



Projecting environmental suitable areas for malaria transmission in China under climate change scenarios

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ABSTRACT

Introduction: The proportion of imported malaria cases in China has increased over recent years, and has presented challenges for the malaria elimination program in China. However, little is known about the geographic distribution and environmental suitability for malaria transmission under projected climate change scenarios.

Methods: Using the MaxEnt model based on malaria presence-only records, we produced environmental suitability maps and examined the relative contribution of topographic, demographic, and environmental risk factors for *P. vivax* and *P. falciparum* malaria in China.

Results: The MaxEnt model estimated that environmental suitability areas (ESAs) for malaria cover the central, south, southwest, east and northern regions, with a slightly wider range of ESAs extending to the northeast region for *P. falciparum*. There was spatial agreement between the location of imported cases and area environmentally suitable for malaria transmission. The ESAs of *P. vivax* and *P. falciparum* are projected to increase in some parts of southwest, south, central, north and northeast regions in the 2030 s, 2050 s, and 2080 s, by a greater amount for *P. falciparum* under the RCP8.5 scenario. Temperature and NDVI values were the most influential in defining the ESAs for *P. vivax*, and temperature and precipitation the most influential for *P. falciparum* malaria.

Conclusion: This study estimated that the ESA for malaria transmission in China will increase with climate change and highlights the potential establishment of further local transmission. This model should be used to support malaria control by targeting areas where interventions on malaria transmission need to be enhanced.

1. Introduction

Malaria, a mosquito-borne infectious disease caused by parasites of the genus *Plasmodium* is a significant public health problem in tropical and subtropical countries (WHO, 2013). In China, malaria has historically been a significant public health burden, reaching 30 million cases annually (Yin et al., 2013). However, several years of control effort have greatly decreased malaria transmission (Xia et al., 2014; Zhou et al., 2014). The nationwide Malaria Control Program initiated in 1955 (Tang, 2000; Yin et al., 2014) was consolidated at different times, including the formulation of the National Malaria Control Programme (NMCP) in 2006 (China Ministry of Health, 2012) and the National Malaria Elimination Programme (NMEP) in 2010 (China Ministry of Health, 2012). Because of investment in malaria control and technical assistance from experts in the field, the burden of malaria has been

reduced substantially. The number of local malaria cases has sharply decreased and has been geographically confined (Feng et al., 2015; Zhang et al., 2014a, 2014b). Nevertheless, the proportion of imported malaria cases has been increasing over recent years, which has presented challenges for the malaria elimination program in China (L. Zhang et al., 2014b; Zhou et al., 2016). This increase has been reported to be due to an increasing number of international travellers in association with growth of international investment, including in some malaria endemic countries (Lai et al., 2016; Liu et al., 2014). Africa and South East Asia are the main source regions for imported cases. (Song et al., 2016; Zhou et al., 2016). Available evidence also has shown a geographic expansion in the distribution of imported malaria cases, especially *P. falciparum* in China (Xia et al., 2014; Zhang et al., 2014a, 2014b). However, little evidence is available on the environmental suitability of areas in which local cases occur. This is despite the

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susceptibility of the malaria vectors in some areas of China to introduced malaria cases (Wang et al., 2015). For example, *An. Sinensis*, one of the four major *Anopheles* mosquitoes in China (*An. sinensis*, *An. minimus*, *An. dirus*, and *An. lesteri*) (Huang et al., 2015) were reported to be susceptible to imported *P. vivax* cases in some areas bordering Myanmar (Wang et al., 2015). This increases the possibility of the establishment of local transmission in previously non-endemic areas from imported malaria. Investigating the environmental suitability for establishment of malaria transmission is important in assisting strategic planning of malaria control.

Suitability of the environment determines the spatial and temporal distributions of infectious diseases. For vector borne-diseases such as malaria, environmental suitability relates to the factors required for survival and development of the transmitting vector, with climatic, topographical and land cover variables being among the best predictors identified by different studies (Ayala et al., 2009; Kulkarni et al., 2010). Remotely sensed land cover and Normalized Difference Vegetation Index (NDVI) were also important predictors of environmental suitability using Maximum Entropy Models (MaxEnt) (Foley et al., 2009; Kulkarni et al., 2010). Despite this, the relative importance of these factors in estimating future malaria risk has not been well investigated in many countries, including China.

The ecological requirements of malaria can be studied using the MaxEnt model relating disease occurrence data to a set of environmental variables (Guisan et al., 2005). The MaxEnt model, also known as the Ecological Niche Model (ENM) or Species Distribution Model (SDM) is a machine-learning algorithm to predict the geographic distribution of species on the basis of their known distribution (i.e. realized niche) in the environmental space. This model has been found to show better predictive ability than other related modelling approaches, such as GARP (Genetic Algorithm for Rule Set Production) (Phillips et al., 2006; Slater et al., 2012). The model is gaining increased attention because of its applicability, especially in a situation when absence data (zero cases) are not available. The MaxEnt model uses variables that are ecologically relevant to the species available in disease presence-only data and a random sample of available environmental conditions (a background sample) to quantify probability of presence (the environmental suitability index), thereby showing the locations where species are most likely to exist. A unique feature of this method is its ability to reduce model complexity by setting regularization – a process of introducing additional information (penalty) to prevent model over-fitting and hence improve the predictive performance of the model (Phillips et al., 2008). Studies conducted in Tanzania (Kulkarni et al., 2010) and Portugal (Capinha et al., 2009), found a high degree of spatial agreement between vector habitat and malaria distribution in human populations. It has been used widely in recent decades to estimate the geographic distribution of vector-borne disease such as cutaneous leishmaniasis (Chalghaf et al., 2016) and lymphatic filariasis (Slater et al., 2012). Other studies have used it to investigate environmental suitability for major malaria vectors and contributing

factors (Kulkarni et al., 2010; Laporta et al., 2011; Obsomer et al., 2012), and to predict the likely range of habitats suitable for mosquitoes under changing global climate scenarios (McIntyre et al., 2017; Ren et al., 2016). One study conducted in China estimated an area suitable for *Anopheles* mosquitoes using bioclimatic and land use variables in the MaxEnt model (Ren et al., 2016). In this study we aim to assess environmental suitability of areas receptive to malaria transmission in China, and the relative contribution of environmental factors. Such findings have significant public health importance in guiding the strategies of disease control programs, by way of mapping areas to be targeted for surveillance and control.

2. Methods

2.1. Occurrence data and environmental layers

Malaria presence data for the period 2005–2014 were obtained from the China Information System for Disease Control and Prevention (CISDCP). A total of 933 *P. vivax* and 1449 *P. falciparum* locations were recorded to have imported malaria cases during the study period. Each observation was assigned a location by matching to geo-coordinates of the county. We selected five environmental variables frequently reported in the literature as determinants of malaria transmission. Meteorological variables (average temperature, rainfall and relative humidity) were available from China Climate Data Sharing Service Center (<http://data.cma.cn/en/?r = data/index>). Daily data recorded at all available weather stations in the country were averaged over the study period (2005–2014) to produce annual data. Kriging interpolation was applied to produce a raster map of meteorological variables at 10 km spatial resolution. Two other environmental variables: Normalized Difference Vegetation Index (NDVI) and elevation were included to assess the effect of vegetation coverage and topography on the transmission of malaria. Monthly NDVI values, from the USGS LP DAAC data (https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/myd13a3) at 1 km resolution were included as a surrogate of vegetation cover. Land cover and elevation data were available from the Global Land Cover Facility (www.landcover.org). Digital Elevation Model (DEM) for the whole country were available from the Consultative Group on International Agricultural Research-Consortium for Spatial Information (CGIAR-CSI) at 90 m resolution (<http://srtm.csi.cgiar.org/>). We maintained the consistency of spatial resolution among environment variables using the spatial re-sampling technique described in Ren et al. (2016). To produce more realistic resolution data, we used a bilinear re-sampling method for continuous variables and the nearest neighbourhood method for categorical variables in ArcGIS 10.3.1 (ESRI, 2014). In this way, all of the environmental variables (Table 1) were re-sampled to the largest cell size of all input datasets (10 × 10 km), and converted to ASCII format for use in MaxEnt Software (Merow et al., 2013). The shapefile of administrative boundaries was obtained from the DIVA-gis open access spatial database, and used

Table 1
Environmental variables used to develop the models for malaria in China.

Dataset	Description and source
Meteorological variables (Temperature, Rainfall, Relative humidity) NDVI	A continuous raster map of meteorological variables created through kriging interpolation of weather station based daily data accessed from China Climate Data Sharing Service Center (http://data.cma.cn/en/?r = data/index). Tiles of Normalized Difference Vegetation Indices (1 × 1 km resolution) accessed from USGS LP DAAC data (https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/myd13a3) overlay with area map, projected, mosaicked, and values extracted by mask.
Land cover	Gridded map of land cover classes obtained from the Global Land Cover Facility (www.landcover.org). Raster maps were extracted by mask (to the boundary map of China), re-sampled, and assigned to presence localities.
Elevation	The Digital Elevation Model (DEM) was accessed from the Consultative Group on International Agricultural Research-Consortium for Spatial Information (CGIAR-CSI) at 90 m resolution (http://srtm.csi.cgiar.org/). Continuous raster data were extracted by mask, re-sampled and assigned to presence localities.
Population	The interpolated county-level population of China was rasterized using kriging techniques.

NDVI = Normalized Difference Vegetation Index.

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