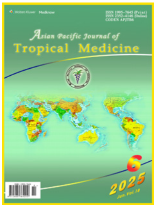

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Modeling the spread risk of dengue vector *Aedes albopictus* caused by environmental factors in Shanghai China

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ABSTRACT

Objective: To predict the distribution of dengue vector *Aedes* (*Ae.*) *albopictus* and identify high-risk areas for dengue fever transmission.

Methods: Data on *Ae. albopictus* occurrences were collected from electronic databases. Ensemble models were developed to assess the impacts of climate, vegetation, and human activity on *Ae. albopictus*. The optimal ensemble model was then used to identify the distribution of suitable areas for *Ae. albopictus*.

Results: After removing duplicate sites and retaining only one location per 100 m × 100 m grid, 189 *Ae. albopictus* breeding sites were identified. The optimal ensemble model revealed that *Ae. albopictus* exhibited higher breeding suitability in Shanghai under specific conditions: a normalized difference vegetation index of 0.1 to 0.6, maximum precipitation in the warmest month ranging from 400 mm to 470 mm, maximum temperature in the warmest month between 30.0 ℃ and 31.0 ℃, and proximity to waterways within 0.5 km. The most suitable habitats for *Ae. albopictus* were primarily concentrated in Shanghai's central urban areas and scattered across the inner suburban districts.

Conclusions: The high-risk areas of *Ae. albopictus* are widely distributed throughout the central urban area and scattered across the inner suburban district of Shanghai, creating conditions conducive to the outbreak of dengue fever. It is essential to enhance targeted control measures for *Ae. albopictus* in the identified risk areas.

KEYWORDS: Dengue; Spread risk; Prediction; Metropolitan; *Aedes albopictus*

1. Introduction

Aedes (*Ae.*) *albopictus*, originally from Southeast Asia, has now spread to over 70 countries worldwide. Due to its strong invasive ability, *Ae. albopictus* has become one of the 100 most invasive

Summary

Question: What are the high-risk areas for dengue fever transmission based on the distribution of the dengue vector *Aedes albopictus* in Shanghai?

Findings: Imported and indigenous dengue have been reported in Shanghai. The study showed a broad distribution across central urban areas and surrounding suburban regions of *Aedes albopictus*. This extensive habitat suitability significantly elevates the risk of dengue outbreaks.

Meaning: Targeted control measures in these high-risk areas are essential to prevent dengue fever outbreaks in Shanghai.

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species globally[1]. It is highly adaptable to arrange of climatic conditions, thriving primarily in tropical and temperate zones, but it can also survive in colder environments through dormancy[2]. A European survey has demonstrated that once *Ae. albopictus* mosquitoes have established themselves in an area, they are exceedingly difficult to eradicate[3].

Ae. albopictus is a significant vector for several diseases, including dengue, Zika virus disease, and yellow fever[4-6]. Dengue is one of the most rapidly spreading mosquito-borne infections worldwide. Currently, approximately half of the global population is at risk of dengue, with annual cases ranging from 100 million to 400 million, and Asia accounting for about 70% of the global disease burden[7]. In recent years, China has experienced numerous outbreaks of dengue in various regions, with the disease's distribution area of dengue gradually expanding[8]. Therefore, it is imperative to identify the factors facilitating the colonization of *Ae. albopictus* and to predict potential areas of invasion in order to implement effective control measures.

In China, the primary vector of dengue is *Ae. albopictus*. The warm and humid climate of the southern coastal areas provides an optimal environment for *Ae. albopictus*, thereby increasing the risk of dengue transmission[9]. The distribution of *Ae. albopictus* is influenced by a variety of environmental factors, with temperature being the most commonly studied[10,11]. Brady *et al* developed a mathematical model to simulate the impact of global temperature on the distribution of *Ae. albopictus* and its ability to transmit dengue virus[12]. Furthermore, precipitation and atmospheric humidity are significant factors influencing the distribution of *Ae. albopictus*[13]. In addition to meteorological factors, human activities such as urbanization and international trade have expanded the habitats and transmission opportunities for *Ae. albopictus*[14]. Areas with high population densities often have increased human activity and more water storage facilities, which create favorable breeding environments for *Ae. albopictus*.

Ecological niche models have been widely used in studying various infectious diseases and their vectors due to their high predictive accuracy[15-17]. These models integrate *Ae. albopictus* distribution data with environmental variables to accurately predict its distribution under diverse conditions. Although individual models such as maximum entropy (MAXENT), boosted regression trees (BRT) and random forest (RF) each have unique advantages, a single model may be not enough to address complex environmental changes and ecological relationships, and its extrapolation capabilities is limited[5,18]. Therefore, in this study we use ensemble models, which leverage the strengths of multiple individual models, to predict the distribution of *Ae. albopictus*.

As the economic center and international metropolis of China, Shanghai has extensive business and personnel exchanges with the world, making it a high-risk area for the transmission of dengue[19]. In recent years, most dengue fever cases reported in Shanghai have been imported from abroad[20]. *Ae. albopictus* is the primary vector of dengue which prefers to breed in crowded urban environments and has become a dominant mosquito species in Shanghai's residential areas. Areas with high population densities typically exhibit more human activity and more water storage facilities, which provide a favorable breeding environment for *Ae. albopictus*.

Ae. albopictus tends to thrive in small water-holding containers commonly found in residential areas and their surroundings, such as tanks, jars, basins, and plant-related containers. This adaptability to human-altered environments and its reliance on such microhabitats make it particularly challenging to control in urban settings. Additionally, the high population density and warm, humid climate of Shanghai provide optimal conditions for the breeding of *Ae. albopictus*, significantly increasing the risk of local epidemics originating from imported cases. Controlling dengue fever largely depends on reducing mosquito density, making it crucial to understand the distribution of *Ae. albopictus*. However, there is a lack of visualizations and future predictions regarding the spatial distribution of *Ae. albopictus* in Shanghai. This gap impairs the ability to identify priority areas and to provide early response.

In this study, we collected data on *Ae. albopictus* and related factors in Shanghai and constructed various ecological niche models, both individual and ensemble. Using these models, we investigated the influences of environmental factors on *Ae. albopictus* population, identified key factors and ranked their importance. Furthermore, these models were employed to predict the spatial distribution of *Ae. albopictus*, thereby facilitating the implementation of targeted prevention and control measures and aligning with the goals of the Global Vector Control Response 2017-2030.

2. Methods

2.1. Study area

Shanghai is situated in the Yangtze River Delta in eastern China, between longitudes 120°52′ and 122°12′ E and latitudes 30°40′ and 31°53′ N. With a population of around 26 million people spread over an area of 63.405 million square kilometers, it is one of the most densely populated regions in the world[21]. It has a subtropical monsoon climate with mild, humid weather, loose soil, and abundant summer rainfall, creating ideal conditions for mosquitoes[22]. *Ae. albopictus*, the primary vector mosquito for dengue fever in China, is also commonly found in Shanghai.

2.2. Data collection

Constructing ecological niche models requires data on species occurrence and environmental factors that influence their distribution. We conducted an extensive literature search using the keywords "*Ae. albopictus*" or "dengue" in PubMed (https://pubmed.ncbi.nlm.nih.gov/), Web of Science (https://www.webofscience.com/), CNKI (https://www.cnki.net/), Wanfang (https://wanfangdata.com.cn/), and VIP (https://www.cqvip.com/) databases from January 2000 to June 2024. Google Earth (https://www.google.com/earth/) was used to acquire the coordinates of the *Ae. albopictus* infested sites. The occurrences with missing geospatial information and absent environmental variable layers were excluded. Duplicate records were removed, and only one presence point per grid (100 m × 100 m) was retained. The 100 m × 100 m grid resolution was chosen to balance computational efficiency and ecological relevance, ensuring sufficient spatial detail to capture environmental heterogeneity while minimizing the risk of spatial autocorrelation, which could bias the model by overemphasizing areas with densely clustered occurrence records[23,24].

The environmental factors that limit the ecological niche of *Ae. albopictus* include climate, geography, vegetation, and socio-economic factors[25]. The climate factors collected in this study encompass conventional climate indicators and extreme climate conditions (Supplementary Table 1). In addition, we collected data on terrain factors (elevation and slope), vegetation indicator (normalized difference vegetation index), water regimes (distance to the waterway), and human activity (human footprint and human influence index). Detailed information on these environmental factors, including name, abbreviation, unit, and source, is provided in Supplementary Table 1.

2.3. Statistical analysis

Eleven individual ecological niche models were constructed using the BioMod2 package to predict the suitable habitats for *Ae. albopictus*[26]: artificial neural network (ANN), classification tree analysis (CTA), flexible discriminant analysis (FDA), generalized additive models (GAM), generalized boosted models (GBM), generalized linear models (GLM), multiple adaptive regression splines (MARS), surface range envelope (SRE), RF, MAXENT, and extreme gradient boosting (XGBOOST). The sample point data were randomly divided into two parts: 75% of the sample points were used as calibration data, and 25% for validation. To reduce overfitting, we repeated the process of dividing the data, calibrating, and evaluating the model 10 times and obtained 110 models in total (11 modeling algorithms × 10 repetitions). Although the ratio of testing to training data in the original datasets remained constant, the specific data points for testing and training varied in each run[21]. The area under the receiver operating characteristic curve (AUC) and the true skill statistic (TSS) were used to evaluate the predictive performance of each model[27]. AUC values range from 0.5 to 1, while TSS values range from -1 to 1. Higher values of these two metrics indicate better predictive performance of the model.

There may be uncertainty in the prediction of a single model. Ensemble models can combine the results from several single model to decrease variance and bias and improve prediction considerably. First, single models with better performance were screened out according to the criteria of AUC> 0.80 and TSS>0.70[28]. Then, ensemble models were constructed using four ensemble algorithms: the mean of probabilities ensemble model, the median of probabilities ensemble model, the committee averaging ensemble model, and the probability weighting mean ensemble model. The best ensemble models were ultimately selected to create the risk classification maps of *Ae. albopictus*. The final output predictions from the ensemble model ranged from 0 to 1, reflecting the likelihood of occurrence. These values were categorized into five risk classes: low suitability (0.00-0.20), moderate-low suitability (0.20-0.40), moderate suitability (0.40-0.60), moderate-high suitability (0.61-0.80), and high suitability zone (0.81-1.00)[15]. All statistical analyses and visualizations were performed using R4.1.3 (R Development Core Team, R Foundation for Statistical Computing, Vienna, Austria) and ArcGIS10.2 (Esri, Redlands, CA, USA).

3. Results

3.1. Occurrence of dengue vector Ae. albopictus and characteristics of reported dengue fever cases

Figure 1 shows the average number of *Ae. albopictus* emerging sites across four periods. A total of 375 emerging sites were collected during the study period (2001 to 2020). During the periods of 2001-2005 and 2006-2010, the average number of *Ae. albopictus* breeding sites was 17 per year. This number decreased to 14 per year during 2011-2015 but then increased to 26 per year during 2016-2020. After removing duplicate sites and retaining only one location per 100 m × 100 m grid, 189 dependent sites remained. The *Ae. albopictus* occurrence records were mainly located in the central urban area and its vicinity (Figure 2). Since 2000, six districts had reported dengue fever cases: Pudong, Changning, Songjiang, Minhang, Baoshan, and Fengxian (Table 1). Among these, Pudong recorded the highest number of imported cases (45) between 2008 and 2020. Songjiang had 20 imported cases between 2014 and 2020, while Changning reported 12 imported cases between 2005 and 2011. Baoshan district reported 1 local infection in 2017 and 3 local infections in 2018.

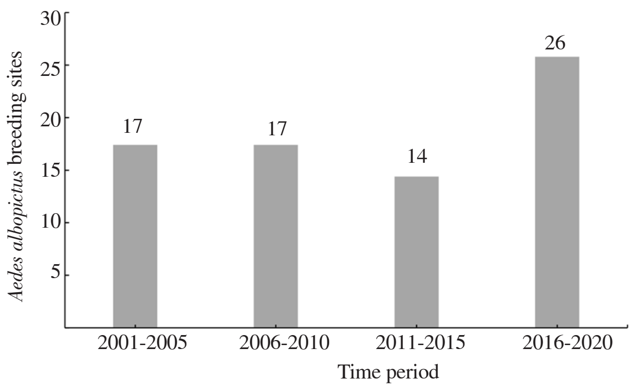

Figure 1. The average number of *Aedes albopictus* emerging breeding sites since 2000.

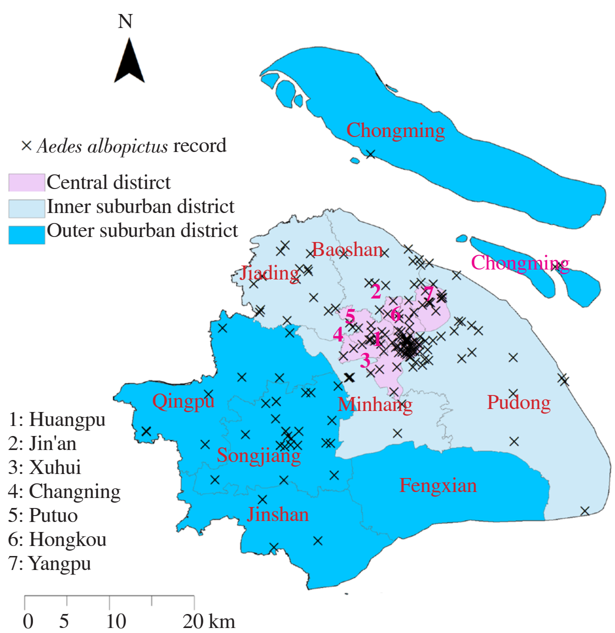

Figure 2. The geographical distribution of *Aedes albopictus* occurrence record collected from literature.

Table 1. Dengue fever cases reported in Shanghai since 2000.

Time	District	Case number	Case source
2008-2020	Pudong	45	Imported case
2005-2011	Changning	12	Imported case
2014-2020	Songjiang	20	Imported case
2017-2018	Baoshan	4	Indigenous case
2019	Minhang	1	Imported case
2019	Fengxian	1	Imported case

3.2. Evaluation of the performance of the Ae. albopictus distribution model

Overall, the GBM (AUC=0.936±0.021; TSS=0.718±0.067), MAXENT (AUC=0.933±0.018; TSS=0.706±0.055), and RF (AUC=0.931±0.024; TSS=0.722±0.052) models demonstrated better predictive performance compared to other models (Table 2). However, the SRE (AUC=0.754±0.052; TSS=0.507±0.104) and GAM (AUC=0.798±0.037; TSS=0.587±0.069) models exhibited poor predictive performance. Due to the varying algorithms underlying each model, individual ecological niche models may suffer from instability and lower accuracy. Therefore, this study opted to filter the results of single models and construct ensemble models to predict the risk areas infested with *Ae. albopictus*. The four ensemble models including mean of probabilities, median of probabilities, committee averaging, probability weighting mean demonstrated strong predictive performance (AUC>0.95, TSS>0.8), with the probability weighting mean ensemble model ranking highest in all metrics (Table 3). Therefore, the following analysis utilized the probability weighting mean ensemble model to examine the response curve of *Ae. albopictus* and predict its habitats distribution.

Table 2. Performance of 11 single ecological niche models of *Aedes albopictus*.

Single model	AUC	TSS
ANN	0.857±0.024	0.612±0.097
CTA	0.837±0.038	0.641±0.07
FDA	0.927±0.017	0.700±0.053
GAM	0.798±0.037	0.587±0.069
GBM	0.936±0.021	0.718±0.067
GLM	0.919±0.024	0.716±0.051
MARS	0.905±0.044	0.673±0.062
MAXENT	0.933±0.018	0.706±0.055
RF	0.931±0.024	0.722±0.053
SRE	0.754±0.052	0.507±0.104
XGBOOST	0.925±0.024	0.690±0.046

Data were expressed as mean±SD. ANN: artificial neural network; CTA: classification tree analysis; FDA: flexible discriminant analysis; GAM: generalized additive models; GBM: generalized boosted models; GLM: generalized linear models; MARS: multiple adaptive regression splines; MAXENT: maximum entropy; RF: random forest; SRE: surface range envelope; XGBOOST: extreme gradient boosting.

Table 3. Performance of 4 ensemble ecological niche models for the distribution of *Aedes albopictus*.

Ensemble model	TSS	AUC
Mean of probabilities	0.828	0.974
Median of probabilities	0.826	0.970
Committee averaging	0.828	0.974
Probability weighting mean	0.837	0.977

3.3. Environmental variables influencing Ae. albopictus and their response curves

Based on the probability weighting mean ensemble model, the six most important variables were normalized difference vegetation index (NDVI, 11.7%), precipitation (BIO16, 11.0%), maximum temperature in the warmest month (BIO5, 10.8%), distance to waterway (DST, 9.3%), annual evaporation (EVP, 7.6%), and annual sunshine hour (SSH, 7.1%) (Figure 3). Conversely, variables such as altitude, slope, and mean annual temperature contributed relatively less to the model predicting suitable habitats for *Ae. albopictus* in Shanghai. Figure 4 shows the response curves of the top 6 most important variables influencing the distribution of *Ae. albopictus* mosquitoes. The suitability probability for *Ae. albopictus* was relatively high when NDVI was between 0.1 and 0.6, but it sharply declined when NDVI exceeded 0.6. BIO6 exhibited an approximately inverted U-shaped relationship with suitability, with higher suitability observed when precipitation ranged from 400 mm to 470 mm. Suitability probability increased with BIO5 between 30.0 ℃ and 31.0 ℃, and remained high between 31 ℃ and 31.5 ℃. Suitability probability decreased with increasing DST, with higher suitability observed within 0.5 km. Suitability was high when EVP ranged from 1 290 mm to 1 310 mm. Suitability decreased with increasing SSH, with higher suitability observed at levels around 1 920 hours.

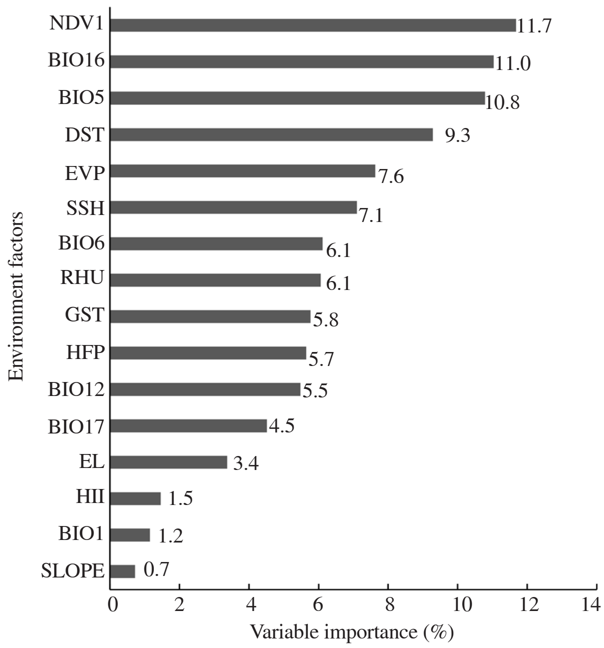

Figure 3. Contribution of individual environmental variables to the distribution of *Aedes albopictus* in the probability weighting mean ensemble model. NDVI: normalized difference vegetation index; BIO16: precipitation in the wettest quarter; BIO5: maximum temperature in the warmest month; DST: distance to waterway; EVP: annual evaporation; SSH: annual sunshine hour; BIO6: minimum temperature in the coldest month; RHU: annual average relative humidity; GST: annual average ground surface temperature; HFP: human footprint; BIO12: annual precipitation; BIO17: precipitation in the driest quarter; EL: elevation; HII: human influence index; BIO1: average annual temperature; SLOPE: slope.

3.4. Predicted distribution of Ae. albopictus habitats

The prediction results (Figure 5) show that the risk areas infested with *Ae. albopictus* in Shanghai were scattered across a relatively large spatial range, with higher clustering in certain local areas. The most suitable habitats for *Ae. albopictus* were primarily distributed in the central urban area, central Jiading, eastern Baoshan, western Pudong, northern Minhang, and central Songjiang.

4. Discussion

The habitat prediction results indicated that the central urban area, along with central Jiading, eastern Baoshan, western Pudong, northern Minhang, and central Songjiang, were at risk for the distribution of *Ae. albopictus*. These areas have higher population densities, and *Ae. albopictus* prefers to inhabit crowded and confined residential environments, which provide a greater abundance of blood sources. A study demonstrated that *Ae. albopictus* was the predominant mosquito species in Shanghai's urban residential environment, accounting for 72% of the total number of mosquitoes captured, with its density significantly higher than that of other species[29]. Moreover, sustained economic growth has led to a surge in cross-border travel and global trade, which has not only increased human mobility but also facilitated the spread and establishment of *Ae. albopictus* in new areas[30]. Therefore, it is imperative that we pay attention to this issue and implement effective measures to address this risk of transmission.

The findings of this study also indicate that vegetation index, precipitation in the wettest quarter, maximum temperature in the warmest month, distance to waterway, evaporation and sunshine hours significantly contribute to the transmission of *Ae. albopictus*. Since 2016, there has been a notable increase in the number of *Ae. albopictus* emergence sites in Shanghai, closely

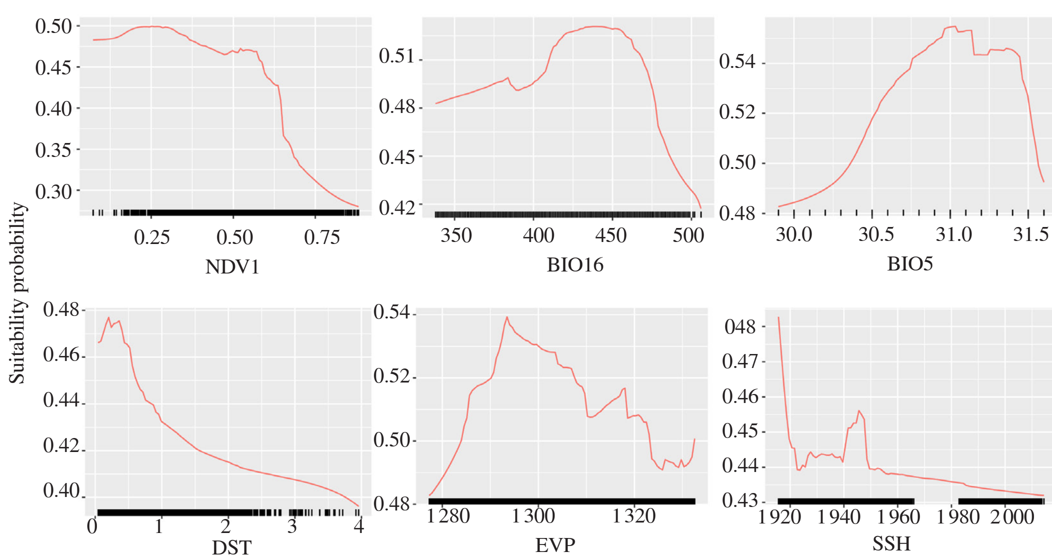

Figure 4. Response curves for the top 6 variables influencing *Aedes albopictus*. NDVI: Normalized difference vegetation index; BIO16: Precipitation in the wettest quarter; BIO5: Maximum temperature in the warmest month; DST: Distance to waterway; EVP: Annual evaporation; SSH: Annual sunshine hour.

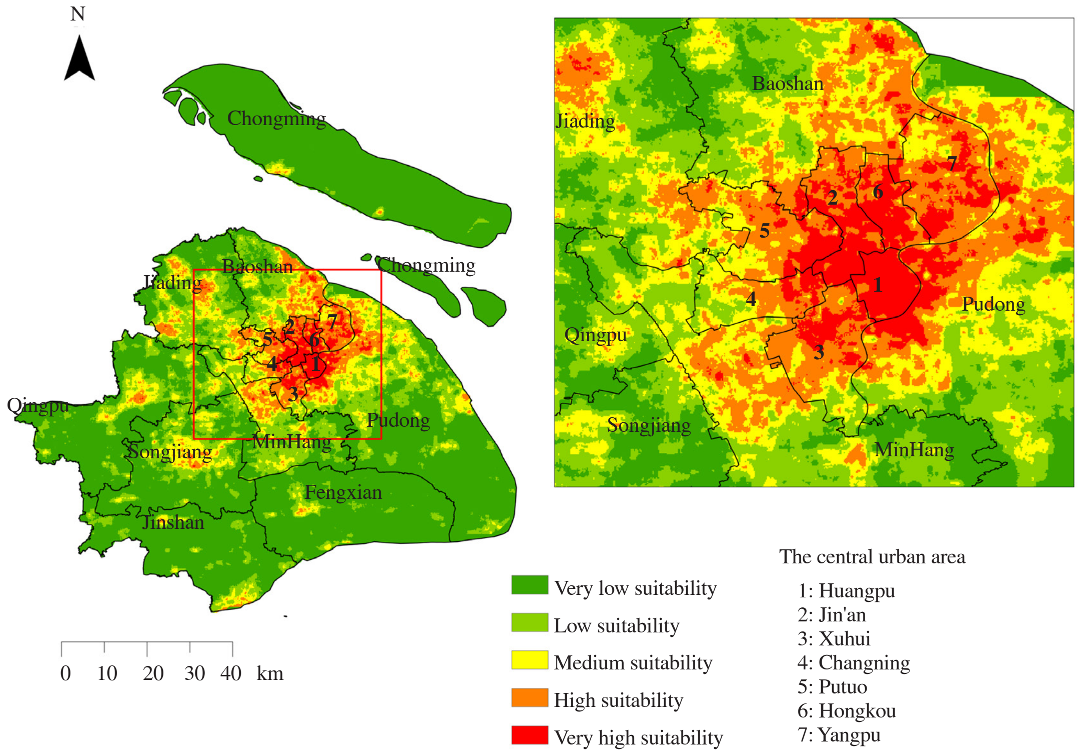

Figure 5. Prediction of habitat suitability for *Aedes albopictus* mosquitoes using the probability weighting mean ensemble model.

associated with the rise of extreme weather events, including heat waves and heavy precipitation, driven by global warming. In recent years, the mean temperature in Shanghai has increased by 0.18 ℃ per decade, promoting the breeding and larval growth of mosquitoes. Concurrently, precipitation has risen by an average of 11.722 mm per decade, providing ample breeding water for *Ae. albopictus*, which typically deposit its eggs in small and stagnant water environment[31,32]. In addition, the presence of vegetation provides a sugar source and shelter for *Ae. albopictus* and has long been recognized as a reliable predictor of mosquito density[33]. The duration of sunlight has been linked to the transmission of *Ae. albopictus*, likely because this species primarily lays its eggs during the daytime; longer sunshine hours result in more active egg-laying activities[34,35].

Since 2000, dengue fever cases in Shanghai have primarily occurred in six districts: including Pudong, Changning, Songjiang, Baoshan, Minhang and Fengxian. Over 95% of these cases were imported. Shanghai's two international airports, Pudong and Changning districts are particularly vulnerable to the risk of dengue due to the high volume of population movement and international contacts. Additionally, out of the 20 reported dengue fever cases in Songjiang District, 19 involved individuals from Southeast Asian countries. Consequently, enhancing monitoring of incoming travelers and implementing environmental disinfection measures are crucial to prevent the transmission of dengue fever.

The introduction of imported dengue cases and the widespread vector populations have established the transmission chain, significantly increasing the risk of local dengue fever outbreaks, as evidenced by four local cases in Baoshan District[36]. These findings highlight the strong correlation between dengue fever incidence and the presence of *Ae. albopictus*. Therefore, future surveillance and prevention efforts should prioritize these high-risk areas and implement effective measures to control the *Ae. albopictus* population, thereby reducing the risk of dengue fever transmission. Key measures should include enhancing environmental hygiene management, eliminating mosquito breeding sites, and increasing public awareness regarding the prevention of mosquito bites. These efforts will be critical in reducing the risk of dengue fever transmission and preventing future outbreaks.

Through the evaluation of several ecological niche models, we found that the ensemble model outperformed individual models in terms of predictive accuracy. Specifically, the probability-weighted mean ensemble model demonstrated the highest performance, with an ROC of 0.977 and a TSS of 0.837. While previous studies have employed single models such as Maxent, Random Forest (RF), and Classification and Regression Trees (CART) to analyze the distribution of *Ae. albopictus*[9,22,30], our results indicate that their predictive effectiveness was comparatively suboptimal. Moreover, it has been noted that no single model can consistently perform well across all cases, owing to differences in their underlying principles and algorithms[37,38]. Ensemble models combine the strengths of multiple algorithms, addressing limitations such as high variance or bias, to enhance predictive reliability and accuracy. In contrast, ensemble models harness the strengths of various algorithms and mitigate the high variance or bias that can occur with individual models, thereby enhancing the reliability and precision of our predictions[15,21]. This approach is particularly valuable for identifying high-risk areas, as it reduces uncertainty and provides balanced, comprehensive risk assessments[39]. By accurately pinpointing risk zones, ensemble models support the efficient allocation of health resources, minimizing waste and ensuring that interventions are both targeted and cost-effective, making them indispensable for ecological research and public health planning.

This study has certain limitations that should be acknowledged. First, while mosquito distribution is influenced by various control measures, these factors were not included in the current analysis due to a lack of available data. Second, some of the study's environmental variables could not be fully covered throughout the study period due to limited data sources, which may introduce potential bias in the results. However, in recent years, the average annual temperature in Shanghai has increased by only 0.2 ℃ per decade, and precipitation has increased slowly by 11 mm per decade. Therefore, it is reasonable to use the temperature and precipitation data for the year 2000 as a proxy for the following two decades. Future research could benefit from integrating more precise and comprehensive datasets, particularly those related to vector control efforts and detailed environmental conditions. Enhanced data collection and monitoring systems, along with advanced modeling techniques, will be critical for refining predictive capabilities and informing more effective public health interventions.

In conclusion, there is a noticeable upward trend in the number of emerging *Ae. albopictus* breeding sites in Shanghai. The predictive model indicates a broad distribution across both central urban areas and surrounding suburban regions. This extensive habitat suitability, coupled with the increasing influx of imported dengue cases and the occurrence of local transmissions, significantly elevates the risk of dengue fever outbreaks. Considering these emerging threats, it is urgent to adopt more precise and proactive vector control strategies. Specifically, targeted management in identified high-risk areas is crucial to curbing the spread of *Ae. albopictus* and preventing future outbreaks of dengue fever.

Conflict of interest statment

The authors declare that there is no conflicting interest.

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Authors' contributions

All authors contributed substantially to drafting, revising, and approving the article's final version. WJM and GYF contributed to the conception and design of the study and acquisition of the data. HJH, ZY, ZLY and SL cleared and analyzed the data. CY and JQW provided critical feedback and revised the manuscript. ZYB oversaw the project, coordinated the research, and provided significant financial support.

Data availability statement

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

References

[1] Gao YH, Yang L, Chen YL, Liu PW, Zhou Y, Chen XG, et al. Aal-circRNA-407 regulates ovarian development of *Aedes albopictus*, a major arbovirus vector, *via* the miR-9a-5p/Foxl axis. *PLoS Pathog* 2023; **19**(5): e1011374.

[2] Wang YG, Liu X, Li CL, Su TY, Jin JC, Guo YH, et al. A survey of insecticide resistance in *Aedes albopictus* (Diptera: Culicidae) during a 2014 dengue fever outbreak in Guangzhou, China. *J Econ Entomol* 2017; **110**(1): 239-244.

[3] Gould EA, Higgs S. Impact of climate change and other factors on emerging arbovirus diseases. *Trans R Soc Trop Med Hyg* 2009; **103**(2): 109-121.

[4] Onyango MG, Lange R, Bialosuknia S, Payne A, Mathias N, Kuo L, et al. Zika virus and temperature modulate *Elizabethkingia anophelis* in *Aedes albopictus*. *Parasit Vectors* 2021; **14**(1): 573.

[5] Kraemer MUG, Reiner RC, Brady OJ, Messina JP, Gilbert M, Pigott DM, et al. Past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. *Nat Microbiol* 2019; **4**(5): 854-863.

[6] Sahu MC, Samantaray RK, Pal A, Pati S. Recent advances on pathogenesis, diagnosis, prevention, immunological aspects, and vectors of dengue: A review. *Asian Pac J Trop Biomed* 2023; **13**(8): 325-338.

[7] Liu HM, Huang XD, Guo XX, Cheng P, Wang HF, Liu LJ, et al. Climate change and *Aedes albopictus* risks in China: Current impact and future projection. *Infect Dis Poverty* 2023; **12**(1): 26.

[8] Zhao N, Guo YH, Wu HX, Liu XB, Yue YJ, Ren DS, et al. National vector surveillance report on mosquitoes in China, 2019. *Chin J Vector Biol & Control* 2020; **31**(4): 395-400.

[9] Liu Y, Wang X, Tang SY, Cheke RA. The relative importance of key meteorological factors affecting numbers of mosquito vectors of dengue fever. *PLoS Negl Trop Dis* 2023; **17**(4): e0011247.

[10] Gao J, Zhang HD, Guo XX, Xing D, Dong YD, Lan CJ, et al. Dispersal patterns and population genetic structure of *Aedes albopictus* (Diptera: Culicidae) in three different climatic regions of China. *Parasit Vectors* 2021; **14**(1): 12.

[11]Little E, Bajwa W, Shaman J. Local environmental and meteorological conditions influencing the invasive mosquito *Ae. albopictus* and arbovirus transmission risk in New York City. *PLoS Negl Trop Dis* 2017; **11**(8): e0005828.

[12]Brady OJ, Golding N, Pigott DM, Kraemer MUG, Messina JP, Reiner

RC, et al. Global temperature constraints on *Aedes aegypti* and *Ae. albopictus* persistence and competence for dengue virus transmission. *Parasit Vectors* 2014; **7**: 338.

[13]Wang X, Tang S, Cheke RA. A stage structured mosquito model incorporating effects of precipitation and daily temperature fluctuations. *J Theor Biol* 2016; **411**: 27-36.

[14]Kraemer MUG, Sinka ME, Duda KA, Mylne AQN, Shearer FM, Barker CM, et al. The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*. *Elife* 2015; **4**: e08347.

[15]Omar K, Thabet HS, TagEldin RA, Asadu CC, Chukwuekezie OC, Ochu JC, et al. Ecological niche modeling for predicting the potential geographical distribution of *Aedes species* (Diptera: Culicidae): A case study of Enugu State, Nigeria. *Parasite Epidemiol Control* 2021; **15**: e00225.

[16]Samy AM, Alkishe AA, Thomas SM, Wang LY, Zhang WY. Mapping the potential distributions of etiological agent, vectors, and reservoirs of Japanese Encephalitis in Asia and Australia. *Acta Trop* 2018; **188**: 108-117.

[17]Manyangadze T, Chimbari MJ, Rubaba O, Soko W, Mukaratirwa S. Spatial and seasonal distribution of *Bulinus globosus* and *Biomphalaria pfeifferi* in Ingwavuma, uMkhanyakude district, KwaZulu-Natal, South Africa: Implications for schistosomiasis transmission at micro-geographical scale. *Parasit Vectors* 2021; **14**(1): 222.

[18]Ding FY, Fu JY, Jiang D, Hao MM, Lin G. Mapping the spatial distribution of *Aedes aegypti* and *Aedes albopictus*. *Acta Trop* 2018; **178**: 155-162.

[19]Zhang M, He JF. Progress in the study of dengue fever epidemiological trends. *Electron J Emerg Infect Dis* 2018; **3**(2): 72-74.

[20]Wang H, Zhu AQ, Xu HM, Zhu WP, Zhou YX. Characterization of dengue fever epidemic in Pudong New Area, Shanghai, 2008-2020. *J Public Health Prev Med* 2022; **33**(3): 68-71.

[21]Tong YX, Xia ZG, Wang QY, Xu N, Jiang HL, Wang ZZ, et al. Prediction of the risk distributions for *Anopheles sinensis*, a vector for malaria in Shanghai, China. *Am J Trop Med Hyg* 2023; **108**(3): 599-608.

[22]Zhou YB, Liu HX, Leng PE, Zhu J, Yao SJ, Zhu YY, et al. Analysis of the spatial distribution of *Aedes albopictus* in an urban area of Shanghai, China. *Parasit Vectors* 2021; **14**(1): 501.

[23]Echeverry-Cárdenas E, López-Castañeda C, Carvajal-Castro JD, Aguirre-Obandoet OA. Potential geographic distribution of the tiger mosquito *Aedes albopictus* (Skuse, 1894) (Diptera: Culicidae) in current and future conditions for Colombia. *PLoS Negl Trop Dis* 2021; **15**(5): e0008212.

[24]Aguiar BS, Lorenz C, Virginio F, Suesdek L, Chiaravalloti-Neto F. Potential risks of Zika and chikungunya outbreaks in Brazil: A modeling study. *Int J Infect Dis* 2018; **70**: 20-29.

[25]Wang F, Zhu YY, Zhang HD, Fan JH, Leng PE, Zhou J, et al. Spatial and temporal analyses of the influences of meteorological and environmental factors on *Aedes albopictus* (Diptera: Culicidae) population dynamics during the peak abundance period at a city scale. *Acta Trop* 2023; **245**: 106964.

[26]Huang LL, Li SF, Huang WY, Jin JH, Oskolski AA. *Cryptocarya chinensis* from the upper Pleistocene of South China and its biogeographic and paleoecological implications. *iScience* 2023; **26**(8): 107313.

[27]Gong YF, Zhu LQ, Li YL, Zhang LJ, Xue JB, Xia S, et al. Identification of the high-risk area for schistosomiasis transmission in China based on information value and machine learning: A newly data-driven modeling attempt. *Infect Dis Poverty* 2021; **10**(1): 88.

[28]Gong YF, Hu XK, Hao YW, Luo ZW, Feng JX, Xue JB, et al. Projecting the proliferation risk of *Oncomelania hupensis* in China driven by SSPs: A multi-scenario comparison and integrated modeling study. *Adv Clim Chang Res* 2022; **13**(2): 258-265.

[29]Zhang ZD, Gao Q, Cao H. Mosquito population dynamics and distribution of residential areas in downtown Shanghai. *Chin J Vec Biol & Control* 2015; **26**(5): 486-490.

[30]Liu Q, Zhang HD, Xing D, Jia N, Du YT, Xie JW, et al. The predicted potential distribution of *Aedes albopictus* in China under the shared socioeconomic pathway (SSP)1-2.6. *Acta Trop* 2023; **248**: 107001.

[31]Zhao DS, Gao X, Wu SH, Zheng D. Trend of climate variation in China from 1960 to 2018 based on natural regionalization. *Adv Earth Sci* 2020; **35**(7): 750-760.

[32]Perugini E, Guelbeogo WM, Guglielmo F, Poggi C, Gabrieli E, Ranson H, et al. The interplay between malaria vectors and human activity accounts for high residual malaria transmission in a Burkina Faso village with universal ITN coverage. *Parasit Vectors* 2023; **16**(1):101.

[33]Zhao JW, Tang T, Wang XX. Effects of landscape composition on mosquito population in urban green spaces. *Urban For Urban Gree* 2020; **49**: 126626.

[34]Lin LQ, Zhang SH, Zhu ZL. The relationship between dengue fever vector *Aedes albopictus* density and meteorological factors in Shenzhen in 2017. *Chin J Hyg Insect & Equip* 2022; **28**(2): 140-143.

[35]Lai HB, Luo LK, Ou QH. Analysis on correlation between the density of dengue fever vector and climatic factors in Yunfu City. *Chin J Hyg Insect & Equip* 2018; **24**(1): 51-55.

[36]Hu YD, Jin K, Wang HJ, Xu JM, Zhang YJ, Xiang LH, et al. Epidemiological investigation and control effect analysis of dengue fever local infection cases in Baoshan District, Shanghai, China, 2017-2018. *Chin Trop Med* 2022; **22**(2): 160-164.

[37]Lei Y, Liu Q. Tolerance niche expansion and potential distribution prediction during Asian openbill bird range expansion. *Ecol Evol* 2021; **11**(10): 5562-5574.

[38]Yang Y, Cheng WT, Wu XY, Huang SY, Deng ZH, Zeng X, et al. Prediction of the potential global distribution for *Biomphalaria straminea*, an intermediate host for *Schistosoma mansoni*. *PLoS Negl Trop Dis* 2018; **12**(5): e0006548.

[39]Xia CC, Hu Y, Ward MP, Lynn H, Li S, Zhang J, et al. Identification of high-risk habitats of *Oncomelania hupensis*, the intermediate host of *Schistosoma japonium* in the Poyang Lake region, China: A spatial and ecological analysis. *PLoS Negl Trop Dis* 2019; **13**(6): e0007386.

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