scientific reports

OPEN

Development and application of a WebGIS-based prediction system for multi-criteria decision analysis of porcine pasteurellosis

Tao Liu[1,2], Lei Cao[1,2], Hao Rang Wang[1,2], Ya Jun Ma[1,2], Xiang Yu Lu[1,2], Pu Jun Li[1,2] & Hong Bin Wang[1,2]✉

Porcine pasteurellosis is an infectious disease caused by *Pasteurella multocida* (*P. multocida*), which seriously endangers the healthy development of pig breeding industry. Early detection of disease transmission in animals is a crucial early warning for humans. Therefore, predicting risk areas for disease is essential for public health authorities to adopt preventive measures and control strategies against diseases. In this study, we developed a predictive model based on multi-criteria decision analysis (MCDA) and assessed risk areas for porcine pasteurellosis in the Chinese mainland. By using principal component analysis, the weights of seven spatial risk factors were determined. Fuzzy membership function was used to standardize all risk factors, and weight linear combination was used to create a risk map. The sensitivity of the risk map was analyzed by calculating the mean of absolute change rates of risk factors, as well as calculating an uncertainty map. The results showed that risk areas for porcine pasteurellosis were predicted to be locate in the south-central of the Chinese mainland, including Sichuan, Chongqing, Guangdong, and Guangxi. The maximum standard deviation of the uncertain map was less than 0.01and the ROC results showed that the prediction model has moderate predictive performance with the area under the curve (AUC) value of 0.80 (95% CI 0.75–0.84). Based on the above process, MCDA was combined with WebGIS technology to construct a system for predicting risk areas of porcine pasteurellosis. Risk factor data was directly linked to the developed model, providing decision support for disease prevention and control through monthly updates.

Keywords Porcine pasteurellosis, Multi-criteria, WebGIS, System

Porcine pasteurellosis is an infectious disease caused by *Pasteurella multocida* (*P. multocida*), which is characterized by septicemia and hemorrhagic inflammation[1]. This pathogen invades the nasal cavity and respiratory tract of pigs, causing pneumonia, focal infection and abscess[2,3]. *P. multocida* can be co-infected with a variety of pathogens (e.g., *Actinobacillus suis, Salmonella choleraesuis, Hemophilus parasuis, Streptococcus suis, and Bordetella bronchiseptica* to increase the prevalence of respiratory diseases in pigs[4]. Porcine pasteurellosis causes serious economic losses to animal feeding and hinders the healthy development of the pig breeding industry[5].

The occurrence of infectious diseases is usually caused by the interaction of various influencing factors[6]. China has a vast territory, and nature, climate, transportation and breeding management are diverse. Many factors, such as climate, geography, and transportation, may affect the outbreak of porcine pasteurellosis. Porcine pasteurellosis occurs mainly in summer in the south-central region of Chinese mainland[7]. The pig breeding industry in China is mainly concentrated in the central and southern regions, and this area has similar climatic characteristics, namely high temperature, humidity and precipitation. Complicated transportation and poor management methods have increased the occurrence and spread of diseases. Therefore, it is important to combine multiple types of risk factors, simulating high-risk areas of infectious diseases. Many models, including multi-criteria decision analysis (MCDA), maximum entropy, boosted regression tree are used to explore the relationship between animal infectious diseases and multiple influencing factors, showing good performance in practical applications[8–10].

[1]College of Veterinary Medicine, Northeast Agricultural University, Harbin, People's Republic of China. [2]Heilongjiang Provincial Key Laboratory of Pathogenic Mechanism for Animal Disease and Comparative Medicine, Harbin, People's Republic of China. ✉email: hbwang1940@neau.edu.cn

1

MCDA is a mathematical method with important decision-making value. Geographic information system (GIS)-based MCDA is a process that combines the value of geographic data with the preferences of decision makers and translates them into decision maps[11]. MCDA is often used in land suitability assessments, environmental planning and infectious disease risk assessments[12–14]. In infectious disease studies, MCDA can clearly show the spatial risk area of the disease by GIS, further understanding the complexity of the spatial risk factors of disease occurrence and epidemic characteristics of the disease[13]. Paul et al.[15] produced a Highly Pathogenic Avian Influenza (HPAI) H5N1 risk map in poultry based on MCDA. The assessment in Cambodian showed that Tonlé Sap watershed was identified as an area of high HPAI H5N1 risk with localized hotspots around the cities of Battambang and Kampong Cham, and in the lower part of the basin bordering Vietnam. Thanapongtharm et al.[16] used natural host factors, intermediate host type and environmental factors based on MCDA to determine that the risk areas for Nipah virus of pigs were mainly distributed around bat colonies. Tran et al.[17] mapped areas suitable for Rift Valley fever amplification and transmission in East African countries (Uganda, Kenya, Ethiopia, and Tanzania) based on MCDA to provide a reference for disease control and risk identification. Alimi et al.[18] assessed the risk of malaria in northern South America and found to be higher in rivers and coastal areas.

In the transmission of infectious diseases, a large amount of data related to infectious diseases has spatial distribution characteristics, and this characteristic becomes the premise of GIS application. Constructing a GIS-based surveillance system can effectively manage and monitor infectious diseases, and can analyze the characteristics and spreading trend of epidemics based on relevant geospatial information. GIS technology has been favored by many researchers for its spatial analysis capability. In the monitoring of diseases and pests in cotton, locust prevention and control, and prediction of avian pasteurellosis, it showed that the application of WebGIS to establish a monitoring and early warning system has a good development prospect[19–21]. Meanwhile, the application of GIS technology in the health field is shown to be an inevitable trend for automation and disease information management[22].

The aim of this study was to develop a system to predict risk areas of porcine pasteurellosis. The main steps can be divided as follows: 1) Developing a predictive model based on MCDA and assessing risk areas for porcine pasteurellosis in the Chinese mainland. 2) Constructing of a WebGIS-based prediction system that considers user requirements and purposes.

Materials and methods
Porcine pasteurellosis outbreak data
According to the Ministry of Agriculture and Rural Affairs of the People's Republic of China, main outbreaks of porcine pasteurellosis in the Chinese mainland were observed in the central and southern China from 2008 to 2020 (http://www.moa.gov.cn/). Sichuan, Chongqing and Guangxi had the most severe outbreaks (Fig. 1a). Between 2008 and 2015, outbreaks of porcine pasteurellosis showed an increasing trend. Since 2015, outbreaks have shown a downward trend (Fig. 1b). Summer (June, July and August) was the main outbreak season for the disease (Fig. 1c).
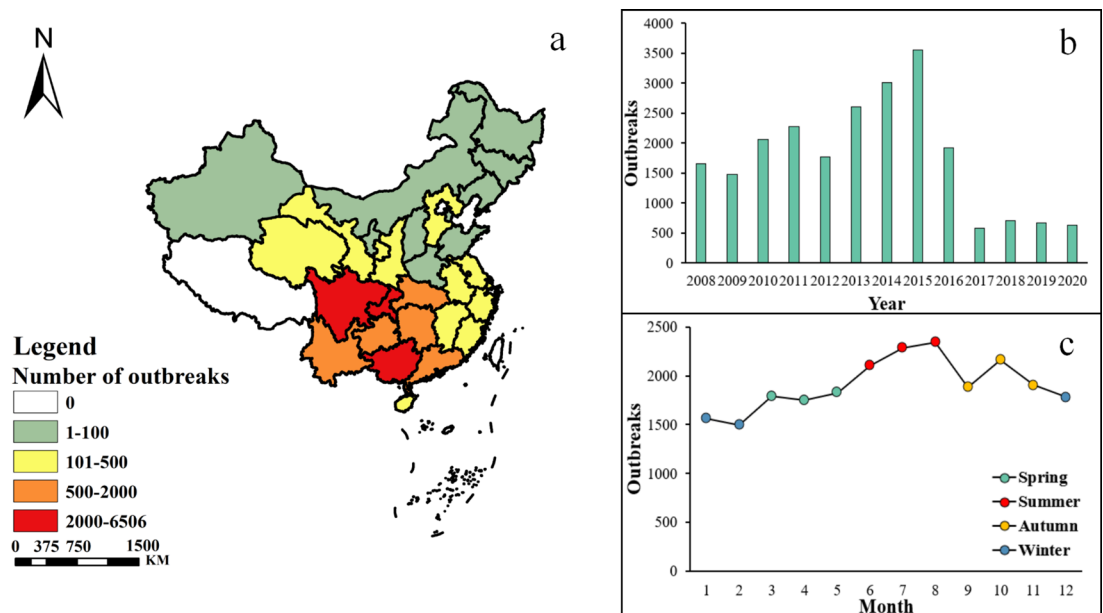

Fig. 1. The outbreaks of porcine pasteurellosis in the Chinese mainland from 2008 to 2020. **a** number of porcine pasteurellosis outbreak in various provinces. **b** annual number of porcine pasteurellosis outbreak. **c** monthly number of porcine pasteurellosis outbreak.

Study framework

In this study, a predictive model for porcine pasteurellosis was developed based on MCDA. According to relevant research, seven spatial risk factors of porcine pasteurellosis were determined[7,23]. The research framework as shown in Fig. 2 and the specific steps are as follows:

1. Different influencing factors have different attributes and units, which need to be standardized for all data. The fuzzy membership function was used to complete the standardization of the data with values between 0 and 1[10].
2. Principal component analysis (PCA) was used to determine the weight of influencing factors. Since the factors used for evaluation have different spatial resolutions, all factors need to be adjusted to a resolution of 2.5 arcmin (approximately 4.65 km × 4.65 km).
3. Weighted linear combination (WLC) was used to construct the risk maps of porcine pasteurellosis by combining all risk factors[16].
4. One-At-a-Time (OAT) was used to calculate the uncertainty map, and mean of absolute change rates (MACRs)[10].
5. C# was used as the development language; MCDA was combined with WebGIS technology to construct a system for predicting risk areas of porcine pasteurellosis[39].

Factors used to risk map

Railway and highway

Transportation plays an important role in spreading animal infectious diseases by increasing the contact rate between sick and healthy animals. The railway and highway data of the Chinese mainland were obtained from Geographic Data Sharing Infrastructure, College of Urban and Environmental Science, Peking University (http://geodata.pku.edu.cn), China. The railway and highway densities in the Chinese mainland were calculated by using kernel density estimation (KDE).

Temperature and precipitation

Temperature and precipitation are the important factors in the prevalence of porcine pasteurellosis[6]. The meteorological data were obtained from WorldClim, and the closest data of the current climate conditions were selected[24].

Pig density and population density

As the most susceptible animal, pigs play an important role in the development and transmission of the porcine pasteurellosis. Moreover, population density can reflect the main areas of livestock farming and *P. multocida* is also pathogenic to humans. The population density and pig density data in this study were obtained from
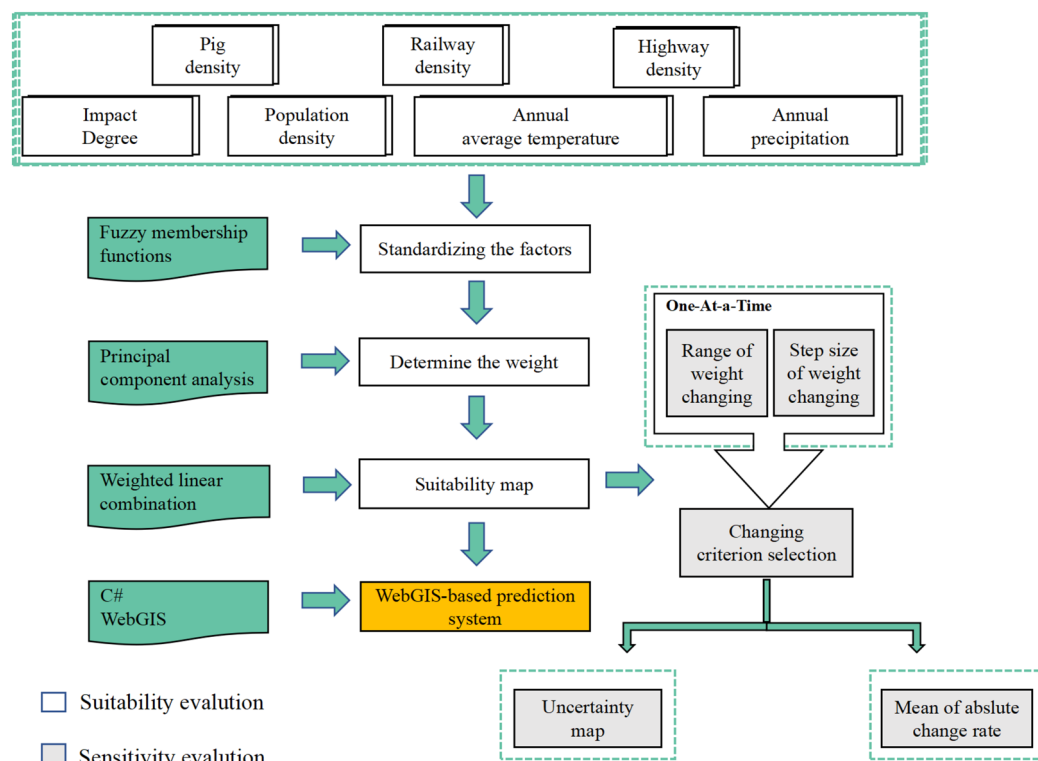

Fig. 2. Study framework to predict risk areas of porcine pasteurellosis based on MCDA.

WorldPop and the Food and Agriculture Organization of the United Nations (FAO), respectively. The obtained data was resampled and adjusted to be consistent with the extent of the Chinese mainland.

Influence degree
Research on animal infectious diseases based on MCDA needs a leading factor to represent the research object. Therefore, used the number of porcine pasteurellosis outbreaks to reflect the degree of outbreak in various regions. According to previous studies, inverse distance weighting (IDW) is the most suitable method to simulate the impact of porcine pasteurellosis compared with ordinary kriging, local polynomials, and simple kriging[25]. In this study, we used IDW to interpolate the number of porcine pasteurellosis outbreaks from 2008 to 2020 in various provinces in the Chinese mainland to obtain the influence degree (degree of outbreak) map.

Standardization of factors
After preprocessing all influencing factors, a raster dataset for the Chinese mainland under the resolution of 2.5 arcmin was obtained. According to studies on other animal infectious diseases, fuzzy membership functions were used to standardize all factors[10,15,16]. Population density, pig density and the influence degree of porcine pasteurellosis were processed by a linear relationship. Railroad density, highway density, average annual temperature and annual precipitation were standardized by sigmoidal relationship. Finally, seven risk factors were normalized to the spatial maps on a 0–1 scale (Supplement 1).

Determining factors weights
Methods in the determination of factor weights include two main categories: subjective assignment and objective assignment. Our study used PCA to determine the weights of each factor. PCA is a kind of recombination of multiple original variables with a strong correlation to generate a few uncorrelated variables and extract information of the original variables. The weight calculation process of the seven factors was as follows:

1. Calculation of the correlation coefficient matrix:

$$R = \begin{bmatrix} r11 & r12 & ... & r1p \\ r21 & r22 & ... & r2p \\ ... & ... & ... & ... \\ rp1 & rp2 & ... & rpp \end{bmatrix} \tag{1}$$

r_{ij} is the correlation coefficient between the original variables x_i and x_j ($i, j = 1, 2, ..., p$).

2. Calculation of eigenvalues and eigenvectors.
   The characteristic equation is $|\lambda E - R| = 0$. E is the unit matrix, calculating all the eigenvalues, arranging them in order of magnitude as $\lambda_1 \geq \lambda_2 ... \geq \lambda_p \geq 0$, and respectively finding the eigenvectors $e_i (i = 1, 2, ..., p)$ corresponding to the eigenvalue λ_i.

3. 3. Calculation of the cumulative contribution rate of the principal components:

$$\frac{\sum_{k=1}^{m} \lambda_k}{\sum_{k=1}^{p} \lambda_k} \tag{2}$$

4. Calculation of the coefficients of the original index in the linear combination of different principal components (L_{ij}):

$$L_{ij} = \frac{e_{ij}}{\sqrt{\lambda_i}} (i = 1, 2, ..., m; j = 1, 2, ..., p) \tag{3}$$

e_{ij} is the loading of the original index (x_j) in the i-th principal component.

5. Calculation of the contribution rate of the principal components (u_i):

$$u_i = \frac{\lambda_i}{\sum_{k=1}^{m} \lambda_k} (i = 1, 2, ..., m) \tag{4}$$

6. Calculation of the co`efficient of the original index in the comprehensive model (d_j):

$$d_j = \sum_{i=1}^{m} u_i L_{ij} (i = 1, 2, ..., m; j = 1, 2, ..., p) \tag{5}$$

7. Normalization of index weight (w_j):

$$w_j = \frac{d_j}{\sum_{k=1}^{p} d_k} (j = 1, 2, ..., p) \tag{6}$$

Construction of risk map
Seven risk factors were weighted using WLC to construct a risk map. The formula is as follows:

$$S = \sum_{i=1}^{n} w_i v(a_i) \tag{7}$$

4

n is the number of risk factors; w is the weight value of risk factor i; v is the value functions of factors at layer i (a_i); and S is the total value of each small grid[26]. ArcGIS 10.2 (ESRI, Redlands, CA, USA) was used to construct the risk map.

Sensitivity analysis and validation

One-At-a-Time is a commonly used sensitivity method, also known as OAT. The purpose of using OAT was to examine the influence of the output factors on the output results[27]. It reflects the degree and regularity of the influence of a single factor on the result by changing the weight of only one factor at a time. The method has a high comparability and the OAT method is simple and easy to implement.

It is necessary to specify a feasible weight deviation range, which can be defined as a range of percent change (RPC) derived from the original standard weight value in basic operations. Various ranges were applied for each criterion, or a single range was used for all criteria. In this study, the RPC was between − 20 and 20%, with a step size of 1%[27]. The adjusted new weight is calculated using the following formula:

$$W(C_m, PC) = W(C_m, 0) + W(C_m, 0) \times PC (1 \leq m \leq n) \tag{8}$$

where $W(C_m, PC)$ is the initial weight of the major changing factor C_m, PC is the percentage of weight change, and n is the number of risk factors.

$$w(C_i, PC) = (1 - w(C_m, PC)) * \frac{W(C_i, 0)}{1 - w(C_m, 0)} (1 \leq i \leq n, i \neq a) \tag{9}$$

where $W(C_i, 0)$ is the weight of i-th criterion (C_i) at the preliminary weight.

Risk factors were compared by calculating the MACRs of the risk map and adjusted-weight map using the following equation:

$$\text{MACRs} = \sum_{k=1}^{N} \left| \frac{R_K - R_0}{R_0} \right| \times 100\% \tag{10}$$

Where R_k is the adjusted-weight risk map; R_0 is the initial risk map; N is the number of pixels.

The uncertainty map was the standard deviation of the risk maps generated after all factors changed the weights[28,29]. Moreover, the outbreak data for porcine pasteurellosis from 2021 to 2022 was used to assess the accuracy of the risk map. The predictive performance of the risk map was evaluated by calculating the receiver operating characteristic (ROC).

Construction of prediction system

Figure 3 showed the research framework for WebGIS-based prediction system. C# was used as a development language to develop the system in Microsoft Visual Studio 2012. Model Builder in ArcGIS 10.2 was used to build models, publish and share services dependent on ArcGIS Server. Silverlight and XAML were used to enable the dynamic presentation of simulation features. The data were stored and processed in Oracle 11 g and ArcGIS. Finally, MCDA was combined with WebGIS technology to construct a system for predicting risk areas of porcine pasteurellosis.

Results

Weight of influencing factors

The scree plot showed that application of two principal components could explain most of the variance of the data (Fig. 4). By calculating the characteristic equations of seven factors, the first two principal components could explain 75% of the variance of all components (Table 1). The coefficients of comprehensive model were normalized to calculate the weights of the factors. The influencing degree of porcine pasteurellosis (0.171), pig density (0.162), and highway density (0.160) had the highest weights in the risk map, followed by the annual average temperature (0.145), precipitation (0.144), and railway density (0.138). In contrast, population density (0.076) had lower importance (Table 2).

Risk map for porcine pasteurellosis

Figure 5 showed the risk map of porcine pasteurellosis in the Chinese mainland. Highly risk areas are mainly located in the central and southern of the Chinese mainland, including parts of Sichuan, Chongqing, Guangxi, Guangdong, Hunan, and Hubei. The low-risk areas were mainly distributed in the northern and western, including parts of Qinghai, Xinjiang, Mongolia, Tibet, Heilongjiang, and Jilin.

Sensitivity analysis

As shown in Fig. 6, the most sensitive factors were annual average temperature, highway density, and pig density, followed by the influence degree of porcine pasteurellosis, railway density, annual precipitation and population density. The sensitivity of annual average temperature was the most sensitive to changes in weights, and its maximum MACRs (6.5532%) was much lower than the corresponding rate of change in weights (± 20%), indicating that the results of risk map were relatively stable.

Uncertainty map and validation

As shown in Fig. 7, the results of the uncertainty map showed that the simulation of the risk map was robust, with the maximum standard deviation less than 0.01. These results indicated that the simulation ability of the
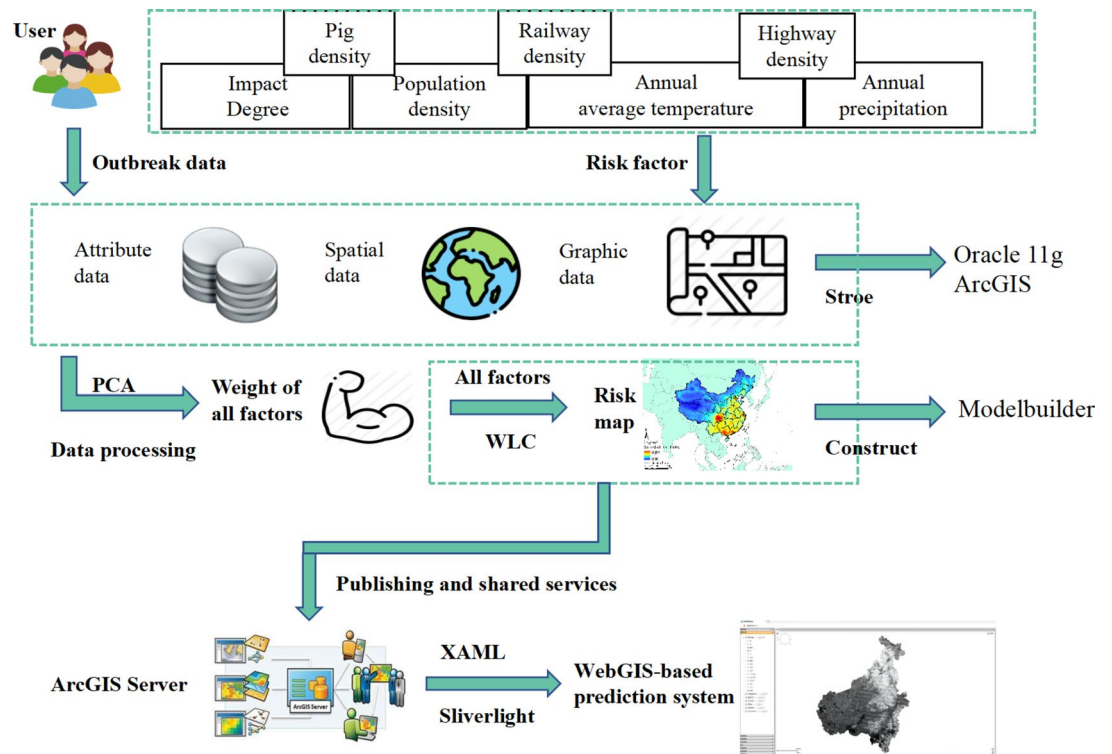
Fig. 3. Study framework for WebGIS-based prediction system. (This map was generated using ArcGIS version 10.2 (Esri, https://www.esri.com/en-us/arcgis/products/arcgis-pro/overview). The base map of China was sourced from the Chinese National Standard Map Service (http://bzdt.ch.mnr.gov.cn/index.html), approval number GS (2020) 4619.)
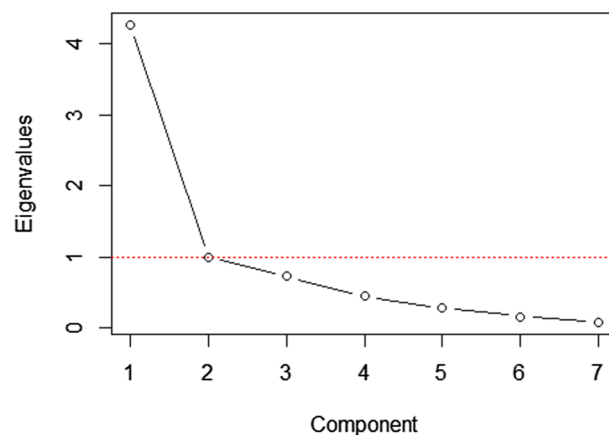

Fig. 4. The number of extracted principal components.

risk map can remain stable, when the weights of the influencing factors are changed. The ROC results showed that the prediction model has moderate predictive performance with the area under the curve (AUC) value of 0.80 (95% CI 0.75–0.84).

WebGIS-based prediction system

MCDA was combined with WebGIS technology to construct a system for predicting risk areas of porcine pasteurellosis. Figure 8 showed the analysis results of the porcine pasteurellosis risk areas in a region of the Chinese mainland in January. This system can predict risk areas based on monthly updates of each factor data, providing users with decision support for disease prevention and control (Supplement 2).

	RC1	RC2	h2	u2
Railway	0.62	0.22	0.43	0.571
People	−0.08	0.97	0.94	0.058
Temperature	0.85	−0.17	0.75	0.251
Precipitation	0.80	−0.08	0.64	0.362
Pig	0.88	−0.05	0.77	0.228
Influence degree	0.94	−0.08	0.89	0.108
Highway	0.91	−0.13	0.84	0.156
Eigenvalue	4.22	1.05		
Contribution Rate	0.60	0.15		
Cumulative Rate	0.60	0.75		
Proportion Explained	0.80	0.20		

Table 1. Results of principal component analysis. RC: Load of principal component; h2: The explanation degree of principal component variance for each variable; u2: The proportion of variance that cannot be explained by principal components.

	Coefficient of PC1	Coefficient of PC2	Coefficient of comprehensive model	Weight
Railway	0.301	0.214	0.284	0.138
People	−0.038	0.946	0.157	0.076
Temperature	0.413	−0.165	0.298	0.145
Precipitation	0.389	−0.078	0.296	0.144
Pig	0.428	−0.048	0.333	0.162
Influence degree	0.457	−0.078	0.350	0.171
Highway	0.442	−0.126	0.329	0.160

Table 2. Weight of the factors.

Fig. 5. Risk map of porcine pasteurellosis in the Chinese mainland.
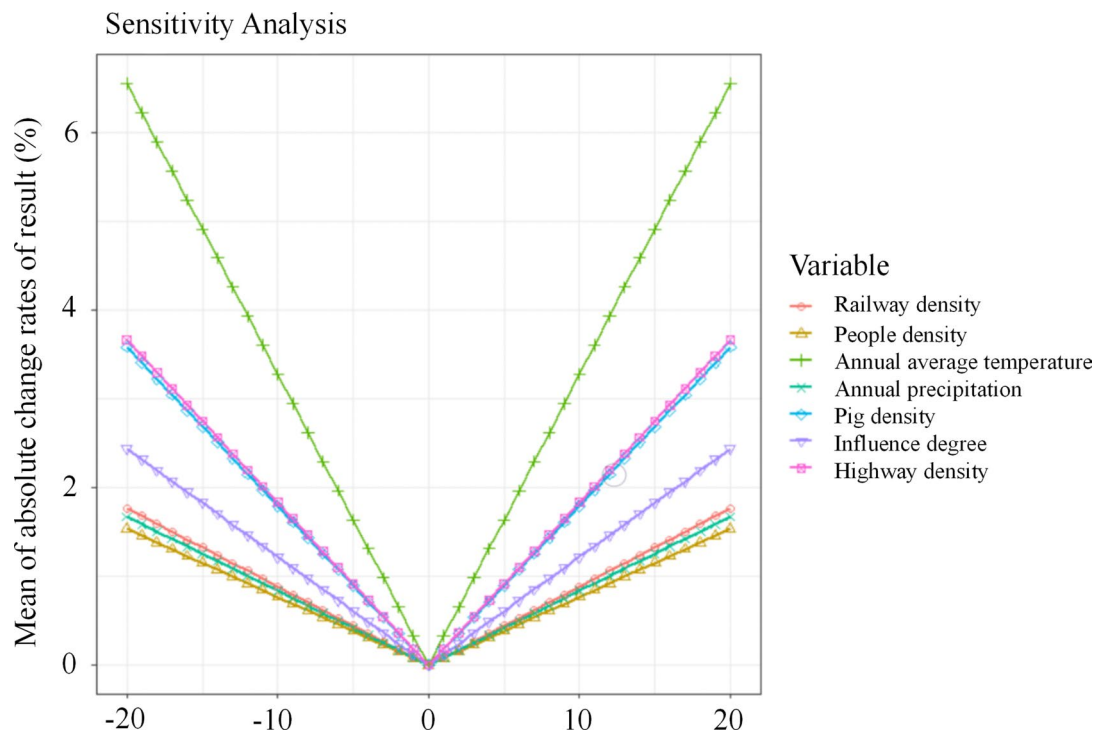
Sensitivity Analysis

Fig. 6. Mean absolute values of the change rate (MACRs) for risk factors.
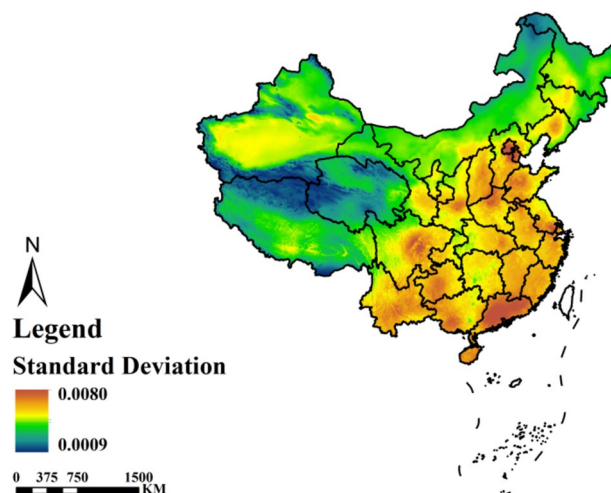

Fig. 7. Uncertainty map (Maximum standard deviation of the adjusted-weight risk map).

Discussion

In the previous study, we constructed the first monitoring and warning system of porcine pasteurellosis based on WebGIS[25]. This system could realize the input and output of disease data, visualization of the epidemic situation, and spatial analysis function, but it cannot combine multiple risks to predict the risk areas of diseases. In this study, we developed a predictive model based on multi-criteria decision analysis (MCDA) and assessed risk areas for porcine pasteurellosis in the Chinese mainland. Then we used this model to construct a WebGIS-based prediction system, which can provide decision support for prevention and control of porcine pasteurellosis through monthly updates of risk factors. High temperatures and humid environments can reduce the immunity and resistance of animal organisms to pathogenic microorganisms.

For the weights of each factor, the differences between the weights of factors other than population density were not very significant. Changes in environmental factors are critical to the spread and occurrence of porcine pasteurellosis, especially climatic factors. High temperature and humidity environment can create conditions for the reproduction of mosquitoes and pathogenic microorganisms. Long-term high temperature and humidity
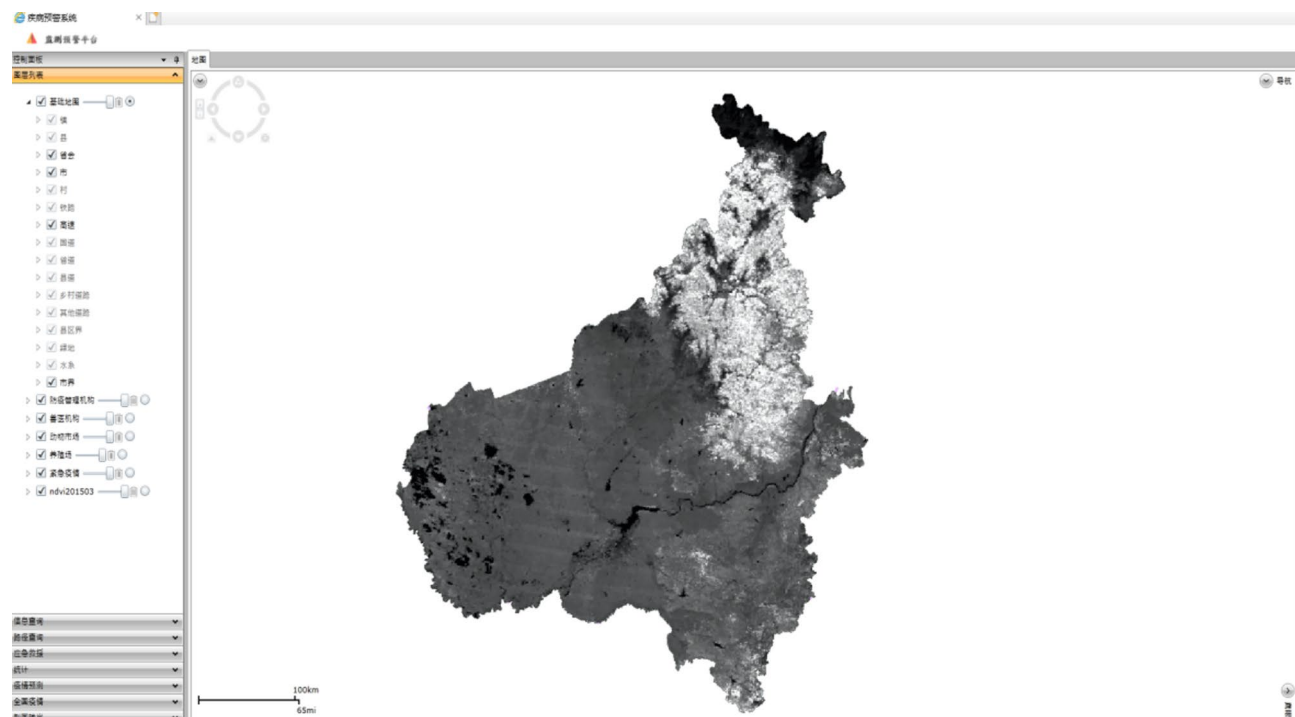
Fig. 8. Prediction results of the porcine pasteurellosis risk areas in a region of the Chinese mainland in January (The risk index increases from white to black).

environment may lead to the deterioration of the breeding environment and reduce the immunity of organisms[7]. The death of more than 200,000 saiga antelopes in central Kazakhstan from *P. multicida* in 2015 was thought to be related to temperature and humidity abnormalities[23]. Therefore, we need to pay attention to changes in the animal habitat and maintain strong veterinary surveillance to address possible future increases in climate and environmental stressors. Areas with high road and rail densities are at greater risk from disease transmission. Livestock trade, free movement of people, and vehicles can increase the prevalence of disease through pathogen-carrying contaminants[30,31]. In addition, pathogens can be present on animals and in the feeding environment for long periods, which is another way in which porcine pasteurellosis can be easily transmitted through contact and animal transport. *P. multocida* can affect a variety of animals and cause many diseases, such as pneumonia in small ruminants, fowl cholera in poultry, and atrophic rhinitis in swine[32]. As the most susceptible animal to porcine pasteurellosis, pigs occupy a higher weight on the risk map. Similarly, humans can also be infected with *P. multocida*, but the incidence rate is lower than that of pigs and other animals, such as rabbits, poultry, cattle, and sheep.

The most important influencing factors involved in the incidence of *P. multocida* in animals are mismanagement, high temperatures, poor air quality, and overcrowding in a limited space[33,34]. High suitability areas are mainly distributed in the south-central of the Chinese mainland, where the climate is humid and hot all year round and the traffic is complex, providing good conditions for the propagation and spread of pathogens. Most breeding patterns in the south-central are small households, and the proportion of intensive livestock farming is relatively small. Insufficient breeding management is one of the inducing factors involved in the incidence of *P. multocida*[7]. The unsuitable areas are mainly distributed in the west and the north, where the climate and geographical conditions are complicated, and most of the farmed livestock are cattle, sheep, and horses that can graze. Some of the people living in this area do not have a high demand for pork due to their ethnic customs. So, the number of pigs is small compared to other livestock. The combination of climate, geography, breeding needs, and other factors can make the western and northern unsuitable for porcine pasteurellosis.

The factor sensitivity analysis was done to evaluate or assist to reduce the uncertainty in the multi-criteria decision analysis by detecting slight changes (± 20%, 1% each time) of the input data. This analysis is very important for the verification and calibration of the numerical model[35]. In the sensitivity analysis of the factors, the annual mean temperature had a relatively high sensitivity to the results. Climate factors affect the entire region of the Chinese mainland and have high spatial heterogeneities, which may be the main reason for high sensitivity.

In this study, we used MCDA to develop a prediction model and construct a prediction system for porcine pasteurellosis. However, this type of research is still in the exploratory stage and there are still some uncertainties due to the constraints of various objective conditions. First, MDCA, as a fuzzy mathematical method, was often used to deal with uncertainty and ambiguity in research[36,37]. Applying this method to assess the risk areas of diseases may produce biased results. In our study, the application of MCDA to develop predictive models for porcine pasteurellosis was mainly due to the limitations of disease information. In further studies, as the disease information increases, we will use machine learning methods, such as random forest, support vector machine, and boosted regression tree, to reconstruct the prediction model of porcine pasteurellosis[38,39]. Compared with

MCDA, machine learning methods may have higher prediction accuracy and lower prediction uncertainty by mining patterns in a large amount of complex data. In addition, the quality and accuracy of the original data, the selection of factors, the calculation of weights, and the grading of factors may cause uncertainties in the results. The weight of the factor is one of the main factors causing controversy and uncertainty in the results. It is impossible to have only one set of weights, and the range of weights is different. So, multiple result data sets will be generated[28]. In further research, we will focus on the issues involved above.

Conclusions

In this study, we developed a predictive model based on multi-criteria decision analysis (MCDA) and assessed risk areas for porcine pasteurellosis in the Chinese mainland. The results showed that risk areas for porcine pasteurellosis were predicted to locate in the south-central of the Chinese mainland, including Sichuan, Chongqing, Guangdong, and Guangxi. The maximum standard deviation of the uncertain map was less than 0.01and the ROC results showed that the prediction model has moderate predictive performance with the area under the curve (AUC) value of 0.80 (95% CI 0.75–0.84). Finally, MCDA was combined with WebGIS technology to construct a system for predicting risk areas of porcine pasteurellosis. These results can provide a theoretical framework for the construction of prediction models in animal infectious disease prediction systems. It also provides decision support for the development and adjustment of control strategies for porcine pasteurellosis.

Data availability

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

References

1. Cardoso-Toset, F. *et al.* Septicaemic pasteurellosis in free-range pigs associated with an unusual biovar 13 of *Pasteurella multocida*. *Vet. Microbiol.* **167**, 690–694. https://doi.org/10.1016/j.vetmic.2013.08.005 (2013).
2. Harper, M., Boyce, J. D. & Adler, B. *Pasteurella multocida* pathogenesis: 125 years after Pasteur. *FEMS Microbiol. Lett.* **265**, 1–10. https://doi.org/10.1111/j.1574-6968.2006.00442.x (2006).
3. Hunt, M. L., Adler, B. & Townsend, K. M. The molecular biology of *Pasteurella multocida*. *Vet. Microbiol.* **72**, 3–25. https://doi.org/10.1016/S0378-1135(99)00183-2 (2000).
4. Ross, R. F. *Pasteurella multocida* and its role in porcine pneumonia. *Anim. Health. Res. Rev.* **7**, 13–29. https://doi.org/10.1017/S1466252307001211 (2006).
5. Davies, R. L., MacCorquodale, R. & Reilly, S. Characterisation of bovine strains of *Pasteurella multocida* and comparison with isolates of avian, ovine and porcine origin. *Vet. Microbiol.* **99**, 145–158. https://doi.org/10.1016/j.vetmic.2003.11.013 (2004).
6. Wang, H. *et al.* Potential risk factors of swine erysipelas outbreak in Northeast the Chinese mainland. *Transbound. Emerg. Dis.* **00**, 1–11. https://doi.org/10.1111/tbed.13840 (2020).
7. Gao, X., Xiao, J., Qin, H., Cao, Z. & Wang, H. Impact of meteorological factors on the prevalence of porcine pasteurellosis in the southcentral of the Chinese mainland. *Prev. Vet. Med.* **125**, 75–81. https://doi.org/10.1016/j.prevetmed.2016.01.002 (2016).
8. Carlson, C. J., Kracalik, I. T., Ross, N., Alexander, K. A. & Blackburn, J. K. The global distribution of *Bacillus anthracis* and associated anthrax risk to humans, livestock and wildlife. *Nat. Microbiol.* **4**, 1337–1343. https://doi.org/10.1038/s41564-019-0435-4 (2019).
9. Ma, J. *et al.* Peste des petits ruminants in China: Spatial risk analysis. *Transbound. Emerg. Dis.* **66**, 1784–1788. https://doi.org/10.1111/tbed.13217 (2019).
10. Sangrat, W., Thanapongtharm, W. & Poolkhet, C. Identification of risk areas for foot and mouth disease in Thailand using a geographic information system-based multi-criteria decision analysis. *Prev. Vet. Med.* **185**, 105183. https://doi.org/10.1016/j.prevetmed.2020.105183 (2020).
11. Malczewski, J. & Rinner, C. *Multicriteria decision analysis in geographic information science* (Springer, 2015).
12. Li, H. & Chen, Y. Assessing potential land suitable for surface irrigation using groundwater data and multi-criteria evaluation in Xinjiang inland river basin. *Comput. Electron. Agr.* **168**, 105079. https://doi.org/10.1016/j.compag.2019.105079 (2020).
13. Santos, D. V. D. *et al.* Identification of foot and mouth disease risk areas using a multi-criteria analysis approach. *Plos One* **12**, e0178464. https://doi.org/10.1371/journal.pone.0178464 (2017).
14. Selim, S., Koc-San, D., Selim, C. & San, B. T. Site selection for avocado cultivation using GIS and multi-criteria decision analyses: Case study of Antalya, Turkey. *Comput. Electron. Agr.* **154**, 450–459. https://doi.org/10.1016/j.compag.2018.09.038 (2018).
15. Paul, M. C. *et al.* Quantitative assessment of a spatial multicriteria model for highly pathogenic avian influenza H5N1 in Thailand, and application in Cambodia. *Sci. Rep.* **6**, 1–10. https://doi.org/10.1038/srep31096 (2016).
16. Thanapongtharm, W. *et al.* A spatial assessment of Nipah virus transmission in Thailand pig farms using multi-criteria decision analysis. *BMC Vet. Res.* **15**, 1–13. https://doi.org/10.1186/s12917-019-1815-y (2019).
17. Tran, A. *et al.* Development and assessment of a geographic knowledge-based model for mapping suitable areas for Rift Valley fever transmission in Eastern Africa. *PLoS Neglect. Trop Dis.* **10**, e0004999. https://doi.org/10.1371/journal.pntd.0004999 (2016).
18. Alimi, T. O. *et al.* A multi-criteria decision analysis approach to assessing malaria risk in northern South America. *BMC Public Health* **16**, 1–10. https://doi.org/10.1186/s12889-016-2902-7 (2016).
19. Gao, X., Xiao, J. & Wang, H. Prediction of *Avian pasteurellosis* basedon ZINB model and meteorological factors. *Trans. Chin. Soc. Agric. Eng.* **34**, 176–182 (2018) (**(in Chinese)**).
20. Yao, X., Zhu, D., Yun, W., Peng, F. & Li, L. A WebGIS-based decision support system for locust prevention and control in China. *Comput. Electron. Agr* **140**, 148–158. https://doi.org/10.1016/j.compag.2017.06.001 (2017).
21. Zhao, Q., Jin, G., Zhou, W., Wang, C. & Dai, J. Information collection system for diseases and pests in cotton field based on mobile. *Trans. Chin. Soc. Agric. Eng.* **31**, 183–190 (2015) (**(in Chinese)**).
22. Pfeiffer, D. U. & Hugh-Jones, M. Geographic information systems as a tool in epidemiological assessment and wildlife disease management. *Rev. Sci. Tech. OIE* **21**, 91–102. https://doi.org/10.1053/rvsc.2002.0554 (2002).
23. Kock, R. A. *et al.* Saigas on the brink: Multidisciplinary analysis of the factors influencing mass mortality events. *Sci. Adv.* **4**, eaao2314. https://doi.org/10.1126/sciadv.aao2314 (2018).
24. Fick, S. E. & Hijmans, R. J. WorldClim 2: New 1km spatial resolution climate surfaces for global land areas. *Int. J. Climatol.* **37**, 4302–4315. https://doi.org/10.1002/Jofrom.5086 (2017).
25. Zhu, Z. *et al.* Monitoring and early warning system of porcine pasteurellosis based on WebGIS. *Inf. Proc. Agric.* **8**, 148–158. https://doi.org/10.1016/10.1016/j.inpa.2020.02.006 (2021).

26. Malczewski, J. *GIS and multicriteria decision analysis* (Wiley, 1999).
27. Haoran, W. *et al.* Assessment of foot-and-mouth disease risk areas in the Chinese mainland based spatial multi-criteria decision analysis. *BMC Vet. Res.* **17**, 1–12. https://doi.org/10.1186/s12917-021-03084-5 (2021).
28. Xu, E. & Zhang, H. Spatially-explicit sensitivity analysis for land suitability evaluation. *Appl Geogr* **45**, 1–9. https://doi.org/10.1016/j.apgeog.2013.08.005 (2013).
29. Feizizadeh, B., Jankowski, P. & Blaschke, T. A GIS based spatially-explicit sensitivity and uncertainty analysis approach for multi-criteria decision analysis. *Comput Geosci* **64**, 81–95. https://doi.org/10.1016/j.cageo.2013.11.009 (2014).
30. Qi, L. *et al.* Neighbourhood contacts and trade movements drive the regional spread of bovine viral diarrhoea virus (BVDV). *Vet. Res.* **50**, 1–15. https://doi.org/10.1186/s13567-019-0647-x (2019).
31. Rosendal, T., Widgren, S., Ståhl, K. & Frösslingab, J. Modelling spread and surveillanceof *Mycobacterium avium* subsp. paratuberculosis in the Swedish cattle trade network. *Prev. Vet. Med.* **183**, 105152. https://doi.org/10.1016/j.prevetmed.2020.105152 (2020).
32. Cuevas, I. *et al.* Antimicrobial resistance of *Pasteurella multocida* type B isolates associated with acute septicemia in pigs and cattle in Spain. *BMC Vet. Res.* **16**, 222. https://doi.org/10.1186/s12917-020-02442-z (2020).
33. Thomson, R., Chander, S., Savan, M. & Fox, M. Investigation of factors of probable significance in the pathogenesis of pneumonic pasteurellosis in cattle. *Can. J. Comp. Med.* **39**, 194 (1975).
34. Slocombe, R. *et al.* Interactions of cold stress and *Pasteurella haemolytica* in the pathogenesis of pneumonic pasteurellosisin calves: Method of induction and hematologic and pathologic changes. *Am. J. Vet. Res.* **45**, 1757–1763 (1984).
35. Delgado, M. G. & Sendra, J. B. Sensitivity analysis in multicriteria spatial decision-making: A review. *Hum. Ecol. Risk Assess* **10**, 1173–1187. https://doi.org/10.1080/10807030490887221 (2004).
36. Chen, H., Wood, M. D., Linstead, C. & Maltby, E. Uncertainty analysis in a GIS-based multi-criteria analysis tool for river catchment management. *Environ. Modell. Softw.* **26**, 395–405. https://doi.org/10.1016/j.envsoft.2010.09.005 (2011).
37. Tenerelli, P. & Carver, S. Multi-criteria, multi-objective and uncertainty analysis for agro-energy spatial modelling. *Appl. Geogr.* **32**, 724–736. https://doi.org/10.1016/j.apgeog.2011.08.013 (2012).
38. Haoran, W. *et al.* Assessment of foot-and-mouth disease risk areas in mainland China based spatial multi-criteria decision analysis. *BMC Vet. Res.* **17**, 1–12 (2021).
39. Wang, H. *et al.* SpatMCDA: An R package for assessing areas at risk of infectious diseases based on spatial multi-criteria decision analysis. *Methods Ecol. Evolut.* https://doi.org/10.1111/2041-210X.14364 (2024).

Acknowledgements

Author contributions

H.B.W.: Designed the study, Supply methodology. L.T.: Collected and analysis data, completed the manuscript. C.L., W.H.R.: Data curation. M.Y.J., L.X.Y. and L.P.J.: Ddited and checked the manuscript for grammar and spelling. All authors read the manuscript and approved the final manuscript.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1038/s41598-024-72350-x.

Correspondence and requests for materials should be addressed to H.B.W.

Reprints and permissions information is available at www.nature.com/reprints.

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.