Assessment of foot-and-mouth disease risk areas in mainland China based spatial multi-criteria decision analysis

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Abstract

Background

Foot-and-mouth disease (FMD) is a highly contagious viral disease of cloven-hoofed animals. As a transboundary animal disease, the prevention and control of FMD are important. This study was based on spatial multi-criteria decision analysis (MCDA) to assess FMD risk areas in mainland China. Ten risk factors were identified for constructing risk maps by scoring, and the analytic hierarchy process (AHP) was used to calculate the criteria weights of all factors. Different risk factors had different units and attributes, and fuzzy membership was used to standardize the risk factors. The weighted linear combination (WLC) and one-at-a-time (OAT) were used to obtain risk and uncertainty maps as well as to perform sensitivity analysis.

Results

Four major risk areas were identified in mainland China, including western (Xinjiang and Tibet), southern (Yunnan, Guizhou, Guangxi and Guangdong), northern (Gansu, Ningxia and Inner Mongolia), and eastern (Hebei, Henan, Anhui, Jiangsu and Shandong). We found spring as the main season for FMD outbreaks. Risk areas were associated with the distance to previous outbreak points, grazing areas and cattle density. Receiver operating characteristic (ROC) analysis indicated that the risk map had good predictive power (AUC = 0.8532).

Conclusions

These results can be used to delineate FMD risk areas in mainland China, and provinces can adopt the targeted preventive measures and control strategies.

Background

Foot-and-mouth disease (FMD) is an acute, febrile, highly contagious disease caused by the foot-and-mouth disease virus, infecting domestic and wild cloven-hoofed animals [1, 2]. The most common signs in infected animals are fever, blister formation and ulceration in the mouth, lower extremities and udders [3]. Globally, between 1995 and 2005, the number of FMD outbreaks reached an all-time maximum and have continued to be an important animal disease of economic concern [4]. The World Organization for Animal Health (OIE) classifies FMD as a notifiable animal infectious disease, and China classifies it as a Class I animal disease.

China is a major producer and consumer of meat products in the world. It is one of the countries more seriously affected by FMD [5]. The FMD virus isolates were first reported in China were in 1958 in Xinjiang Uyghur Autonomous Region (serotypes O and A) and Yunnan Province (serotype Asia1) of China [6, 7].
2005, the FMD virus was first detected in cattle in Wuxi, Jiangsu Province (serotype Asia 1). The disease spread rapidly in mainland China, causing severe economic losses in 17 provinces between 2005 and 2009 [8]. Cattle are the main animals infected by serotype Asia 1. Due to the efforts of the government and farmers, FMD virus (serotype Asia 1) did not appear in mainland China after 2009. Since 2010, FMD virus (serotypes O and A) have been endemic and sporadic in many provinces, mainly in northwestern and southeastern China [9]. According to official data, 140 outbreaks have occurred in China since 2010. In October 2020, a total of 70 cattle and 6 cattle were affected in Heshuo County, Xinjiang Uyghur Autonomous Region. Xinjiang and Tibet are the provinces with the highest outbreaks of FMD in mainland China, which may be related to the high population density of susceptible species in the regions [9]. Also, the farming pattern in these regions is mostly small households and grazing, which may increase the risk of outbreaks.

Risk factors associated with FMD outbreaks have been reported in previous studies, including climatic factors, livestock density, transportation and breeding factors [10–12]. Given the considerable impact of FMD, a significant number of studies focused on evaluating risks, which have sought to provide guidance it mitigates risk, conduct contingency planning, and insights to potential economic outcomes [13]. The majority of this work has likely resulted from OIE requirements to conduct risk and economic consequence assessments, resulting in most available assessments being narrowly focused on specific geographic regions and often addressing OIE guidelines [14]. To avoid inaccuracy of assessment, countries have conducted FMD risk assessments based on local prevalence and risk factors, including Thailand and Brazil [15, 16].

Multi-criteria decision analysis (MCDA) is a mathematical approach that provides great value in decision systems [17]. By combining spatial geographic data and its weighted, it is converted into a decision map [18]. It has a wide range of applications, mainly in environmental studies, land suitability assessment and epidemiological risk area assessment [19–21]. In health geography, this approach can reflect the complexity of spatial risk factors that affect the disease occurrence and consider multiple criteria for better understanding of disease characteristics [18]. For example, Sangrat et al. modeled FMD risk areas in Thailand based on MCDA and showed that some regions in western, central, upper northern, northeastern, and southern Thailand were identified as risk areas for FMD, which were associated with a large number of previous FMD epidemics, distribution of livestock markets, and high density of cattle [15]. Weerapong et al. identified three types of spatial risk factors for Nipah virus transmission in pig farms through expert assessment, which included natural host factors, intermediate host factors, and environmental factors, and the results indicated that risk areas were mainly concentrated around bat colonies [21]. Alimi et al. evaluated the risk areas for Malaria epidemics in northern South America, and the results showed that areas along rivers and coasts have higher risk than other areas [22].

The aim of this study is to assess the risk areas of foot-and-mouth disease in mainland China based on MCDA. The results of this study will support disease control measures and implementation of risk-based surveillance strategies.
Results

Prevalence of FMD in mainland China from 2010 to 2020

In this study, a total of 140 FMD outbreaks were recorded between 2010 and 2020, including Serotype O (99), Serotype A (34) and uncertain Serotype (7). The outbreak was mainly distributed in the western and south-central of mainland China, including Xinjiang, Tibet, and Guizhou (Figure 2A). Most outbreaks of FMD occurred in 2010 and 2018, with the main prevalent Serotype O (Figure 2B). For the season, spring (March, April, May) was the season of high FMD prevalence (Figure 2C). Of all domestic animals, cattle were the main susceptible animals (54.76%), followed by pigs (32.74%), and goats and sheep (12.50%) (Figure 2D).

Between 2010 and 2020, twenty-one provinces in mainland China were affected by FMD in varying degrees. The sum-outbreaks, sum-cases and sum-destroyed in every province showed that the western of mainland China was severely affected because the sum-outbreaks, sum-cases and sum-destroyed were higher than other provinces (Figure 3A-C). The sum-deaths were relatively low due to the aggressive control measures taken by the government and farmers, preventing large-scale livestock deaths (Figure 3D).

Risk factors weight

Ten important risk factors, such as buffalo density, cattle density, pig density, goat density, sheep density, distance to previous outbreak points, distance to national boundaries, distance to livestock market and slaughterhouse, major road density and grazing area were identified (Table 1). These factors were considered appropriate for the construction of the risk map, which are important for the FMD outbreaks. Decreasing sigmoidal was used in fuzzy affiliations for distance to previous outbreak points, distance to national boundaries and distance to livestock market and slaughterhouse. Increasing sigmoidal was used in other risk factors. After standardizing all risk factors, AHP was used to determine the weights. Distance to previous outbreak points, grazing area, and cattle density were considered as the most important risk factors for FMD outbreaks.

Risk map of FMD in mainland China

Figure 4 shows the risk map of FMD in mainland China, including continuous risk map, classified risk map, and major risk areas map. Four major risk areas were identified in mainland China, including western (Xinjiang and Tibet), southern (Yunnan, Guizhou, Guangxi and Guangdong), northern (Gansu, Ningxia and Inner Mongolia), and eastern (Hebei, Henan, Anhui, Jiangsu and Shandong). We assessed a risk province (western Shandong) where FMD had never occurred.

Uncertainty map

The uncertainty map represents the maximum standard deviation of the 4000 adjusted-weight risk maps (Figure 5). The FMD risk map predicted based on risk factors was robust, with a maximum standard
deviation less than 0.01, indicating that the predictive ability of the risk map is stable when the weights of risk factors are changed. The uncertainty map highlighted spatial heterogeneity, with higher uncertainty in high-risk FMD regions.

**Sensitivity analysis**

As shown in Figure 6, the MACRs showed an approximately linear increase with the absolute value of the change rate of the weights. The MACRs were the same for the same change factor when the absolute value of the change rate of the weights was the same. The same factor weight increased or decreased by the same value, and its sensitivity to the results was the same. The most sensitive factors were distance to previous outbreak points, followed by grazing area, distance to livestock market and slaughterhouse, distance to the national boundaries, goat density, major road density, buffalo density, cattle density, sheep density and pig density. Distance to previous outbreak points showed the highest sensitivity to weight changes, with the highest MACRs (4.4916%), which is much lower than the corresponding weight change rate (20%), indicating that the assessment of the FMD risk map is relatively stable.

**Risk map validation**

A total of thirty-five FMD outbreaks from 2018 to 2020 were used for model validation. Most of the outbreak points were found in the high-risk areas of the risk map. ROC results also showed that the prediction capacity of the risk map was good (AUC = 0.8532 [Figure 7]).

**Discussion**

Due to the prevalence of FMD in China, only some literature have explored the history and viral characteristics of outbreaks through phylogenetic analysis, and the risk of entering China through animal migration through geographic information systems, risk assessment and epidemiological models [28]. However, studies assessing risk areas in China are scarce. This study constructed an FMD risk map in mainland China-based on spatial MCDA.

Four major risk areas were identified in mainland China, including western (Xinjiang and Tibet), southern (Yunnan, Guizhou, Guangxi and Guangdong), northern (Gansu, Ningxia and Inner Mongolia), and eastern (Hebei, Henan, Anhui, Jiangsu and Shandong). We assessed a risk province (western Shandong) where FMD had never occurred. Therefore, it is necessary to take measures to prevent outbreaks of FMD in mainland China. These areas are different in geographic location, climatic conditions, transportation, trade and livestock feeding management. In this study we presented some recommendations based on the characteristics of each region.

Western mainland China (Tibet and Xinjiang), has always been a high outbreak area of FMD. China shares its borders with thirteen countries. Location may face the risk of FMD epidemic caused by cross-border transportation of wild animals or illegal livestock in other countries. Elnekave's research results showed that the risk of FMD infection in livestock in areas near the border was relatively high [29]. The
highlands, mountains and basins are the dominant geographical features, which have made grazing the dominant livestock rearing and management practice in the region. Grazing is done in areas close to borders, leading to encounters with other FMD-affected livestock and wildlife, whose common behavior may increase the risk of disease transmission [30]. Previous studies reported the aggregation of different animals at the same watering points and pastures as a cause of FMD transmission and persistence [31]. However, the risk of epidemics exists in natural rearing and farmers captive breeding methods, even if farmers do not regularly practice grazing. Mixed rearing of cattle, sheep and goats is one of the risk factors for FMD outbreaks and transmission [32]. Balinda's investigation concluded that the prevalence of FMD in small ruminants in Uganda was associated with outbreaks in cattle [33]. This may be related to the fact that small ruminants exhibit less severe clinical signs of FMD and are usually not on vaccination schedules [34]. The outbreaks that occurred in Tibet in 2013 were distributed along the main traffic routes, reflecting the association of animal movement with the occurrence of outbreaks [35]. The combination of grazing, mixed feeding, animal movement and livestock trade with border countries increases the probability of FMD outbreaks in these areas. These aspects, improvement of herders' knowledge of the disease and increase of vaccination rates should be considered for the prevention of FMD.

During 2010–2020, we found a higher outbreak in spring. According to Guerrini’s study showed that the season affects the timing of FMD outbreaks across regions [36].

The reason for the outbreak may be that the climate has just warmed up and farmers need to cultivate and graze, which increases the risk of FMD for livestock. These conditions also apply to northern mainland China, including Gansu, Ningxia and Inner Mongolia. Although these regions have different climatic conditions, the northern region with large grasslands and adjacent borders is also dominated by grazing as a feeding management practice.

For the eastern and southern parts of mainland China, small-scale farming is the dominant feeding practice [37]. Animals are usually kept in free-range grazing systems and open barns, which are managed in a simpler way. Vaccination is the most reported preventive measure in surveys of small-scale farms [38]. So necessary vaccination programs and vaccine effectiveness are key to preventing outbreaks of FMD on small farms. Some farmers mistakenly identify FMD as stomatitis, a mucosal disease. Therefore, it is extremely important for small-scale farmers to improve their knowledge and understanding of FMD and the role of the vaccine. In the risk map, the complex transportation and aggregated livestock in the south had a great weight in the risk assessment [39, 40]. Human transmission by mechanical transfer or transportation is a factor that is not controlled easily. The government needs to strengthen regulation during animal import and export, regular spot checks and monitoring of livestock trading markets and slaughterhouses [41].

In this study, western Shandong Province was assessed as a risk area, where no FMD was observed. There were some errors in the assessment with empirical data. Considering the risk factors in Shandong,
we believe that need to keep an eye on this province in the future. Because, outbreaks of FMD in nearby regions are likely to increase the risk of epidemics [42].

In this study, we assessed the FMD risk areas in mainland China-based on spatial MCDA and identified four major risk areas. Spring was the main season for FMD outbreaks in China. Risk areas were related to distance to previous outbreak points, grazing areas, and cattle density. These results can be used to delineate FMD risk areas in China and take target preventive measures and control strategies.

**Materials And Methods**

**Study framework**

In this study, MCDA was applied to assess the risk areas for FMD in China based on FMD outbreak data between 2010 and 2020 (Figure 1). We provided detailed data on outbreaks during this period from the Ministry of Agriculture of the People's Republic of China (MAPRC) and OIE.

1. We used Web of Science, PubMed and Google Scholar to select and evaluate the risk factors associated with the occurrence and spread of FMD. The five-Likert scale is used to select the ten most important spatial risk factors.

2. Analytic hierarchical process (AHP) was applied to assess the weights occupied by ten risk factors in FMD outbreaks.

3. Weighted linear combination (WLC) was used to transform the empirical data into risk map after standardization of all risk factors.

4. Sensitivity and uncertainty analysis was performed on the risk map.

**Data transformation and standardization**

We selected fifty risk factors from the literature and self-assessment (Supplement 1), these factors were obtained from actual surveys and analyses. The selected risk factors were classified and scored using the five-Likert scale [23]. Ten professional veterinarians participated in this work, including three Ph.D. and seven M.S. Ten most important risk factors for FMD outbreaks were selected, including livestock distribution, environment, transportation and location conditions.

Density data for buffalo, cattle, pigs, goats and sheep were collected to the extent of mainland China, and resampling was applied to transform them into map layers with a spatial resolution of 2.5 min. Proximity analysis was used to calculate the distance of each region in mainland China from outbreak points, national boundaries, livestock markets and slaughterhouses. The data were transformed into map layers with distances in km to each location. The kernel density estimation (KDE) was used to calculate densities of major railroads and roads in mainland China. Complex distance was used to measure local density changes in this method.
In this study, five types of relationships were proposed (linear, increasing sigmoidal, decreasing sigmoidal, symmetrical, and bi-directional). Based on previous literature for the relationship between these risk factors and FMD, sigmoidal was finally determined [15]. Standardized spatial layer maps of all risk factors were calculated by fuzzy membership functions at a scale of 0–1 (unsuitable to perfectly suitable, Supplement 2).

All geographic data were calculated and transformed using ArcGIS 10.2 (ESRI, Redlands, CA, USA). The standardization of the risk maps was performed using IDRISI (Clark Labs, Worcester, USA).

**Risk factors weight**

AHP was used to determine the weights of risk factors. The factors were grouped according to their characteristics. The elements of the same level were dominated by the elements of the previous level. It dominated certain elements of the next level. The judgment matrix was constructed by comparing the importance of all factors at each level using a 9-level scale. "1" means that the two elements are of equal importance; "3" means that the former is moderately important than the latter; "5" means that the former is strongly important than the latter; "7" means that the former is very strongly important than the latter; "9" indicates that the former is extremely important than the latter; 2, 4, 6 and 8 are the intermediate values of the above judgments. The importance of all factors was determined according to the scores in 2.2. For weight calculation and hierarchical single ranking, we applied the square root to calculate the eigenvectors and eigenvalues. The resulting eigenvectors are the weight ranking of the factors. Equation 1 is given as follows:

\[ M_i = \prod_{j=1}^{n} P_{ij} \quad (i, j = 1, 2, \ldots, n) \]

\[ \bar{\omega} = \sqrt[n]{M_i} \]

\[ w = (w_1, w_2, \ldots, w_n) \]

\[ \lambda_{\text{max}} = \sum_{i=1}^{n} \left( \frac{P_{ij}}{\bar{\omega}} \right) \]

Where \( M_i \) is the product of the elements in the i-th row in the judgment matrix \( P \); \( \bar{\omega} \) is the geometric mean of \( M_i \); \( W_i \) is the weight of the i-th factor; \( W \) is the eigenvector; \( \lambda_{\text{max}} \) is the maximum eigenvalue. The judgment matrix was constructed by comparing the scores of two elements. Equation 2 is given as follows:

\[ CI = \frac{\lambda_{\text{max}} - n}{n - 1} \]

\[ CR = \frac{CI}{RI} \]

Where \( CI \) is the consistency of the indicator; \( CR \) is the relative consistency of the indicator; \( \lambda_{\text{max}} \) is the maximum eigenvalue; \( RI \) is the average random consistency indicator.
CR < 0.10 indicates a high level of consistency in the pairwise comparisons. However, if CR ≥ 0.10, the original values in the pairwise comparison matrix should be reconsidered and revised. R software version 4.0.3 (R Foundation for Statistical Computing, Vienna, Austria) was used for the application of AHP, and we provided the R code in this study (Supplement 3).

**Risk map**

A risk map was produced from the selected spatial risk factor layers and weighted using WLC. Equation 3 is given as follows:

\[ R = \sum_{i=1}^{n} w_i v(a_i) \]

Where n is the number of risk factors; w is the weight of factor i; v is the value function of risk factors at level i (a_i). R is the total value of risk factors at each cell level in the end [24]. ArcGIS 10.2 was used to map and classify the risk map.

**Sensitivity analysis and uncertainty**

The one-at-a-time (OAT) was used to conduct sensitivity analysis. The change in the weight value of only one factor at a time (other factors remain unchanged as much as possible) reflects the degree of influence and regularity of the single factor weight change for results. For the adjustment weight (wa) of each main factor, the rate of change was between -20% and 20%, and the step size was 1%. The weights of other factors (wi) were calculated as follows (Equation 4):

\[ w_i = (1 - wa) \times \frac{W_i}{1 - W_{a_0}} \quad 1 \leq i \leq n, i \neq a \]

Where Wi_0 is the initial weight of each risk factor; Wa_0 is the initial weight of the main change risk factor. The sum of all weights is equal to 1 [25].

The mean of absolute change rates (MACRs) of the adjusted-weight risk maps were calculated as follows (Equation 5):

\[ MACRs = \frac{1}{N} \sum_{k=1}^{N} \left| \frac{R_k - R_0}{R_0} \right| \times 100\% \]

Where R_k is the adjusted-weight risk map; R_0 is the initial risk map; N is the number of pixels [15].

The uncertainty map was the standard deviation of the risk maps generated after all factors changed the weights [26]. The weights were randomly selected for each iteration through Monte Carlo sampling (between ±20%), and the process was repeated 400 times. The total number of output risk maps was calculated by multiplying the number of iterations with the number of criteria. Finally, 400 weight-adjusted values per criteria throughout this range were combined to compute 4000 risk maps [27].
Risk map validation

The FMD outbreak data in mainland China from 2018 to 2020 were used to test the accuracy of the map. Areas with coefficients greater than 0.7 in the risk map were considered to have an outbreak of FMD. Combining predicted and actual data, the receiver operating characteristic (ROC) analysis was used to assess the predictive ability of the risk map. The R package-InformationValue was used to calculate the ROC.

Abbreviations

FMD: Foot-and-mouth disease; MCDA: multi-criteria decision analysis; AHP: analytic hierarchy process; ROC: receiver operating characteristic; WLC: weighted linear combination; OAT: one-at-a-time; OIE: World Organization for Animal Health; KDE: kernel density estimation; MACRs: mean of absolute change rates; AUC: area under the ROC curve.

Declarations

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Authors’ contributions

All authors have directly participated in the planning, execution & analysis of this study. Wang Haoran and Xiao Jianhua participated in data collection, analysis and writing up of the final manuscript. Ouyang MaoLin, Gao Hongyan and Bie Jia participated in data collection and editing of the manuscript. Gao Li and Gao Xiang checked the manuscript. Wang Hongbin assisted in the analysis of results and editing of the final manuscript. All authors read and approved the final manuscript.

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Availability of data and materials

The FMD data came from the World Organization for Animal Health (https://www.oie.int/) and the Ministry Agriculture and Rural Affairs of the People's Republic of China (http://www.moa.gov.cn/gk/yygl_1/yqfb/). The other datasets supporting the conclusions of this article are available in the supplementary materials.

Ethics approval and consent to participate

Not application.
Consent for publication

Not applicable.

Competing Interest

All the authors declare that they have no competing interests.

References

1. Grubman MJ, Baxt B (2004) Foot-and-mouth disease. Clinical Microbiology Reviews. 17:465-493.
2. Food and Agriculture Organization of the United Nations (2012) Foot-and-mouth disease frequently asked questions. http://www.fao.org/3/an384e/an384e00.pdf.
3. Jamal SM, Belsham GJ (2013) Foot-and-mouth disease: past, present and future. Veterinary Research 44:116.
4. OIE (2020). World Animal Health Information Database (WAHIS) Interface. https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home/indexcontent/newlang/en.
5. Ma J, Xiao J, Gao X, Liu B, Wang H (2017) Spatial pattern of foot-and-mouth disease in animals in China, 2010–2016. Peerj 5:e4193.
6. Bai XW, Li PH, Cao YM, Li D, Lu ZJ, Guo JH, Sun DH, Zheng HX, Pu S, Liu XT (2009) Engineering infectious foot-and-mouth disease virus in vivo from a full-length genomic cdna clone of the a/akt/58 strain. Science in China Series C: Life Sciences 52:155-162.
7. Li D, Liu ZX, Bao HF, Lu ZJ, Guo JH, Cao YM, Li PH, Bai XW, Chen YL, Xie BX (2007) The complete genome sequence of foot-and-mouth disease virus O/Akesu/58 strain and its some molecular characteristics. Archives of Virology 152:2079-2085.
8. Bai XW, Li PH, Bao HF, Liu ZX, Liu XT (2011) Evolution and molecular epidemiology of foot-and-mouth disease virus in China. Chinese Science Bulletin 56:2191-2201.
9. Chen J, Wang J, Wang M, Liang R, Lu Y, Zhang Q, Chen Q, Niu B (2020) Retrospect and Risk Analysis of Foot-and-Mouth Disease in China Based on Integrated Surveillance and Spatial Analysis Tools. Frontiers in Veterinary Science 6:511.
10. Jiang F, Song P, Zhang J, Cai Z, Chi X, Gao H, Qin W, Li S, Zhang T (2020) Assessing the impact of climate change on the spatio-temporal distribution of foot-and-mouth disease risk for elephants. Global Ecology and Conservation 23:e01176.
11. Chhetri BK, Perez AM, Thurmond MC (2010) Factors associated with spatial clustering of foot-and-mouth disease in Nepal. Tropical animal health and production 42:1441-1449.
12. Udahemuka JC, Aboge GO, Obiero GO, Lebea PJ, Onono JO, Paone M (2020) Risk factors for the incursion, spread and persistence of the foot and mouth disease virus in Eastern Rwanda. BMC veterinary research 16:1-10.
13. Knight JT, Rushton J (2013) The economic impacts of foot and mouth disease—What are they, how big are they and where do they occur? Preventive veterinary medicine 112:161-173.

14. Brown VR, Miller RS, McKee SC, Ernst KH, Didero NM, Maison RM, Grady MJ, Shwiff SA (2020) Risks of introduction and economic consequences associated with African swine fever, classical swine fever and foot-and-mouth disease: A review of the literature. Transboundary and Emerging Diseases, in press.

15. Sangrat W, Thanapongtharm W, Poolkhet C (2020) Identification of risk areas for foot and mouth disease in Thailand using a geographic information system-based multi-criteria decision analysis. Preventive Veterinary Medicine 185:105183.

16. Santos DV, Silva GS, Weber EJ, Hasenack H, Groff FHS, Todeschini B, Borba MR, Medeiros AAR, Leotti VB, Canal CW (2017) Identification of foot and mouth disease risk areas using a multi-criteria analysis approach. PloS one 12:e0178464.

17. Linkov I, Moberg E (2011) Multi-criteria decision analysis: environmental applications and case studies. CRC Press.

18. Malczewski J, Rinner C (2011) Multicriteria Decision Analysis in Geographic Information Science. Springer.

19. Psomas A, Vryzidis I, Spyridakos A, Mimikou M (2018) MCDA approach for agricultural water management in the context of water–energy–land–food nexus. Operational Research 1-35.

20. Zarin R, Azmat M, Naqvi S R, Saddique Q, Ullah S (2021) Landfill site selection by integrating fuzzy logic, AHP, and WLC method based on multi-criteria decision analysis. Environmental Science and Pollution Research 1-16.

21. Thanapongtharm W, Paul M C, Wiratsudakul A, Wongphruksasoong V, Kalpravidh, Wantanee (2019) A spatial assessment of Nipah virus transmission in Thailand pig farms using multi-criteria decision analysis. BMC veterinary research 15: 1-13.

22. Alimi, T.O., Fuller, D.O., Herrera, S.V., Arevalo-Herrera, M., Quinones, M.L., Stoler, J.B., Beier, J.C (2016). A multi-criteria decision analysis approach to assessing malaria risk in northern South America. BMC Public Health 16:221.

24. Jeong JS (2018) Design of spatial PGIS-MCDA-based land assessment planning for identifying sustainable land-use adaptation priorities for climate change impacts. Agricultural Systems 167:61-71.

25. Paul MC, Goutard FL, Roulleau F, Holl D, Thanapongtharm W, Roger FL, Tran A (2016) Quantitative assessment of a spatial multicriteria model for highly pathogenic avian influenza H5N1 in Thailand, and application in Cambodia. Scientific reports 6:31096.

26. Xu E, Zhang H (2013) Spatially-explicit sensitivity analysis for land suitability evaluation. Applied Geography 45:1-9.

27. Feizizadeh B, Jankowski P, Blaschke T (2014) A GIS based spatially-explicit sensitivity and uncertainty analysis approach for multi-criteria decision analysis. Computers & geosciences 64:81-
28. Zhang J, Jin Z, Yuan Y (2019) Assessing the spread of foot and mouth disease in mainland China by dynamical switching model. Journal of theoretical biology 460:209-219.

29. Elnekave E, van Maanen K, Shilo H, Gelman B, Storm N, Berdenstain S, Berke O, Klement E (2016) Prevalence and risk factors for foot and mouth disease infection in small ruminants in Israel. Preventive Veterinary Medicine 125:82-88.

30. Sansamur C, Arjkumpa O, Charoenpanyanet A, Punyapornwithaya V (2020) Determination of Risk Factors Associated with Foot and Mouth Disease Outbreaks in Dairy Farms in Chiang Mai Province, Northern Thailand. Animals 10:512.

31. Abbas T, Younus M, Muhmmad S, Ijaz M, Shakoor A (2014) Some challenges to progressive control of foot and mouth disease in Pakistan—findings of a pilot survey. Transboundary and emerging diseases 61:81-85.

32. Wungak Y, Olugasa B, Ishola O, Lazarus D, Ularamu G (2016) Foot-and-mouth disease (FMD) prevalence and exposure factors associated with seropositivity of cattle in north-central, Nigeria. African Journal of Biotechnology 15:1224-1232.

33. Balinda SN, Tjørnehøj K, Muwanika VB, Sangula A, Mwiine FN, Ayebazibwe C, Masembe C, Siegismund HR, Alexandersen S (2009) Prevalence estimates of antibodies towards foot-and-mouth disease virus in small ruminants in Uganda. Transboundary and emerging diseases 56:362-371.

34. Kitching R, Hughes G (2002) Clinical variation in foot and mouth disease: sheep and goats. Revue scientifique et technique (International Office of Epizootics) 21:505-512.

35. He J, Guo J, Liu X (2015) Current situation and prevention suggestion on foot-and-mouth disease in China. China Animal Health Inspection 32:10-14.

36. Guerrini L, Pfuenyri DM, Etter E, Bouyer J, Njagu C, Ndlovu F, Bourgarel M, de Garine-Wichatitsky M, Foggin C, Grosbois V (2019) Spatial and seasonal patterns of FMD primary outbreaks in cattle in Zimbabwe between 1931 and 2016. Veterinary research 50:1-12.

37. Gao X, Xiao J, Qin H, Cao Z, Wang H (2016) Impact of meteorological factors on the prevalence of porcine pasteurellosis in the southcentral of Mainland China. Preventive Veterinary Medicine 125:75-81.

38. Nyaguthii DM, Armsen B, Kitala PM, Sanz-Bernardo B, Di Nardo A, Lyons NA (2019) Knowledge and risk factors for foot-and-mouth disease among small-scale dairy farmers in an endemic setting. Veterinary research 50:33.

39. Hayama Y, Yamamoto T, Kobayashi S, Muroga N, Tsutsui T (2016) Potential impact of species and livestock density on the epidemic size and effectiveness of control measures for foot-and-mouth disease in Japan. Journal of Veterinary Medical Science 78:13.

40. Hamoonga R, Stevenson MA, Allepuz A, Carpenter TE, Sinkala Y (2014) Risk factors for foot-and-mouth disease in Zambia, 1981–2012. Preventive Veterinary Medicine 114:64-71.

41. Ann Lindholm EH, Pablo Torres-Lasso, Medardo Lasso, Carlos Echeverria, John Shaw, Jorge Hernandez (2007) Epidemiologic Aspects of a Foot-and-Mouth Disease Epidemic in Cattle in
42. Bessell PR, Shaw DJ, Savill NJ, Woolhouse MEJ (2010) Statistical modeling of holding level susceptibility to infection during the 2001 foot and mouth disease epidemic in Great Britain. International Journal of Infectious Diseases 14:e210-e215.

Table

Table 1 The standardization and weight of risk factors for risk mapping.

| Risk factors                     | Unit       | Weight | Standardization     | Source | Reference                 |
|----------------------------------|------------|--------|---------------------|--------|--------------------------|
| Buffalo density                  | head/km²   | 0.12   | Sigmoidal increase  | FAO    | Chhetri et al. (2010)    |
| Cattle density                   | head/km²   | 0.16   | Sigmoidal increase  | FAO    | Chhetri et al. (2010)    |
| Pig density                      | head/km²   | 0.08   | Sigmoidal increase  | FAO    | Hayama et al. (2016)     |
| Sheep density                    | head/km²   | 0.04   | Sigmoidal increase  | FAO    | Self assessment           |
| Goat density                     | head/km²   | 0.04   | Sigmoidal increase  | FAO    | Chhetri et al. (2010)    |
| Distance to previous outbreak points | Km         | 0.18   | Sigmoidal decrease  | FAO    | Bessell et al. (2010a)   |
| Distance to national boundaries  | Km         | 0.08   | Sigmoidal decrease  | NGCC   | Elnekave et al. (2016b)  |
| Distance to livestock market and slaughterhouse | Km | 0.10 | Sigmoidal decrease | AMAP | Lindholm et al. (2007) |
| Major road density               | Km         | 0.06   | Sigmoidal decrease  | NGCC   | Hamoonga et al. (2014)   |
| Grazing area                     | Km         | 0.14   | Sigmoidal increase  | LUH    | Sansamur et al. (2020)   |

FAO: The Food and Agriculture Organization; NGCC: National Geomatics Center of China; LCH: Land-Use Harmonization.

Figures
Figure 1

Study framework of FMD risk areas in mainland China based on spatial MCDA. Uncertain: an outbreak of FMD at this location, but its serotype was not reported.
Figure 2

The prevalence of FMD in mainland China from 2010 to 2020. A) Geographical distribution. B) Annual outbreaks. C) Monthly outbreaks. D) The proportion of species affected. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.
Figure 3

Spatial distribution of FMD in mainland China from 2010 to 2020. A) Number of FMD outbreaks. B) Number of FMD cases. C) Number of FMD destroyed. D) Number of FMD deaths. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.
Figure 4

Risk map of FMD in mainland China. A) Classified risk map. B) Continuous risk map. C) Main risk areas (risk coefficient > 0.7). Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.
Figure 5

Uncertainty map (The maximum standard deviation of 4000 adjusted-weight risk map). Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.
Figure 6

Mean absolute values of the change rate (MACRs) for the risk maps under simulations. (Buffalo: buffalo density; Cattle: cattle density; Dis_Ls: distance to livestock market and slaughterhouse; Dis_Nb: distance to national boundaries; Dis_Ou: distance to previous outbreak points; Gazing: grazing area; Goat: goat density; Pig: pig density; Road: major road density; Sheep: sheep density.)
Figure 7

ROC of risk map.

Supplementary Files

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- Sup.1Listofriskfactors.d1.docx
- Sup.2riskfactormapsd1.docx
- Sup.3AHPRcoded1.docx