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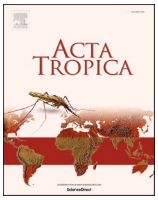

Assessing the risk of malaria local transmission and re-introduction in China from pre-elimination to elimination: A systematic review

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ABSTRACT

Assessing the risk of malaria local transmission and re-introduction is crucial for the preparation and implementation of an effective elimination campaign and the prevention of malaria re-introduction in China. Therefore, this review aims to evaluate the risk factors for malaria local transmission and re-introduction in China over the period of pre-elimination to elimination. Data were obtained from six databases searched for studies that assessed malaria local transmission risk before malaria elimination and re-introduction risk after the achievement of malaria elimination in China since the launch of the NMEP in 2010, employing the keywords "malaria" AND ("transmission" OR "re-introduction") and their synonyms. A total of 8,124 articles were screened and 53 articles describing 55 malaria risk assessment models in China from 2010 to 2023, including 40 models assessing malaria local transmission risk (72.7%) and 15 models assessing malaria re-introduction risk (27.3%). Factors incorporated in the 55 models were extracted and classified into six categories, including environmental and meteorological factors (39/55, 70.9%), historical epidemiology (35/55, 63.6%), vectorial factors (32/55, 58.2%), socio-demographic information (15/26, 53.8%), factors related to surveillance and response capacity (18/55, 32.7%), and population migration aspects (13/55, 23.6%). Environmental and meteorological factors as well as vectorial factors were most commonly incorporated in models assessing malaria local transmission risk (29/40, 72.5% and 21/40, 52.5%) and re-introduction risk (10/15, 66.7% and 11/15, 73.3%). Factors related to surveillance and response capacity and population migration were also important in malaria re-introduction risk models (9/15, 60%, and 6/15, 40.0%). A total of 18 models (18/55, 32.7%) reported the modeling performance. Only six models were validated internally and five models were validated externally. Of 53 incorporated studies, 45 studies had a quality assessment score of seven and above. Environmental and meteorological factors as well as vectorial factors play a significant role in malaria local transmission and re-introduction risk assessment. The factors related to surveillance and response capacity and population migration are more important in assessing malaria re-introduction risk. The internal and external validation of the existing models needs to be strengthened in future studies.

1. Introduction

Significant progress has been achieved on the road to global malaria eradication over the past decades. According to the *World Malaria Report 2022*, 25 countries that were malaria endemic in 2000 have achieved three consecutive years of zero indigenous malaria cases, and 12 of these

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countries were certified malaria-free by the World Health Organization (WHO) between 2000 and 2021 (WHO, 2022b). Despite the fact that malaria elimination efforts were largely be affected by the COVID-19 pandemic since 2020, two countries achieved this goal. Of which, China was certified as a malaria-free country by the WHO on June 30, 2021 (WHO, 2021a, 2022b).

In 2010 and in response to a global malaria eradication initiative proposed at the UN Millennium Development Goals high-level meeting, the Chinese government launched the National Malaria Elimination Program (NMEP) and planned to achieve malaria elimination by 2020 (Cao et al., 2021). Malaria transmission risk assessment has played an important role in implementing an effective malaria elimination program in China. The malaria local transmission risk was assessed and stratified at a city- or even county-level to guide the NMEP. With the initiation of the malaria elimination program, a nationwide malaria transmission risk prediction model was established in China by incorporating temperature, relative humidity, and rainfall factors (Yang et al., 2010). According to the model, malaria local transmission risk in China was classified into four strata, namely non-endemic, sporadic-endemic, hypo-endemic, and meso-endemic, of which the latter two have been particularly focused on in the last mile of elimination (Yang et al., 2010). Later, Zhou et al. innovatively assessed the malaria local transmission risk by incorporating the malaria transmission risk index during the pre-elimination phase in China. Based on the assessment, four types of risk areas were categorized among 2,147 counties in 24 endemic provinces in China, including super-high risk areas, high-risk areas, moderate risk areas, and low risk areas (Zhou et al., 2014). Modeling the transmission risk provided a practical tool to stratify the malaria transmission risk and implement an effective elimination campaign in China.

Since China was certified as a malaria-free country in 2021, strengthening the malaria surveillance and response system by assessing the risk of malaria re-introduction became a particularly important intervention to sustain the malaria elimination success (Cao et al., 2022; Lu et al., 2022b; Lu et al., 2016). Besides constructing malaria re-introduction risk assessment models using the Delphi method, scholars are developing the malaria re-introduction risk prediction model by adopting machine learning techniques and by incorporating multiple risk factors (Kamana et al., 2022; Lan et al., 2022; Li et al., 2022; Li et al., 2021a; Liu et al., 2023; Mo et al., 2021; Wang et al., 2016). The main objective of this study is to determine the lessons gained in modeling malaria risk from pre-elimination to elimination stage in China, which are expected to benefit malaria-eliminating countries globally.

2. Methods

This study followed Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement guidelines (Page et al., 2021). The protocol of this study was registered on the international prospective register of systematic reviews database (CRD42023415657).

2.1. Inclusion and exclusion criteria

Studies that assessed malaria local transmission or re-introduction risk in China since 2010 were incorporated. Whether the risk assessment was conducted for malaria local transmission or re-introduction was defined based together on the statement by the authors and a comprehensive analysis of the malaria epidemiological context of the study (e.g., the number of reported cases in the study location). Malaria re-introduction here refers to the occurrence of introduced cases (cases of the first-generation transmission that are epidemiological linked to a confirmed imported case) in a country or area where the disease had previously been eliminated (WHO, 2021b). If multiple articles described the same assessment model, it was recorded only once, and all relevant information was extracted from these articles.

2.2. Search strategy and screening

A comprehensive literature search was performed both in English databases (PubMed, Web of Science, Cochrane Library), and in Chinese databases including China National Knowledge Infrastructure (CNKI), China Science and Technology Journal Database (VIP), and Wanfang database by using the following keywords “malaria”, “Malaria, *Vivax*”, “Malaria, *Falciparum*”, “transmission”, “re-introduction”, “re-establishment”, “re-emergence”, “resurgence” and “China” (supplementary material appendix 1). All searches were conducted in April 2023 and covered the databases between 2010 and 2023. After removing duplicate entries, two reviewers (LYC and GYL) independently screened the identified titles and abstracts for eligibility. Subsequently, the full-text articles were screened for inclusion, and any disagreements were resolved through consensus. The citations of relevant articles were also manually screened to identify additional studies.

2.3. Data extraction and synthesis

The data extraction was carried out independently by two investigators (LYC and GYL). Information extracted including the first author, the year of publication, the study site, the source of data, the year of the reported last indigenous case in the study area, the purpose of models (local transmission or re-introduction risk assessment), the methodology of models, variables incorporated in the established models, the performance of the model, and the validity of the models.

2.4. Quality assessment

The risk of bias in incorporated studies was assessed using an adapted Newcastle-Ottawa Scale (aNOS) by the two independent reviewers (LYC and GYL). The aNOS scale incorporates the assessment of the sample selection, comparability, and outcomes. Scores on this instrument range from 1 to 10, with higher scores indicating higher quality (Ottawa Hospital Research Institute, 2021). Considering the quality of the reported models was reflected by the model performance, we adapted the domain of “comparability” into “model performance”. The domain “model performance” was assessed according to the existing tool used in evaluating prediction models in clinical settings, titled “Prediction model Risk of Bias Assessment Tool (PROBAST)” (Wolff et al., 2019) (Supplementary Material Appendix 2).

3. Results

A total of 6,339 articles were identified after the electronic searches of six databases and removal of duplicate studies. The titles and abstracts were screened and 251 articles were subjected to full-text review. Of these, 198 were excluded after reading full texts with various reasons. Finally, 53 articles were incorporated into the analysis (Fig. 1).

3.1. General characteristics of the incorporated studies

The general characteristics of the 53 articles reporting 55 malaria risk prediction or assessment models in China from 2010 to 2023 were summarized in Table 1, including 40 models in malaria local transmission risk (72.7%) and 15 models in malaria re-introduction risk (27.3%). One-third of the incorporated studies (36/53, 67.9%) were published in Chinese. Geographically speaking, of 55 incorporated models, seven models were established at a national level and 43 were at a provincial level, including 16 were developed for Yunnan province, 14 for Anhui province, six for Henan province, six for Hainan province, four for Hubei province, two for Hunan, Fujian and Taiwan province respectively, and one for Jiangxi and Shandong province.

Of the 55 incorporated models, the majority were developed based

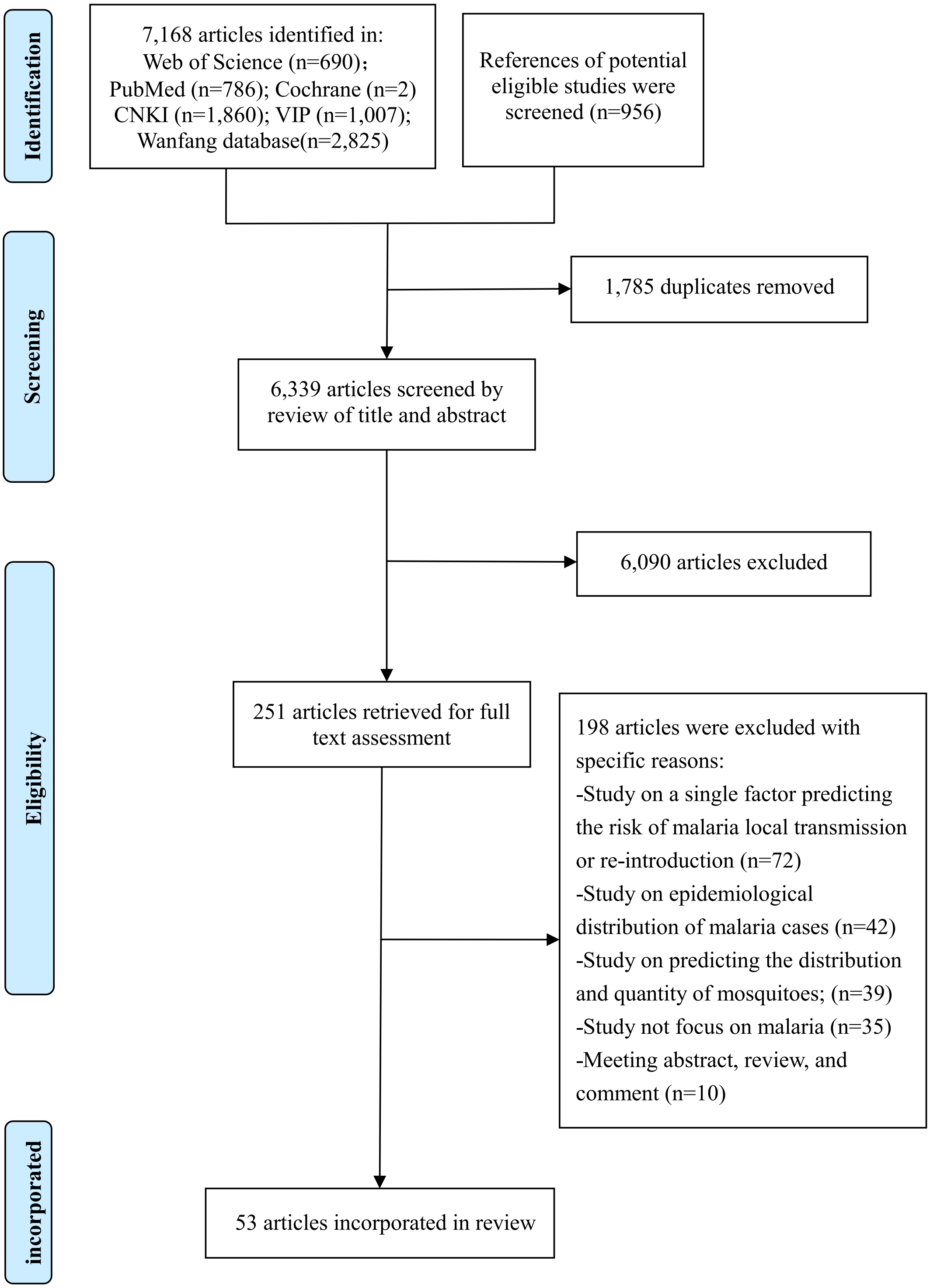

Fig. 1. A summary flow of the study selection process

on routine surveillance data (35/55, 63.6%). In terms of methodology, 22 models (22/55, 40%) were developed by statistical method, followed by mathematical methods (16/55, 29.1%), Delphi method (12/55, 21.8%), and machine learning (5/55, 9.1%). Of four studies assessing the malaria re-introduction risk, three models have used the Delphi method.

3.2. *Variables incorporated in malaria risk assessment model*

Variables incorporated in the 55 models were identified and classified into six categories, namely environmental and meteorological factors, historical epidemiology, vectorial factors, surveillance and response-related factors and population migration.

3.2.1. *Environmental and meteorological factors*

Environmental and meteorological factors were considered in 40 models and finally incorporated in 38 models (38/55, 69.1%). Rainfall (32/39, 82.1%), temperature (29/39, 74.4%), and relative humidity (15/39, 38.5%) were most frequently incorporated in these models. Remote sensing data was as defined as predictors only for malaria local transmission risk, including normalized difference vegetation index (NDVI) (4/39, 10.3%), land surface temperature (3/39, 7.7%), evapotranspiration (2/39, 5.1%), slope (2/39, 5.1%), water density index (1/39, 2.6%), and drainage density (1/39, 2.6%). Extreme weather events such as Multivariate ENSO Index were identified in two prediction models (Gao et al., 2012). Land use was studied in 3 models, but only one model incorporated it. Topography, wind velocity, and barometric pressure were identified in one model.

3.2.2. Historical epidemiology

Historical epidemiology was incorporated in 35 models (35/55, 63.6%). The most commonly incorporated was the number of malaria cases (34/35, 97.1%). Of which, 21 models incorporated both the number of indigenous and imported cases (21/34, 61.8%), and 12 models only incorporated the number of imported cases (12/34, 35.3%). Six models incorporated the malaria species and historical epidemic strength separately.

3.2.3. Vectorial factors

Vectorial factors were incorporated in 32 models (32/55, 58.2%). The most commonly incorporated vectorial factors were vector suitability (a combination of *Anopheles* species, density, number and biological characteristics) (26/32, 81.3%), human-vector contact (biting rate and human blood index) (15/32, 46.9%) and vectorial capacity, which was defined by a formula including the parasite's extrinsic incubation period, the ratio of mosquitoes to humans, mosquito survival through one day and human biting rates (Brady et al., 2016) (9/32, 28.1%).

3.2.4. Socio-demographic information

Socio-demographic information was incorporated in 26 models (26/55, 47.3%). Population structure (the number of populations, population density, fertility or mortality of population, male population, occupation) (15/26, 53.8%) was the most commonly used indicator in the domain. Moreover, economic level (GDP, industrial structure, economic growth rate, and income per capita) was incorporated in seven models (7/26, 26.9%), and the quantity of medical and health services (number of medical institutions and number of practicing physicians) were incorporated in two models (2/26, 7.7%).

3.2.5. Surveillance and response-related factors

Surveillance and response-related factors were incorporated in 18 models (18/55, 32.7%). Construction of a malaria prevention and control team (establishment of malaria working group, number of malaria staff, implementation of the malaria training program, number of microscopists, and number of microscopy stations, etc.) (10/18, 55.6%). and awareness and behavior of malaria prevention and health seeking, (10/18, 55.6%) were the most common predictors. This was followed by financial support (8/18, 44.4%) and treatment capacity (8/18, 44.4%). Surveillance and diagnostic capacity were incorporated in five models (5/18, 27.8%). Multi-sectorial prevention and control mechanism (4/18, 22.2%), stock of anti-malarial drugs and other equipment (4/18, 22.2%), government's attention (3/18, 16.7%), implementation of "1-3-7" malaria surveillance and response strategy (3/18, 16.7%) were only incorporated in malaria re-introduction risk assessment models.

3.2.6. Population migration

Population migration was incorporated as a predictor in 13 models (13/55, 23.6%). Of these, half of the models assessed malaria re-introduction risk (7/14, 50%). The number of migrants from malaria-endemic regions was the most common indicator used in presenting the population migration in assessing the malaria risk (14/14, 100%). Moreover, the length of stay in the malaria endemic area and the number of trips were incorporated in two models (2/14,14.3%) respectively, and the original country of the migrated population was incorporated in one model (1/14, 7.1%).

3.3. Shifting of the variables used in assessing malaria local transmission risk to malaria re-introduction risk

Among the 40 models in assessing malaria local transmission risk, the most commonly incorporated variables were environmental and meteorological factors (29/40, 72.5%), followed by historical epidemiology (25/40, 62.5%), demographic and social statistic information (22/40, 55%), and vectorial factors (21/40, 52.5%). Surveillance and response-related factors (9/40, 22.5%). and population migration (7/40, 17.5%) were less frequently incorporated in the models.

Differently, among the 15 models in assessing malaria re-introduction risk, the vectorial factors (11/15, 73.3%) were the most commonly incorporated. Moreover, it is important to notice that 60% of the models for assessing malaria re-introduction risk incorporated surveillance and response-related factors (9/15), which is significantly higher compared with local transmission risk prediction models. Similarly, population migration (6/15, 40.0%) was more frequently incorporated in malaria re-introduction risk models than in local transmission risk models. Demographic and social statistic information was only incorporated in four models assessing malaria re-introduction (4/15, 26.7%).

3.4. Performance and validation of the malaria transmission and re-introduction models

Of the 55 incorporated models, only 18 models reported their performance. The commonly evaluated metrics include Akaike's information criterion (7/18, 38.9%), mean absolute error (6/18, 33.3%), Root mean square error (5/18, 27.8%), and R square (5/18, 27.7%).

Of the 55 incorporated models, six were validated internally and five were validated externally. Only four models from one study were validated both internally and externally (Kamana et al., 2022). The methods used in validation include traditional methods, such as splitting the data into training and validation sets according to a defined proportion (Hundessa et al., 2018a; Shi et al., 2020). In addition, some models were validated by splitting data following a time series to ensure that the validation set and test set results are more realistic (Kamana et al., 2022). For example, four machine learning models for malaria re-introduction (by XGBoost model, LSTM model, GRU model, and LSTMSeq2Seq model) were established by data collected from 2004-2012, validated by data from 2013-2014, and further tested by data from 2015-2016.

3.5. Quality assessment

Scores of the aNOS scale of 53 incorporated studies ranged from five to ten. Of these, 45 studies scored seven and above as the models were established based on the surveillance data, with adequate sample size, good representation, and data quality. The missing scores in the quality assessment are mainly due to the lack of measurement of the models' performance (Supplementary Material Appendix 3).

4. Discussion

This study analyzed and summarized the establishment and findings of 40 malaria local transmission risk models and 15 malaria re-introduction risk models established in China from the pre-elimination to elimination phase. A total of one hundred factors incorporated into the risk assessment models were identified and further classified into six categories, including environmental and meteorological factors, historical epidemiological factors, vectorial factors, socio-demographic information, surveillance and response-related factors, and population migration aspects. Factors related to surveillance and response capacity and population migration are more commonly incorporated in malaria re-introduction risk assessment models. Although existing models generally lack strong internal or external validation, the predictors considered, the methods used, and the lessons gained in establishing the risk assessment models from China over the past decade may benefit other countries aiming for malaria elimination and prevention of malaria re-introduction.

Nearly one-third of the included models were established in Yunnan Province, including 15 malaria local transmission risk assessment models and 1 malaria re-introduction risk assessment model. Yunnan Province has been long-term regarded as the last mile of the malaria elimination program in China (Li et al., 2021b; Yang et al., 2021). It's climate and natural conditions are suitable for vector breeding and *Plasmodium* development, and thus malaria outbreaks and epidemics were frequently reported in this province (Liu et al., 2018; Xu et al., 2016; Yang et al., 2017). Moreover, Yunnan Province shares long porous international borders with malaria-endemic countries, such as Lao People's Democratic Republic, Myanmar, and Vietnam (Yang et al., 2021). Therefore, migrants from endemic countries into Yunnan Province are at high risk of carrying malaria-infected individuals and can easily reintroduce malaria transmission in China's border areas (Liu et al., 2022; Yang et al., 2021). In addition, there was a concern that the risk of border-spill malaria due to the infected *Anopheline* mosquitoes may cause malaria outbreaks in Yunnan Province (Lin et al., 2022). Continuing to strengthen the public health response capacity and malaria surveillance capacity, particularly in border areas, is crucial to maintaining malaria elimination success.

All malaria local transmission risk models established in the Huang-Huai River region only incorporated environmental and climatic factors (n=14) (Lin et al., 2022; Liu et al., 2022; Liu et al., 2018; Xu et al., 2016; Yang et al., 2017; Yang et al., 2021; Zhou et al., 2010). The Huang-Huai River region is situated in central China, bordered by the Yellow River to the north and the Huaihe River to the south, covering 116 counties in four provinces of Henan, Anhui, Shandong, and Jiangsu (Zhang et al., 2014). This region experiences a diverse range of climates, including arid, semi-arid, semi-humid, and humid zones, characterized by complex weather patterns and distinct continental monsoonal features (Guan et al., 2021). Due to global climate change, this area occasionally experiences abrupt alternations between droughts and floods (Zhang et al., 2021). In addition, the Huang-Huai River region serves as a major population center in the northern part of the country and plays a crucial role in food production, accounting for nearly 35% of the population and 34% of the cultivated land (Ren et al., 2023). Under the context of global climate change, drought-flood abrupt alternation occurs from time to time in this region (Ren et al., 2023). Historically, a malaria epidemic occurred in this region in the 1960s, and the reason is largely attributed to the increase of breeding sites, as dry fields in the region were generally converted into paddy fields (Li, 2013). In the early 21st century, malaria re-emergence, and outbreaks again occurred in this region, which was attributed to the high vectorial capacity of *Anopheles sinensis* (Zheng et al., 2008; Zhou et al., 2010). These epidemic histories explain well a large proportion of environmental and climatic factors that were incorporated in the risk assessment models in this region, including classical ones (e.g., temperature, humidity, and rainfall) and rare ones such as NDVI and land use, etc. (Gao et al., 2012; Liu et al., 2021; Zhai et al., 2018; Zhou et al., 2010).

Although one local transmission risk assessment model and one re-introduction risk assessment model excluded environmental and meteorological factors, more than half of both local transmission risk assessment models and re-introduction risk assessment models incorporated them (Hu, 2017; Lei et al., 2019). This is consistent with the majority of findings that environmental and meteorological factors are closely linked to vectorial activities (Castro, 2017; Lu et al., 2023). In particular, rainfall creates many suitable sites for mosquitoes to breed and temperature accelerates the development of *Plasmodium,* which are both the major drivers of malaria transmission (Gething et al., 2011; Paaijmans et al., 2007; Ren et al., 2016; Zhou et al., 2010). Other environmental and meteorological factors such as altitude, topography, and extreme weather events were less frequently incorporated in the risk assessment models, which may be due to the inherent complexity of the environment and the variability of environments in different regions (Bødker et al., 2006; Cao et al., 2023; Ewnetu and Lemma, 2022; Kovats et al., 2003; Stresman, 2010; van de Straat et al., 2022). Moreover, environmental remote sensing data was gradually being used in assessing the risk of transmission of malaria in more recent studies, such as NDVI, land surface temperature, evapotranspiration, water density index et al. In this case, epidemiologists and geographers should be in collaboration from the onset of a study so that the remote sensing data are fully applicable to the needs of public health concerns (Herbreteau et al., 2007).

Surveillance and response capacity play a crucial role in reducing the burden of malaria, eliminating the disease, and preventing its re-introduction. Our study demonstrated that surveillance and response factors are given more weight in assessing malaria re-introduction risk than in transmission risk. However, the factors related to malaria surveillance and response capacity incorporated in models were inconsistent. WHO has developed a Malaria Surveillance Assessment Toolkit, which can be used to track the progress towards surveillance system strengthening (WHO, 2022a). But the tool maybe not fully applicable to the malaria surveillance and response system of China. Thus, there is a need to develop a standard tool to regularly assess malaria surveillance and response capacity in China.

Only about one-fifth of malaria local transmission risk assessment models and two-fifths of re-introduction risk assessment models incorporated the factors related to population migration. The main reason for this is the persistent challenge of accessing information on migrant populations. Firstly, migrant population is excluded from public management and health services, especially irregular migrants (Guan, 2020). Secondly, migrant worker management is not totally standardized by labor export organizations or companies (Qian et al., 2014). Thirdly, the origin country and length of stay of migrated population may be imprecise because they often visit multiple countries over a period of time (Qian et al., 2014; Wang et al., 2012). Fourthly, migrant population may have a recall bias on preventive or high-risk behaviors during their long-term travel. So far, many efforts have been conducted to characterize population migration patterns and the translation of these into parasite dispersion (Pindolia et al., 2012). For example, scholars replaced the number of migrant populations with various data sets, such as flight data, census data, health survey data, GPS records or mobile phone records (Kugler and Fitch, 2018; Schick et al., 2008; Vazquez-Prokopec et al., 2009). Moreover, scholars investigated the demographics of human movement and migration patterns based on population censuses and sampling surveys (Chen, 2018; Lu et al., 2022a; Pindolia et al., 2013).

Only few models in our study have been validated internally or externally, mainly due to a lack of adequate and high-quality validation datasets. In terms of the risk factors incorporated, the models that were validated all incorporated environmental and vectorial factors, while none of the models that incorporated factors related to surveillance and response capacity as well as migration population were validated, which could be explained by the difficulties in collecting such data (Gao, 2012; Hundessa et al., 2018b; Kamana et al., 2022; Shi et al., 2020). Finding a suitable separate dataset for outbreaks and epidemics of infectious diseases can also be challenging (Walters et al., 2018). Additionally, transmission potential of pathogens may have evolved significantly over time, that those datasets which do exist may not be appropriate for comparison (Ding et al., 2021). Access to surveillance data or multi-source public data and big-data mining can vastly facilitate model validation (Bansal et al., 2016). When validated datasets are indeed lacking, researchers should try alternative methods to illustrate the stability and accuracy of model predictions, such as by comparing multiple models, or to make it as clear as possible why validation cannot be performed (Walters et al., 2018).

5. Implications for public health practice

Based on the 40 malaria transmission risk models and 15 malaria re-introduction risk assessment models incorporated in this study, we recommend that researchers incorporate the following factors for malaria risk assessment: environmental and meteorological factors, historical epidemiology, vectorial factors, population migration, as well as surveillance and response related factors. Although datasets of factors related to surveillance and response capacity as well as population migration are challenging to obtain, they play an irreplaceable role in malaria risk assessment, particularly for malaria re-introduction risk assessment. Malaria risk assessment models established on the basis of Delphi method can be a useful tool for stratifying malaria risk areas in countries that are in pre-elimination or elimination phase of malaria. To make full use of the experts' knowledge and practical experience while ensuring that the results of risk assessment are objective and scientific, Delphi method can be combined with objective weighting methods, such as analytic hierarchy process and entropy weighting. Given the rapid and constant evolution of infectious disease models, a standard tool for evaluating the risk of bias in the modeling studies of infectious diseases should be developed.

6. Limitations

This is the first study to summarize the efforts made in predicting or assessing malaria risk in China since the initiation of the Malaria Elimination Program in 2010. However, there are some limitations in this study. Firstly, we were unable to conduct a meta-analysis for the factors incorporated in the models because incomplete information on the incorporated studies. Moreover, we used an aNOS scale for quality assessment because the PROBAST scale generally applies to clinical prediction model studies but not to infectious disease prediction models, which may have resulted in higher quality scores.

7. Conclusion

China has made considerable efforts in assessing malaria local transmission and re-introduction risk. Both malaria local transmission and re-introduction risk assessment models were established based on environmental and meteorological factors, historical epidemiology, vectorial factors, demographic and social statistic information, surveillance and response-related factors, and population migration. Factors related to surveillance and response capacity as well as population migration are more important in malaria re-introduction risk assessment models than in malaria local transmission risk assessment models. But it is undeniable that environmental and meteorological factors and vectorial factors play a significant role in both malaria local transmission and re-introduction risk assessment models. Existing models for malaria local transmission and re-introduction risk lack general applicability due to the lack of internal and external validation. There is still a lack of a quality assessment tool applicable to infectious disease models.

CRediT authorship contribution statement

Guangyu Lu: Conceptualization, Funding acquisition, Writing – review & editing. **Li Zhao:** Data curation, Writing – original draft. **Liying Chai:** Methodology, Writing – original draft. **Yuanyuan Cao:** Data curation, Formal analysis. **Zeyin Chong:** Data curation, Methodology. **Kaixuan Liu:** Data curation, Methodology. **Yan Lu:** Data curation. **Guoqiang Zhu:** Data curation. **Pengpeng Xia:** Data curation. **Olaf Müller:** Writing – review & editing. **Guoding Zhu:** Supervision, Writing – review & editing. **Jun Cao:** Supervision, Writing – review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

I have shared my data at the supplementary material.

Ethics approval

Not applicable

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Availability of data and materials

All data generated or analyzed during this study are incorporated in this published article and its supplementary information files.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.actatropica.2023.107082.

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