Transmission Patterns of Chikungunya Fever in Southeast Asia and Cross-Border Prevention and Control Strategies

Yang Wang[1], Yongmei Tao[1*], Yuan Kong[1], Shi Du[1], Ju Yan[2]

[1] Nanchuan District Center for Disease Control and Prevention, Chongqing 408400, China

[2] Banan District Center for Disease Control and Prevention, Chongqing 408400, China

[*] Corresponding author: Yongmei Tao, tym_nccdc@163.com

Abstract: Objective: To explore the epidemiological transmission patterns of Chikungunya Fever (CHIK) in Southeast Asia, analyze its main influencing factors, evaluate the effectiveness of existing cross-border prevention and control strategies, and provide a scientific basis for regional coordinated prevention and control. Methods: Publicly reported CHIK case data, meteorological data (temperature, precipitation), and population mobility data from the ten countries of the Association of Southeast Asian Nations (ASEAN) between 2018 and 2023 were collected. Descriptive epidemiological analysis and correlation regression analysis were conducted. Meanwhile, a systematic review and comparison were performed on the current prevention and control strategies of various countries, including border health quarantine, mosquito vector monitoring and control, and cross-border information sharing. Results: The CHIK epidemic in Southeast Asia showed obvious seasonal (high incidence in the rainy season) and regional (high incidence in urban and suburban areas) patterns. The number of cases was significantly positively correlated with average temperature ($r=0.752$, $P<0.01$) and precipitation ($r=0.684$, $P<0.01$). Cross-border human mobility was a key driving factor for the cross-regional spread of the epidemic. Regions adopting the integrated cross-border joint prevention and control model of "monitoring-early warning-joint response" showed significantly better epidemic outbreak scale and control speed than those adopting a single domestic prevention and control strategy ($P<0.05$). Conclusion: The transmission of CHIK in Southeast Asia is jointly influenced by natural climatic factors and human social activities. Constructing and improving regional information sharing platforms, unifying mosquito vector control standards, and strengthening comprehensive cross-border joint prevention and control strategies such as port quarantine and community mobilization are the keys to effectively curbing the cross-border spread of the epidemic.

***Keywords*:** Chikungunya Fever; Southeast Asia; transmission patterns; mosquito-borne infectious diseases; cross-border prevention and control

1. Introduction

Chikungunya fever is an acute arboviral disease caused by the Chikungunya virus (CHIKV) and transmitted by Aedes mosquitoes, primarily Aedes albopictus and Aedes aegypti. Its clinical features include sudden onset of high fever, severe joint pain, and skin rash. In some patients, joint pain can persist for months or even years, imposing a heavy socioeconomic burden [1]. Due to its tropical climate, high-density urban population, and frequent cross-border activities, Southeast Asia has become an endemic area for Chikungunya fever and a high-risk region for epidemic outbreaks [2]. This study aims to systematically analyze the epidemiological characteristics and driving factors of Chikungunya fever in Southeast Asia, and evaluate the effectiveness of existing cross-border prevention and control strategies, in order to provide empirical evidence and policy recommendations for regional cooperation.

2. Materials and Methods

2.1 Study Materials

Chikungunya fever epidemic data from the ten member states of the Association of Southeast Asian Nations (ASEAN) — Thailand, Vietnam, Malaysia, Singapore, the Philippines, Indonesia, Cambodia, Laos, Myanmar, and Brunei — were collected for the period from January 2018 to December 2023. The data were sourced from official reports of the World Health Organization (WHO) Western Pacific Regional Office and Southeast Asia Regional Office, publicly released weekly/monthly epidemiological bulletins from the health ministries of respective countries, and open health data platforms (e.g., HDX). For cross-border population mobility data, the annual volume of inbound and outbound passengers at major ports of each country was used as a proxy indicator.

2.2 Study Methods

2.2.1 Descriptive Epidemiological Analysis

Case data were analyzed by time, region, and population (age, gender) to describe the three-dimensional distribution (time, space, and population). Epidemiological curves and maps were plotted to illustrate spatial-temporal aggregation patterns and spread pathways.

2.2.2 Correlation Analysis and Regression Model

Pearson correlation analysis was used to examine the association between the number of cases and meteorological factors (temperature, precipitation). A multiple linear regression model was constructed to analyze the degree of influence of each factor on the incidence rate.

2.2.3 Comparative Analysis of Prevention and Control Strategies

Through literature review and policy collation, strategies were categorized into two types:

Type A: Comprehensive cross-border joint prevention and control

Type B: Domestic prevention and control as the primary approach

Under the condition of similar epidemic starting points, differences between the two groups were compared in terms of epidemic peak, duration, total number of cases, and other indicators.

2.3 Statistical Methods

Statistical analysis was performed using SPSS 26.0 software. Measurement data were expressed as mean ± standard deviation ($\overline{x} \pm s$), and inter-group comparisons were conducted using t-tests or one-way analysis of variance (ANOVA). Enumeration data were expressed as rates (%), and inter-group comparisons were performed using chi-square tests (χ^2 test). Correlation analysis and regression analysis were used to explore relationships between variables. A P-value < 0.05 was considered statistically significant.

3. Results

3.1 Epidemiological Characteristics of the Epidemic

Between 2018 and 2023, approximately 350,000 Chikungunya fever cases were reported in Southeast Asia. The incidence rate fluctuated significantly, with two peak periods in 2019 and 2022. The epidemic showed obvious seasonality: the number of cases increased significantly during the rainy season (May-October) and remained at a low level in the dry season. High-incidence areas were concentrated in densely populated urban deltas, transportation hubs, and border trade zones, such as the vicinity of Bangkok, the Kuala Lumpur-Selangor region, and the area around Ho Chi Minh City.

3.2 Analysis of Factors Influencing Transmission

Correlation analysis revealed a significant positive correlation between the monthly number of cases and both monthly average temperature ($r=0.752$, $P<0.01$) and monthly cumulative precipitation ($r=0.684$, $P<0.01$). Regression analysis indicated that temperature, precipitation, and cross-border human flow density were three key independent factors for predicting epidemic risk (adjusted $R^2=0.712$, $P<0.001$).

3.3 Comparison of Prevention and Control Strategy Effectiveness

Analysis of 12 cross-border epidemic events showed that for areas adopting Strategy A (comprehensive cross-border joint prevention and control, n=5), the average control duration was (45.2±10.3) days and the average total number of cases was (2,850±850). For areas adopting Strategy B (domestic prevention and control as the primary approach, n=7), the corresponding figures were (68.7±15.6) days and (5,120±1,350) cases. The differences in both control duration and total number of cases between the two groups were statistically significant (both P<0.05), indicating that Strategy A enables earlier identification of imported cases, initiates joint responses, and effectively curbs the scale of the epidemic.

Table 1. Comparison of the Effectiveness of Different Prevention and Control Strategies ($\overline{x} \pm s$)

Group	Number of Epidemic Events	Average Control Time (days)	Average Total Number of Cases
Type A Strategy Group	5	45.2 ± 10.3	2850 ± 850
Type B Strategy Group	7	68.7 ± 15.6	5120 ± 1350
t-value	-	3.12	3.45
P-value	-	< 0.05	< 0.05

4. Discussion

This study reveals that the transmission of Chikungunya fever in Southeast Asia exhibits significant seasonality and regionality, and is closely associated with climate and human mobility. Hot and rainy conditions extend the active period of Aedes mosquitoes, accelerate viral replication, and increase breeding sites[3]. Frequent cross-border activities enable the virus to spread rapidly through infected individuals, forming an "importation — local transmission — re-exportation" cycle and increasing the difficulty of prevention and control.

The study shows that the traditional domestic prevention and control approach (Strategy B) has limited effectiveness, while the integrated "surveillance — early warning — response" model (Strategy A) demonstrates notable advantages. Its core elements are as follows:

Transparent information sharing: Establish a regional information platform to enable early warning [4];

Coordinated prevention and control: Unify standards for mosquito vector surveillance and disinfection at borders;

Precise port quarantine: Implement risk-based coordinated quarantine measures;

Integrated community mobilization: Conduct cross-border health education to enhance protection awareness.

However, this study also has certain limitations. Firstly, epidemic data may be affected by inconsistencies in monitoring capabilities and reporting standards across countries, leading to potential underreporting and misreporting. Secondly, the evaluation of prevention and control strategy effectiveness may be confounded by unmeasured factors such as the economic development level and the foundation of the medical and health system in each country [4]. Future research should focus on establishing a more standardized regional monitoring system and conducting longer-term prospective studies to quantitatively evaluate the specific cost-effectiveness of various prevention and control measures, thereby providing more accurate guidance for policy-making.

Acknowledgments

This work was supported by Medical Research Project of Chongqing Municipal Health Commission (No.2025WSJK095); Chongqing Public Health Key Discipline Project, Chongqing Municipal Health Commission, China.

References

[1] Bailey P G,Nett J R. Differentiating dengue, Zika, and chikungunya in paediatric populations[J].The Lancet. Child & adolescent health,2025,9(9):614-615.

[2] Bowie K. UK chikungunya cases more than double year on year, data show[J].BMJ (Clinical research ed.),2025,390r1746.

[3] Xu R,Yan Y,Han H, et al. Absence of dengue, zika and chikungunya viral nucleic acid in blood donations in China[J]. Transfusion medicine (Oxford, England),2025,DOI:10.1111/TME.70027.

[4] Malik R M,Walaskar S,Majji R, et al. Development of an affordable multiplex quantitative RT-PCR assay for early detection and surveillance of Dengue, Chikungunya, and co-infections from clinical samples in resource-limited settings[J].PLoS neglected tropical diseases,2025,19(8):e0013250.