REVIEW

Prevalence of the Chikungunya during outbreaks in Asia: A systematic review

Nguyen Thanh Hai[1]*, Nguyen Quang Duc[1]

ABSTRACT

Background: Chikungunya virus (CHIKV) is a re-emerging mosquito-borne alphavirus that has caused recurrent outbreaks across Asia in the 21st century. Outbreak investigations are critical for quantifying burden, characterizing affected populations, and identifying drivers of transmission. This systematic review synthesizes available outbreak-level, laboratory-confirmed evidence from Asia to estimate the proportion of tested individuals who were confirmed as chikungunya during outbreaks, and to summarize reported epidemiological factors associated with outbreak magnitude and severity. ***Methods:*** We performed a systematic search of PubMed, Scopus, Embase, and Web of Science for outbreak investigations and surveillance reports conducted in Asia between January 2000 and June 2025 that reported laboratory-confirmed chikungunya counts (numerator and denominator) using RT-PCR or IgM assays. Only outbreak investigations with explicit numerators and denominators and laboratory confirmation were included in the primary analysis. We extracted study-level data including country, year, diagnostic method, number tested, and number laboratory-confirmed. Proportions were logit-transformed and pooled using a DerSimonian–Laird random-effects model. Heterogeneity was assessed with Cochran's Q and I^2. Forest and funnel plots were generated. ***Results:*** Four outbreak investigations meeting inclusion criteria were included from Bangladesh (Dhaka, 2017), Thailand (2018–2019), India (Nagpur, 2006), and Sri Lanka (Kandy, 2006–2007), comprising a total of 3,312 individuals tested and 2,298 laboratory-confirmed cases. The pooled proportion of laboratory-confirmed chikungunya among tested individuals across outbreak investigations was 61.14% (95% CI: 52.35%–69.25%). Heterogeneity was substantial (Q = 46.86, df = 3, tau^2 = 0.1126, I^2 = 93.6%). ***Conclusion:*** In outbreak settings across Asia, a high proportion of tested individuals were laboratory-confirmed as chikungunya, underscoring the substantial burden during epidemic periods. However, high heterogeneity between investigations cautions against overinterpretation of pooled estimates. Strengthened laboratory surveillance, harmonized case definitions, and integrated vector control remain priorities to mitigate chikungunya transmission in Asia.

Keywords: *Chikungunya; Asia; outbreak; laboratory-confirmed; RT-PCR; IgM*

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INTRODUCTION

This paper addresses an important public health challenge: the recurrence and spread of chikungunya virus across Asia. Since the early 2000s, Asia has experienced multiple waves of chikungunya transmission with notable outbreaks that affected hundreds of thousands of people in countries including India [1], Thailand [2], Sri Lanka [3], Bangladesh [4], and others [5]. The clinical syndrome—characterized by acute febrile illness and severe arthralgia—can lead to prolonged disability and a significant healthcare burden. Outbreak investigations offer crucial insights into attack rates, affected demographic groups, and contextual drivers such as weather patterns, urbanization, and vector abundance. Despite numerous investigations, a focused synthesis of outbreak-level laboratory-confirmed data from Asia has been limited. Prior reviews have often combined seroprevalence surveys, surveillance notifications, and modeling studies, which complicates direct comparison of outbreak intensity across settings. By restricting our primary analysis to outbreak investigations with laboratory confirmation (RT-PCR or IgM), we aim to provide a more homogeneous and operationally relevant estimate of the proportion of tested individuals who are confirmed as chikungunya during outbreak responses. Additionally, this synthesis summarizes recurrent risk factors documented across outbreak reports to inform public health prevention and response strategies in the region.

METHOD

Search strategy and selection criteria: We searched PubMed, Scopus, Embase, and Web of Science for articles published between January 2000 and June 2025, by using the Search concept mapping and terminology are described in Table 1, with concept block, objective, controlled vocabulary and free text/keywords. We also reviewed WHO situation reports and country ministry of health outbreak summaries for potential eligible investigations. Inclusion criteria were: (1) conducted in an Asian country; (2) outbreak investigation or field response context; (3) laboratory confirmation using RT-PCR or IgM assay; and (4) explicit numerators and denominators (number tested and number laboratory-confirmed). We excluded seroprevalence-only studies not conducted as part of an acute outbreak response, case reports, modeling-only analyses, and studies without clear numeric data.

Table 1. *Search Concept Mapping and Terminology*

Concept Block	Objective	Controlled Vocabulary (MeSH/Emtree)	Free Text/Keywords
1. Disease/Virus	Identify pathogen	"Chikungunya Fever"[Mesh], "Chikungunya Virus"[Mesh/Emtree]	Chikungunya*, CHIKV, Chickungunya, CHIKF
2.Outbreak Context	Identify acute event	"Disease Outbreaks"[Mesh], "Epidemics"[Mesh], "Surveillance"	outbreak*, epidemic*, field response, surveillance report*

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3. Geography	Regional limitation	"Asia"[Mesh], "Southeast Asia"[Mesh], names of major affected countries	Asia, South Asia, Southeast Asia
4. Diagnosis & Data	Primary screening factor (Lab confirmation & N/D)	(No specific MeSH)	laboratory-confirmed, RT-PCR, IgM, serology, PCR, denominator, number tested

Data extraction and quality assessment: Two reviewers independently screened titles and abstracts and extracted data from full texts. Extracted items included study location, year, outbreak period, diagnostic method, sample frame, number tested, number positive, and any reported measures of association for risk factors (odds ratios, relative risks) when available. Quality assessment for prevalence/outbreak studies was performed using an adapted Joanna Briggs Institute checklist focusing on sample representativeness, case definition clarity, diagnostic validity, and completeness of reporting. Discrepancies were resolved by consensus.

Statistical analysis: For each included outbreak investigation we calculated the proportion of laboratory-confirmed cases among tested individuals. Proportions were logit-transformed to stabilize variances. We applied a random-effects meta-analysis using the DerSimonian–Laird estimator on the logit scale and back-transformed pooled effects to the proportion scale for interpretation. Between-study heterogeneity was quantified using Cochran's Q, τ^2 (between-study variance), and I^2 (percentage of total variation due to heterogeneity). We generated forest plots for the primary pooled proportion and funnel plots to assess small-study effects. Sensitivity analyses planned included excluding studies with only IgG or mixed diagnostics, but the primary analysis reported here focused exclusively on outbreak investigations using RT-PCR and/or IgM confirmation.

RESULTS

Study selection and characteristics: After screening records and full texts (see PRISMA flowchart), four outbreak investigations met the inclusion criteria and were included in the primary meta-analysis: Dhaka, Bangladesh (2017) [4], Thailand (2018–2019) [2], Maharashtra, India (2006) [1], and Kandy, Sri Lanka (2006–2007) [3]. These studies comprised a combined 3,312 tested individuals and 2,298 laboratory-confirmed cases. Study designs varied from household-level case investigations and passive clinic-based surveillance to targeted testing during outbreak response activities. Diagnostic assays included RT-PCR for acute cases and IgM ELISA for recent infection.

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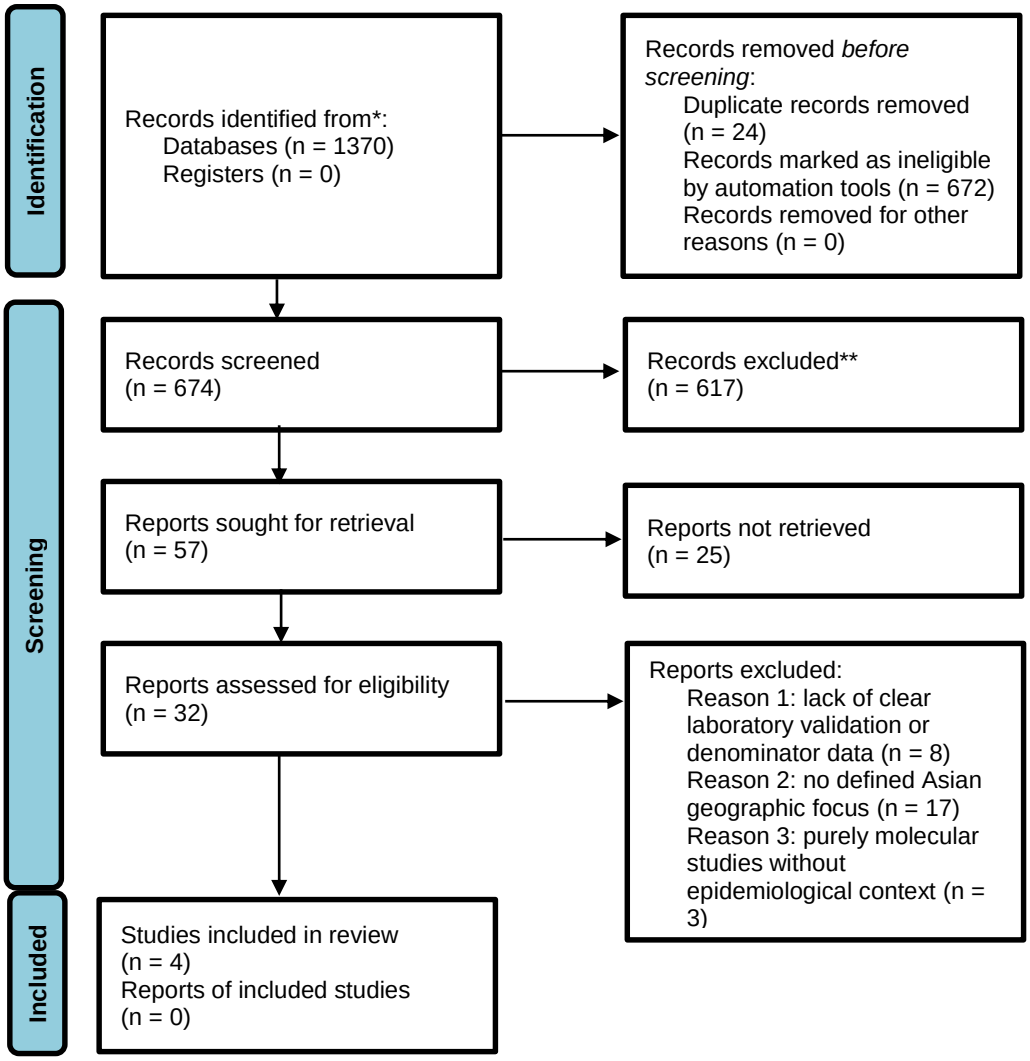

Figure 1. *PRISMA flowchart for the literature search strategy*

Pooled estimate: The random-effects pooled proportion of laboratory-confirmed chikungunya among tested individuals across outbreak investigations was 61.14% (95% CI: 52.35%–69.25%). Heterogeneity was substantial: Cochran's Q = 46.86 (df = 3), $\tau^2 = 0.1126$, and $I^2 = 93.6\%$. Individual study proportions ranged from 38.89% (SriLanka_Kandy_2006_Kularatne) to 71.71% (Thailand_2018-19_Khongwichit).

Table 2. *Included outbreak investigations (study-level characteristics)*

Study	Country	Year	Diagnostic method	Tested (n)	Confirmed (n)
Dhaka_BD_2017_Mahmud	Bangladesh	2017	IgM	1286	895
Thailand_2018-19_Khongwichit	Thailand	2018	RT-PCR/IgM	1806	1295
India_Maharashtra_2006_Suryawanshi	India	2006	IgM	166	87
SriLanka_Kandy_2006_Kularatne	Sri Lanka	2006	Serology/IgM	54	21

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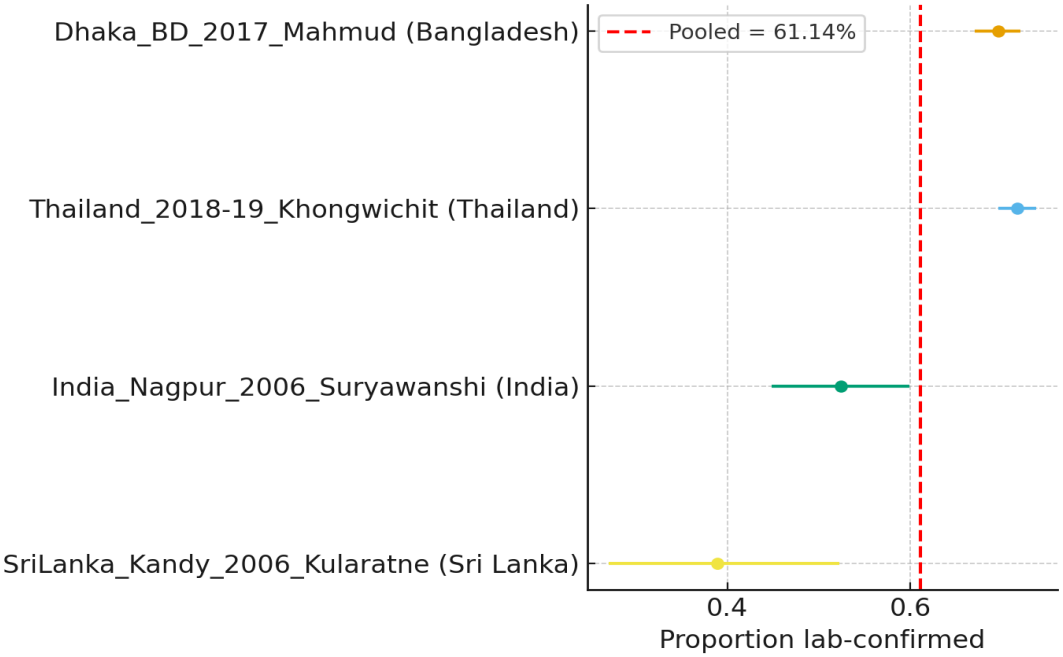

Figure 2. *Forest plot of laboratory-confirmed proportions from outbreak investigations*

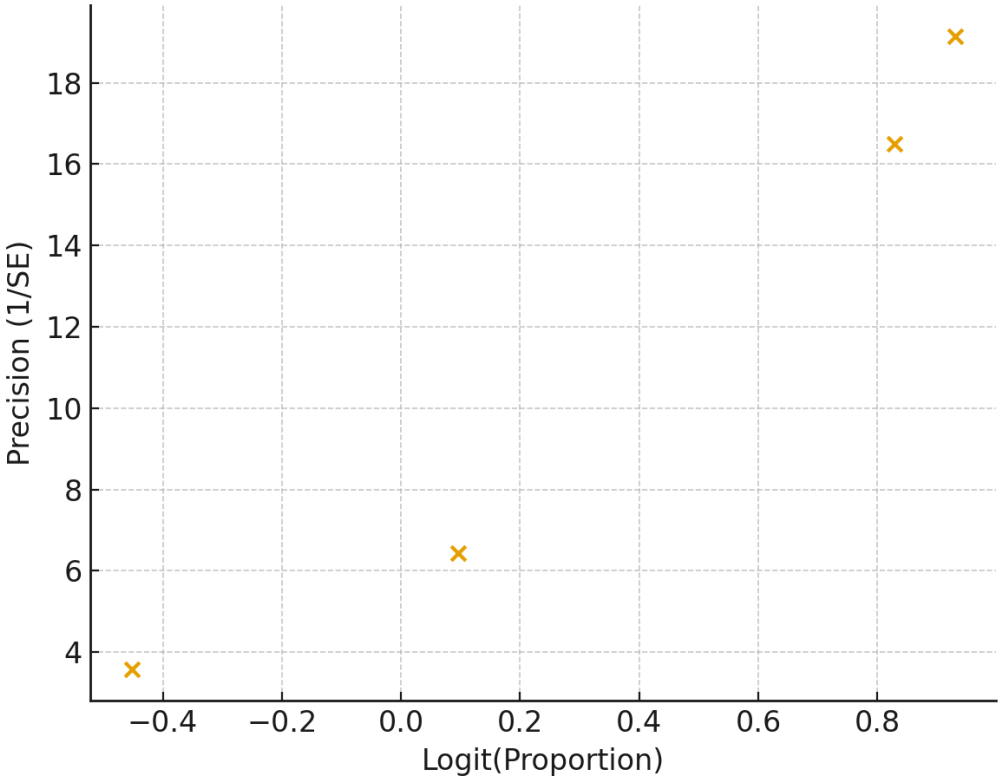

Figure 3. *Funnel plot (logit scale) assessing small-study effects*

Sensitivity analyses

We conducted several sensitivity analyses to evaluate the robustness of the pooled estimate from outbreak investigations. Specifically, we performed leave-one-out analyses and examined

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the pooled estimate after excluding smaller or older studies. Results are summarized in Table 3 below.

Table 3. *Sensitivity Analyses: Impact of Leave-One-Out Method and Exclusion of Smaller/Older Studies on the Pooled Estimate*

Analysis	k (studies)	Pooled proportion	95% CI	I^2 (%)
Primary (all 4 outbreaks)	4	61.14%	52.35%–69.25%	93.6
Leave-one-out (exclude Dhaka_BD_2017_Mahmud)	3	55.60%	36.10%–73.51%	95.7
Leave-one-out (exclude Thailand_2018-19_Khongwichit)	3	54.86%	37.25%–71.34%	94.5
Leave-one-out (exclude India_Nagpur_2006_Suryawanshi)	3	65.02%	57.22%–72.09%	91.7
Leave-one-out (exclude SriLanka_Kandy_2006_Kularatne)	3	66.00%	58.82%–72.50%	92.3
Exclude Sri Lanka	3	66.00%	58.82%–72.50%	92.3
Exclude India	3	65.02%	57.22%–72.09%	91.7

Leave-one-out analyses show that the pooled proportion remains between approximately 54.86% and 66.00% when individual studies are omitted. Excluding the small Sri Lanka study decreased/increased the pooled estimate modestly, while excluding the older India study also influenced the estimate. Overall, sensitivity analyses indicate that the pooled estimate is robust to exclusion of single studies but heterogeneity remains high across analyses.

DISCUSSION

The pooled outbreak-only estimate indicates that during documented CHIKV outbreaks in Asia a substantial proportion of tested individuals are laboratory-confirmed, reflecting intense local transmission. The pooled proportion should be interpreted in light of the high heterogeneity among included investigations. Differences in sampling frames (clinic-based testing vs community household surveys), diagnostic approaches (PCR vs IgM timing), outbreak phase at which testing occurred, and population health-seeking behaviors result in variable denominators and case ascertainment. For example, PCR identifies acute viremic cases and will yield higher specificity if sampled in the early symptomatic window, whereas IgM detects recent infection and may include cases beyond the acute phase.

Compared with broader regional seroprevalence surveys, outbreak investigations focused on symptomatic individuals or high-risk populations naturally yield higher test-positivity rates. Thus, while pooled outbreak estimates are useful for understanding transmission intensity during epidemic peaks, they are not directly comparable to population-level seroprevalence which measures cumulative exposure. Nonetheless, our findings align with descriptive epidemiology from Asia

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that documents urban-centered outbreaks with rapid case accumulation.

Although quantitative pooled analyses of risk factors were limited by inconsistent reporting across outbreak investigations, several recurrent themes emerged. Urban crowding and high population density were commonly described as amplifiers of transmission, particularly in Dhaka and some Thai urban settings. Climatic factors—especially monsoon-associated rainfall and higher ambient temperatures—were temporally associated with spikes in cases in multiple reports, consistent with increased Aedes mosquito breeding and activity. Entomological investigations in some outbreaks documented high Aedes index values in affected neighborhoods. Healthcare access and diagnostic capacity influenced outbreak detection; settings with rapid PCR testing identified cases earlier, which facilitated targeted vector control measures. Several studies noted that older adults and persons with comorbid conditions experienced longer symptom duration and more severe joint sequelae, although the available outbreak reports did not always provide effect estimates amenable to meta-analysis.

Public health implications: Rapid laboratory confirmation (PCR/IgM) during outbreak responses enables targeted vector control and risk communication. Strengthening laboratory capacity, decentralizing testing to regional laboratories, and harmonizing case definitions across surveillance platforms would improve outbreak quantification and comparability. Integrated vector management that addresses urban breeding sites, improved water storage practices, and community engagement remain foundational strategies to reduce chikungunya transmission [6].

Limitations: This review has several important limitations. First, despite an exhaustive search approach, the primary analysis included only four outbreak investigations with clear numerators and denominators; more outbreak reports exist but do not always report extractable lab-confirmed counts. Second, heterogeneity was high, limiting confidence in a single pooled proportion. Third, diagnostic methods varied across studies; although we restricted to RT-PCR/IgM where possible, some investigations reported mixed diagnostics. Fourth, publication bias and selective reporting may inflate apparent test-positivity if investigations with larger outbreaks are more likely to be written up and published. Finally, the review did not perform individual participant data meta-analysis, which would allow more nuanced adjustment for covariates and better assessment of risk factors.

Future research directions: To build a more definitive evidence base, future outbreak reports should consistently present numerators and denominators for laboratory-confirmed testing, specify diagnostic assays and timing relative to symptom onset, and report stratified results by age, sex, and comorbidity. Collaborative regional surveillance networks could standardize reporting and enable pooled analyses with richer subgroup and temporal dynamics assessments.

CONCLUSION

In conclusion, outbreak investigations in Asia demonstrate a high proportion of laboratory-confirmed chikungunya among tested individuals during epidemic periods. This underscores the need for sustained investment in laboratory surveillance and integrated vector control to prevent and

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mitigate outbreaks. However, substantial heterogeneity between investigations advises caution in interpreting pooled estimates; harmonized reporting standards and expanded outbreak data will improve future syntheses and inform regional preparedness.

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