International Journal of Biological Innovations
http://ijbi.org.in | http://www.gesa.org.in/journals.php
https://doi.org/10.46505/IJBI.2025.7212
IJBI 7(2): 202-210 **(2025)**
E-ISSN: 2582-1032

CHIKUNGUNYA AND DENGUE CO-INFECTION IN INDIA: A SYSTEMATIC REVIEW AND META-ANALYSIS

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Article Info:
Review article
Received
03.07.2025
Reviewed
15.08.2025
Accepted
27.08.2025

Abstract: Dengue and chikungunya co-infections are increasing in India due to their shared vector *Aedes* mosquito. The overlap of clinical symptoms often results in cases of chikungunya going undiagnosed in regions where dengue is endemic. This study offers an extensive meta-analysis of the occurrence of chikungunya and chikungunya-dengue coinfection across seven different Indian states: Tamil Nadu, Odisha, New Delhi, Punjab, Telangana, Karnataka, and Gujarat. This analysis compiled data from 16 peer-reviewed articles and employed graphical, tabular, and chart-based techniques to represent the trends and prevalence rates. The findings indicated that New Delhi (~61.7%) had the highest chikungunya incidence rates, while Punjab (~32.4%) had recorded the highest chikungunya-dengue co-infection rates in relation to the overall sample. These results emphasize notable geographical differences in infection patterns and point to potential hotspots that may need targeted public health measures. The study highlights the importance of future research to investigate the links between environmental factors and infection rates, which could aid in developing more effective strategies for preventing and controlling vector-borne diseases in India.

Keywords: *Aedes*, chikungunya, chikungunya dengue co-infection, Disease, India, Vector.

Cite this article as: Siwal N., Mishra A. and Panwar A. (2025). Chikungunya and Dengue co-infection in India: A systematic review and Meta-analysis. *International Journal of Biological Innovations*. 7(2): 202-210. https://doi.org/10.46505/IJBI.2025.7212

INTRODUCTION

The vector-borne diseases continue to pose substantial public health challenges in tropical and subtropical regions, with countries like India bearing a considerable burden of arboviral infections (Kaur *et al.,* 2017; Dey *et al.,* 2023). Among the most prevalent are dengue and chikungunya: mosquito-borne viral diseases transmitted primarily by *Aedes aegypti* and *Aedes albopictus* (Afreen *et al.* 2014). These viruses frequently co-circulate during the monsoon and post-monsoon periods, resulting in concurrent outbreaks that pose challenges to clinical diagnosis and management, while placing considerable strain on the public health infrastructure (Monira, 2020).

Dengue, caused by four different serotypes of the dengue virus (DENV 1-4), is closely associated with a broad clinical spectrum ranging from asymptomatic infection to severe forms such as dengue hemorrhagic fever and dengue shock syndrome (Hasan *et al.* 2025). Chikungunya, on the other hand, caused by the chikungunya virus (CHIKV), is known for acute febrile illness and persistent polyarthralgia. The similarity in clinical manifestations especially fever, rash, and joint pain finally poses a diagnostic challenge, particularly in resource-limited settings (Powers and Logue, 2007). These diseases share several clinical signs, such as fever, joint pain, rash, nausea, vomiting, and fatigue (Lahariya and Pradhan, 2006). The likelihood of co-infections increases due to the mosquitoes' feeding habits in regions where both viruses are present (Nunes *et al.,* 2015). Since the clinical symptoms of both viruses are alike, CHIKV infections may go undiagnosed in areas where DENV is endemic (Chahar *et al.,* 2009).

Coinfection with dengue and chikungunya has emerged as a significant epidemiological concern in India, a country with endemic transmission of both viruses. Numerous studies have reported the prevalence and clinical outcomes of these infections separately; however, the landscape of coinfection remains inadequately understood (Furuya-Kanamori *et al.,* 2016; Salam *et al.,* 2018). The simultaneous occurrence of both viruses in a single host can potentially alter disease severity, immune response, and treatment outcomes.

Present systematic review and meta-analysis aim to integrate literature published between 2006 and 2024 to evaluate the prevalence, geographic distribution, clinical characteristics, and public health implications of dengue and chikungunya co-infection in India. Drawing on evidence from the past two decades, this study aims to provide a comprehensive understanding of the syndemic interaction among these diseases and to guide future efforts in surveillance, diagnosis, and policy development.

MATERIALS AND METHODS

This study is a systematic review and meta-analysis conducted according to the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. The objective was to assess the prevalence, clinical features, diagnostic challenges, and outcomes of chikungunya and dengue virus coinfection cases reported in India between January 2006 and March 2024. Following inclusion criteria was included: multiple states in India where this type of study was conducted, article published between January 2006 and March 2024, the reporting cases of laboratory-confirmed co-infection with both dengue and chikungunya viruses, authors included observational studies including cross-sectional, cohort, and case-control designs and only those studies which are published in English.

A comprehensive literature was searched in the following electronic databases: like PubMed/ MEDLINE, Scopus, Web of Science, Google Scholar, EMBASE and IndMED. The keywords and medical subject headings (MeSH) used during study survey includes chikungunya, dengue, co-infection, India, epidemiology, and prevalence. The Boolean operators AND/OR were used to refine the search. Additional studies were identified through manual screening of reference lists of relevant articles and gray literature. The exclusion criteria included in this study were based on:

a) Case studies, review articles, editorials, and conference abstracts
b) Studies lacking laboratory confirmation of both viruses.
c) Studies not specifying the Indian population.
d) Duplicate studies or overlapping datasets.

For data extraction/collection, the two reviewers independently screened titles and abstracts, followed by full-text exploration. A standardized data extraction form was used to collect the following information: like, author (s), year of publication, study design and location, sample size, diagnostic methods used (e.g., RT-PCR, IgM ELISA), number and proportion of coinfected cases, demographic characteristics and the clinical features and outcomes. This data was systematically organized in a Prisma flow chart (Fig. 1), Microsoft Excel sheet, formatted into tables (Table 1) and Venn diagram (Fig. 2), visual representations (including map), pie chart (Fig. 3), clustered column and line graph line (Fig. 4) for analytical purposes.

Furthermore, a statistical relationship was seen/ identified between the cases positive for chikungunya and those involving coinfection with chikungunya and dengue, based on calculations utilizing the Pearson Correlation Coefficient.

RESULTS AND DISCUSSION

A comprehensive search initially yielded a total 216 publications after removing the duplicate articles relevant to the investigation of dengue, chikungunya and chikungunya-dengue co-infections. After a comprehensive screening, 108 records were excluded as full-text access was restricted by pay walls or access limitations (Fig. 1). Following an initial identification of 80 publications, a multi-stage exclusion process was applied. First, 29 studies were removed as they reported data from countries outside India, which fell beyond the scope of this review. Subsequently, 13 studies were excluded due to reliance solely on clinical presentation or microscopic diagnosis without laboratory confirmation (e.g., PCR or serology), failing to meet the required diagnostic standard for confirmed coinfection.

Furthermore, 8 studies were eliminated as they were review articles and did not present original data. Finally, an additional 4 publications were excluded because they provided only national-level data without specifying Indian states or regions, thus lacking the geographic granularity required for our analysis. This rigorous screening resulted in a final inclusion of 26 studies for data extraction and synthesis.

The study selection process, encompassing data gathering, screening, processing, and analytical outcomes, is depicted in the PRISMA flowchart (Fig. 1). These studies encompassed both isolated cases of chikungunya and cases of chikungunya-dengue coinfection, offering a highly valuable epidemiological insight across seven Indian states: Tamil Nadu, Odisha, Karnataka, New Delhi, Telangana, Punjab, and Gujarat. The time frame of data collection spans ranging from 2006 to 2024, capturing nearly two decades of nicely reported incidence and providing a longitudinal perspective on co-infection trends within the country; shown in Table 1.

Importantly, the scope of this analysis is not confined by age or gender, thereby representing a broader demographic spectrum and such representation strengthens the applicability of the findings across the Indian population. Most of the included studies employed enzyme-linked immunosorbent assay (ELISA) and polymerase chain reaction (PCR) as their primary diagnostic techniques. These laboratory methods are well-established for their sensitivity and specificity, and their frequent usage underscores a consistent methodological approach among researchers for the accurate identification of chikungunya and dengue virus infections. This reliance on standardized diagnostic tools enhances the reliability and comparability of findings across studies, making the data robust for drawing meaningful conclusions about coinfection prevalence and patterns.

A Venn diagram (Fig. 2) illustrates the case distribution, including the total sample (n = 59,438), chikungunya mono-infections (n = 8,379), and chikungunya-dengue coinfections (n = 547). Analysis of chikungunya (CHIKV) and chikungunya-dengue coinfection cases across seven Indian states (2006–2024) revealed distinct geographic trends, as shown in figure 3. Out of the total sample, authors found that New Delhi exhibited the highest burden of CHIKV infections alone, with 61.7% of cases relative to its sample size, followed by Gujarat (38.8%) and Odisha (33.2%). In contrast, Punjab (32.4%) and New Delhi (29.4%) reported the highest coinfection rates. Notably, New Delhi emerged as the only state with elevated rates of both CHIKV alone and coinfection, underscoring its dual public health challenge.

The Pearson correlation coefficient between CHIKV-positive cases and coinfection cases was 0.3535, indicating a weak positive association. The relationship was not statistically significant ($p = 0.437$), indicating no sufficient evidence to reject the null hypothesis at the 0.05 level. This suggests that the observed correlation may arise from random variation rather than a systematic linkage between the CHIKV incidence and coinfection risk across states.

Table 1: The data collected on chikungunya and chikungunya-dengue coinfection burden in 7 states of India (retrieved from 16 different research papers spanning from 2006 to 2024).

S. No.	States	Population co-ordinates	Total sample	Positive cases	Coinfection with dengue	References
1.	Tamil Nadu	13°N 80.27°E 10°N 77.47°E	13454 16997	1589 388	103	Balasubramaniam *et al.* (2011); Gopinath *et al.* (2023)
2.	Odisha	20.95 °N85.09 °E 20.18 °N 85.61°E 20.29 °N 85.82°E	678 204 5198	174 28 1816	28	Mohanty *et al.* (2013) Saswat *et al.* (2015) Subhadra *et al.* (2021)
3.	Telangana	18 °N 79.58 °E 17.82 °N 79.18°E	3344 11768	313 2365	153\2103	Sreedevi and Krishna (2023) Vatkuri *et al.* (2021)
4.	New Delhi	28.56 °N 77.28°E 28°N 77 °E 28 °N 77 °E	65 200 600	26 77 525	5\55 23 152	Hisamuddin *et al.* (2018) Abhishek and Chakravarti (2019) Kaur *et al.* (2017)
5.	Gujarat	23.25 °N 69.66°E 23 °N 72.58 °E	305 1430	55 618	6	Chotaliya *et al.* (2024) Patel *et al.* (2023)
6.	Karnataka	11.92 °N 76.94°E 12.97 °N 77.59°E	1308 547	123 55	1	Naik *et al.* (2018) Ashokumar *et al.* (2025)
7.	Punjab	31 °N 74 °E 31.63 °N 74.87°E	370 373	142 127	34 27\283	Awal and Swu (2024) Kaur *et al.* (2018)

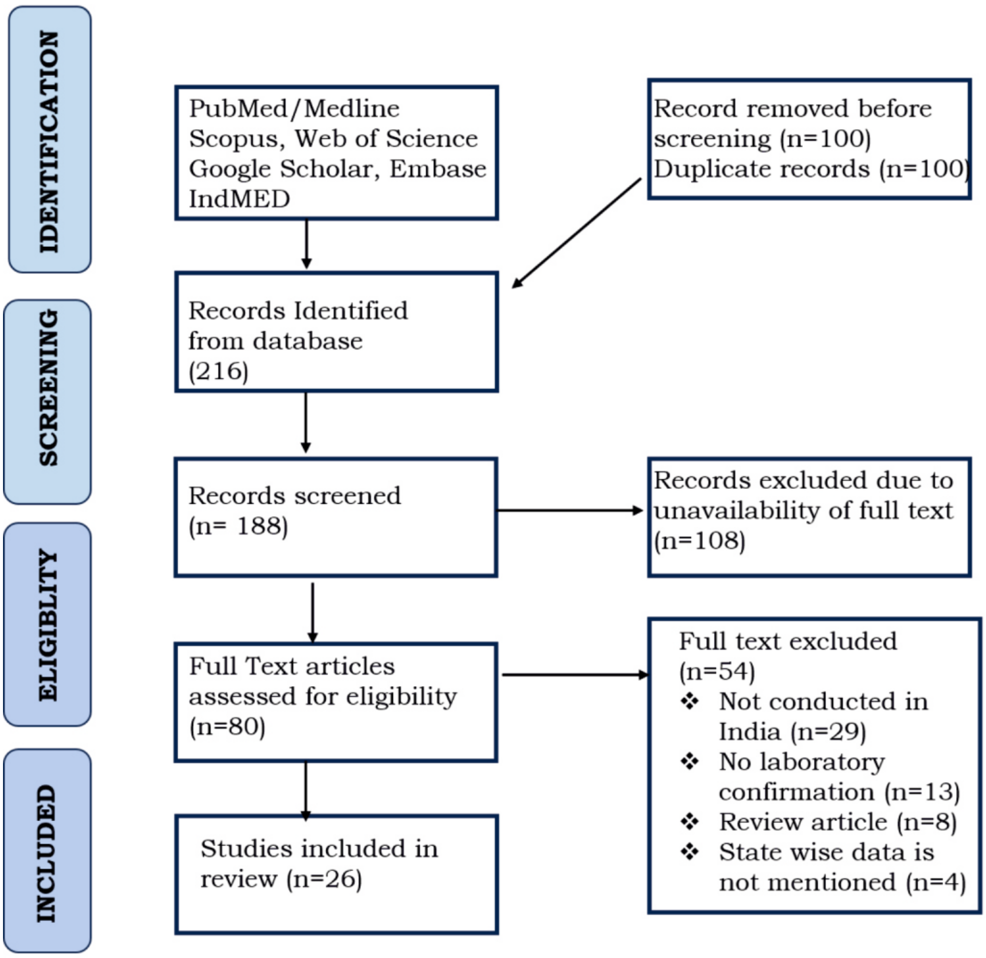

Fig. 1: Flowchart representation of data collection, screening, processing and data analysis steps involved.

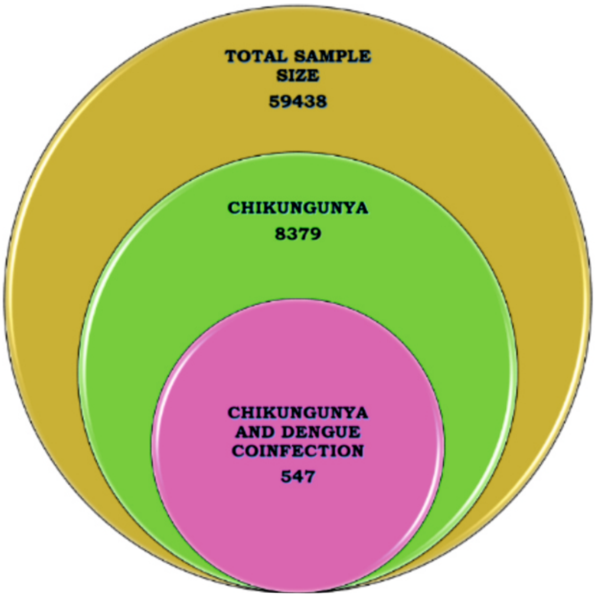

Fig. 2: Venn diagram- style nested circle chart illustrating the proportion of chikungunya-dengue co-infected cases within the context of both total sample size and chikungunya-specific cases. The outermost red circle represents the total sample size (59,438). The middle green circle comprises exclusively of chikungunya-only cases (8,379). Finally, the innermost yellow circle depicts the chikungunya-dengue coinfection cases (547).

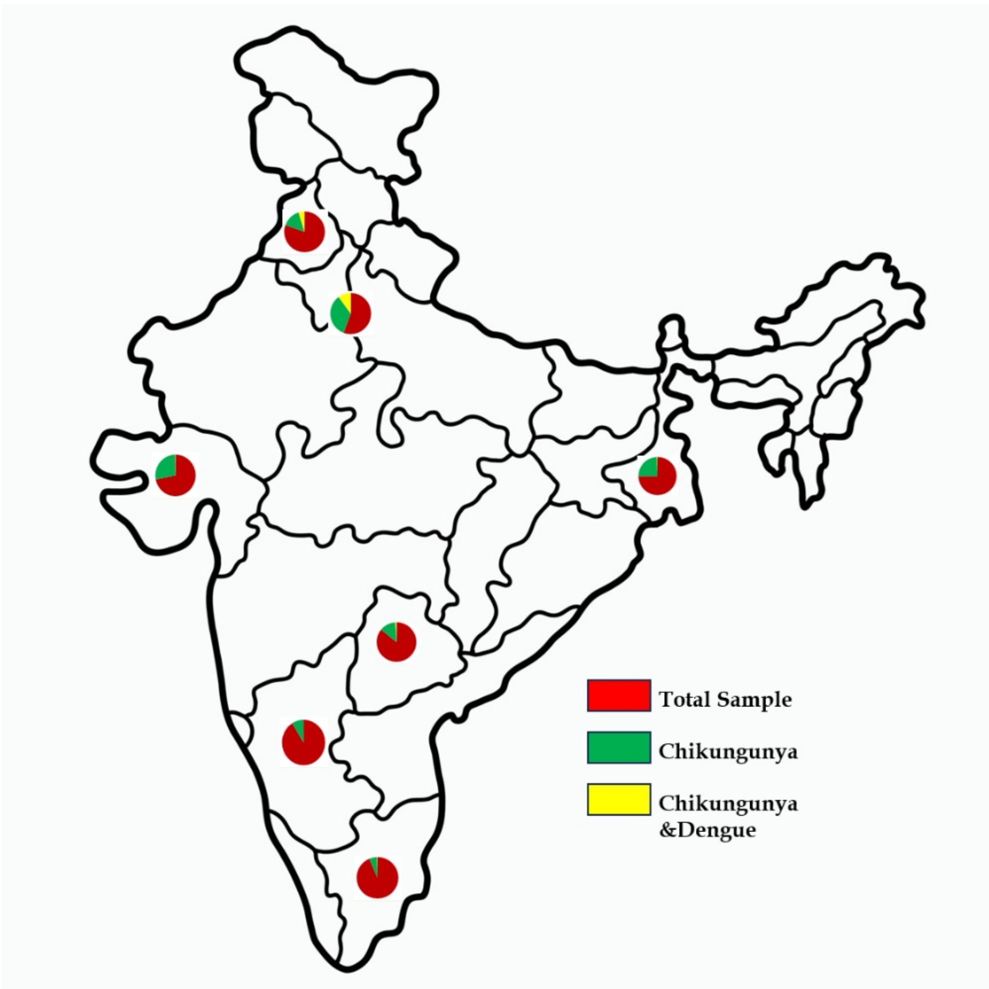

Fig. 3: A map of India depicting the burden of chikungunya and chikungunya-dengue coinfections across selected states from year 2006 to 2024.

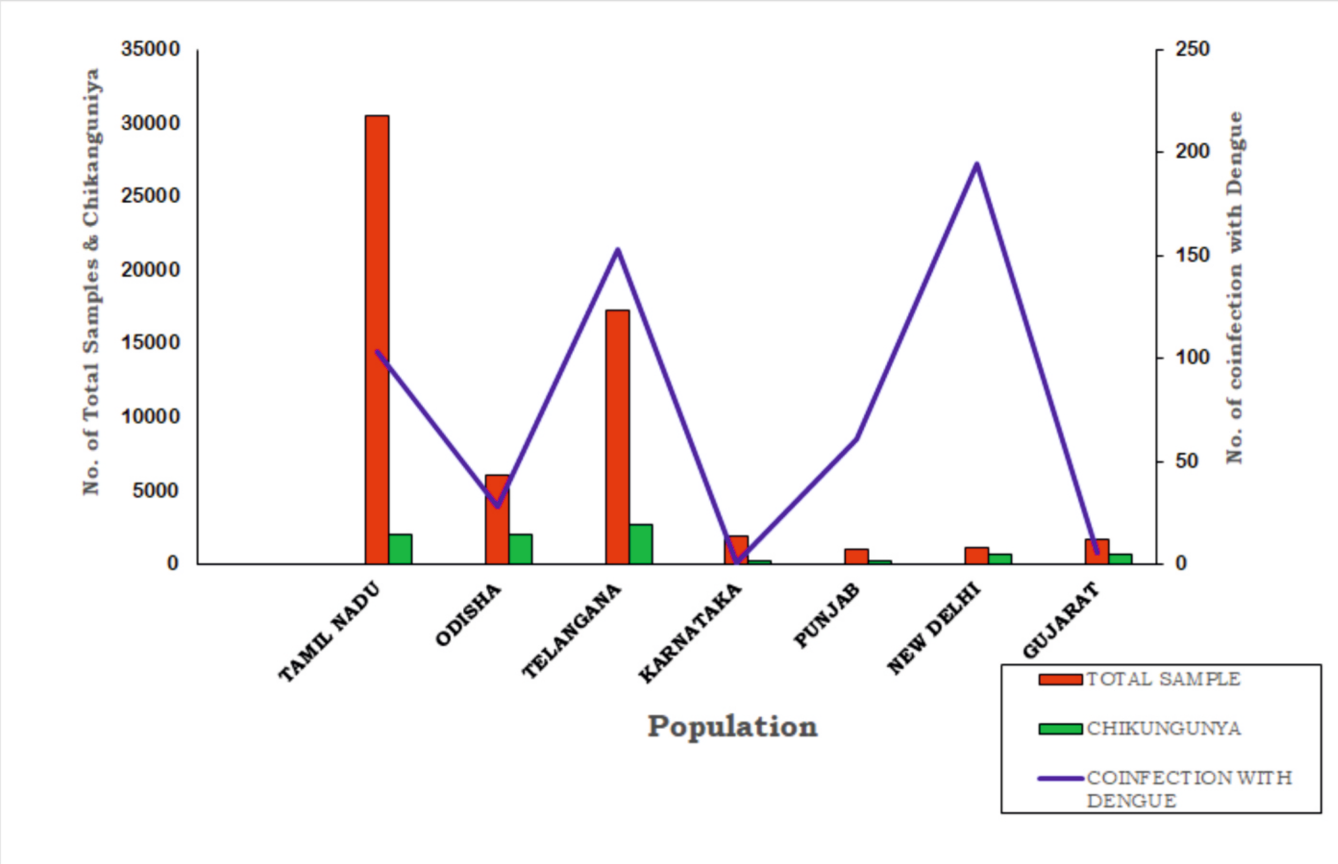

Fig. 4: Clustered column and line graph. This graph provides a comparative visual representation of chikungunya and chikungunya-dengue co-infection data across seven Indian states using both bar and line elements. X-axis represents different Tamil Nadu, Odisha, Telangana, Karnataka, Punjab, New Delhi, and Gujarat. Primary Y-Axis (left side) represents the number of individuals (0 to 35,000) for: Red bars: indicates the total sample size per state. 2. Green bars: indicates the number of Chikungunya-positive cases per state. Secondary Y-Axis (right side): Represents the number of co-infections (0 to 250) for blue line: indicates the number of Chikungunya and Dengue co-infections.

The findings highlight a significant regional disparity among CHIKV and co-infection epidemiology across the India. New Delhi's prominence in both CHIKV and coinfection rates may clearly reflect overlapping ecological and demographic factors, such as high population density, widespread *Aedes aegypti* mosquito prevalence, and urban environmental conditions conducive to arboviral transmission. However, the weak, non-significant correlation between CHIKV and coinfection rates across all seven states implies that high CHIKV incidence does not inherently predict coinfection burden. For instance:

a) Punjab's high coinfection rate (32.4%) contrasts with its absence from the top CHIKV-alone list, perfectly suggesting localized dengue transmission dynamics or diagnostic practices that favor coinfection detection, as shown in figure 4.

b) Gujarat and Odisha, despite high CHIKV rates, exhibited clearly lower co-infection rates, potentially due to temporal or spatial mismatches in dengue and CHIKV outbreaks, differences in vector species dominance, or population immunity, as shown in figure 4.

The non-significant correlation (*p* = 0.437) further challenges assumptions of a universal relationship between CHIKV incidence and coinfection risk. This aligns with studies highlighting the role of stochastic factors such as outbreak timing, diagnostic bias, or cross-protective immunity in shaping coinfection patterns. For example, simultaneous circulation of both viruses during overlapping transmission seasons may increase coinfection likelihood in specific regions, such as New Delhi, but not in others.

CONCLUSION

This study examined 26 eligible and authentic publications from 2006 to 2024, concentrating on chikungunya and chikungunya-dengue coinfections across seven Indian states. From an initial pool of 216 records, rigorous inclusion criteria were applied to ensure relevance, accessibility, and a regional focus. The findings indicate that New Delhi consistently reported the highest incidence of chikungunya alone (~61.7%) and chikungunya-dengue coinfection (~29.4%), highlighting a significant public health concern in the capital of India. Gujarat and Odisha (western and eastern region of India) also demonstrated notably high chikungunya positivity rates, whereas Punjab exhibited a disproportionately high coinfection rate relative to its chikungunya cases. Statistical analysis revealed a weak positive correlation ($r = 0.3535$) between chikungunya and coinfection cases; however, this relationship was not statistically significant ($p = 0.4367$). This suggests that while coinfection may co-occur with high chikungunya incidence in certain regions, it does not follow a predictable or consistent pattern across all states. Overall, these insights underscore the necessity for state-specific surveillance and control strategies. Additionally, further studies could explore the relationship between environmental factors and disease in regions with high chikungunya incidence to develop effective control strategies addressing both chikungunya and its potential overlap with dengue infections.

LIMITATIONS

This systematic review and meta-analysis provide a compelling evidence of the co-circulation and co-infection of chikungunya and dengue viruses in India from 2006 to 2024. The findings highlight a significant public health concern, particularly in endemic regions where overlapping outbreaks frequently strain the diagnostic, clinical, and surveillance capacities. Coinfection cases often exhibit overlapping clinical presentations, complicating accurate diagnosis and timely treatment, and in some instances, have been associated with increased disease severity. This review indicates that coinfection is not a rare event and may be underreported due to diagnostic limitations and lack of integrated vector surveillance. The co-endemicity of Aedes mosquito vector further exacerbates the risk, especially during monsoon seasons. These findings underscore the urgent need for improved/updated diagnostic protocols, integrated vector management strategies, and public health awareness campaigns.

Future research should prioritize elucidating the immunopathogenesis of coinfections, so that clinical outcomes related to mono-infections, and developing rapid multiplex diagnostic tools especially for coinfection detection can be established properly. Strengthening coordinated surveillance and response systems is critical to mitigate the impact of these concurrent arboviral threats in countries like India.

However, it is important to acknowledge that this systematic review and meta-analysis have several limitations. Firstly, substantial heterogeneity was clearly observed among the included studies, attributable to differences in study design, diagnostic methods, geographical distribution, and sample sizes. Many studies relied on serological tests, which may have limited specificity and can result in cross-reactivity between dengue and chikungunya viruses, potentially affecting the accuracy of coinfection rates. Additionally, there was a clear cut lack of standardized definitions and reporting protocols across studies, making direct comparisons difficult. The temporal and seasonal patterns of outbreaks were not consistently addressed, which may influence coinfection prevalence but could not be accounted for. Furthermore, some publication bias might be present, as studies with significant findings are more likely to be published, and some relevant data from unpublished or non-English sources may have been neglected. And last but not the least, the evolving epidemiology and surveillance systems over the nearly two-decade span may have introduced inconsistency in data quality and completeness.

ACKNOWLEDGEMENT

Authors would like to express heartfelt gratitude to Prof. Sangeeta Avasthi, Head of the Zoology Department, AND NNM Mahavidyalaya, Kanpur, India for continuous motivation and valuable suggestions while preparing this manuscript.

CONFLICT OF INTEREST

Authors declare that there is no competing interest regarding this article.

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