e-ISSN: 0976-822X, p-ISSN:2961-6042

Available online on http://www.ijcpr.com/

International Journal of Current Pharmaceutical Review and Research 2026; 18(8); 1250-1258

Original Research Article

Dual Threat: Assessing the Impact of Dengue and Chikungunya Co-Infections on Hospital Admissions in Tertiary Care Hospital in Pune

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Received: 01-05-2026 / Revised: 15-06-2026 / Accepted: 21-07-2026
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Conflict of interest: Nil

Abstract

Background: Vector-borne diseases like dengue and chikungunya pose significant public health challenges in Pune. Despite their endemic nature, comprehensive data on their seroprevalence and clinical manifestations remain limited, particularly regarding co-infections.

Objective: To investigate the seroprevalence and clinical profile of dengue, chikungunya, and their co - infections in tertiary care hospitals of Pune.

Methods: We conducted a retrospective analysis of medical records from tertiary care hospitals across Pune between January 2022 and December 2024. Serological confirmation was done using ELISA for dengue NS1 antigen, IgM, and IgG antibodies, and chikungunya IgM antibodies. Clinical and laboratory parameters were analyzed using appropriate statistical methods.

Results: Among 569 patients included in the study, dengue seroprevalence was 21.65%, chikungunya 13.71%, and co-infections 7.26%. Dengue patients predominantly presented with fever (98.61%), headache (86.22%), retro-orbital pain (72.1%), and thrombocytopenia (68.9%). Chikungunya cases typically manifested with high-grade fever (97.8%), severe arthralgia (94.2%), and characteristic rash (67.5%). Co-infected patients exhibited more severe clinical manifestations, with significantly higher rates of hemorrhagic complications ($p<0.01$) and prolonged hospitalization (mean 6.8 days vs. 4.2 days for mono-infections, $p<0.001$). Age >60 years, presence of comorbidities, and delayed presentation (>5 days) were identified as significant risk factors for severe disease.

Conclusion: Our findings highlight the substantial burden of dengue and chikungunya in Pune, with co-infections presenting unique diagnostic and therapeutic challenges. The distinct clinical profiles identified can aid clinicians in early recognition and appropriate management. Enhanced surveillance, vector control measures, and public awareness campaigns are urgently needed to reduce the disease burden in this endemic region.

Keywords: Dengue, Chikungunya, Co-infection, Seroprevalence, Pune, Clinical profile.

DOI: 10.25258/ijcpr.18.8.187

Introduction

Dengue and Chikungunya are two mosquito-borne viral infections that have emerged as major global health concerns, particularly in tropical and subtropical regions where environmental conditions favor the proliferation of Aedes mosquitoes. These diseases are transmitted by the same mosquito species, primarily Aedes aegypti and Aedes albopictus, which thrive in urban and semi-urban areas. [1] The increasing incidence of these infections over recent decades can be attributed to several interconnected factors. Rapid urbanization has created densely populated areas with poor waste management and stagnant water, providing ideal breeding grounds for mosquitoes. Climate change, with rising temperatures and altered rainfall patterns, has further expanded the habitats of these vectors, allowing them to survive in regions previously unsuitable for their survival. Additionally, globalization and increased human mobility have facilitated the spread of these diseases to new areas, making them a growing concern for public health systems worldwide. Dengue, caused by the Dengue virus (DENV), is a flavivirus with four distinct serotypes (DENV 1 to

DENV 4). [2] The disease manifests in a wide clinical spectrum, ranging from mild febrile illness to severe and potentially life-threatening complications such as Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS). [3] The initial symptoms often include high fever, severe body pain, retro-orbital pain, rash, and, in severe cases, bleeding tendencies. A unique challenge with Dengue is the phenomenon of antibody-dependent enhancement (ADE), where a secondary infection with a different serotype can lead to more severe disease outcomes. This occurs because pre-existing antibodies from the first infection may enhance the replication of the new serotype, exacerbating the immune response and increasing the risk of severe complications.

Chikungunya, on the other hand, is caused by the Chikungunya virus (CHIKV), an alphavirus. The disease is characterized by an acute febrile illness accompanied by severe joint pain or arthritis, which can persist for months or even years in some cases. [4] While Chikungunya is not associated with high mortality rates, its long-term effects on joint health can significantly impair the quality of life for affected individuals. The debilitating nature of the disease, even after the acute phase has resolved, poses a substantial burden on individuals and healthcare systems in endemic regions.

In areas where both Dengue and Chikungunya are endemic, co-infections with both viruses are increasingly being reported. These co-infections present unique clinical challenges, as the symptoms of the two diseases often overlap and can mimic other febrile illnesses such as Zika virus infection, malaria, and leptospirosis. This overlap complicates the diagnostic process, making it difficult for healthcare providers to accurately identify and treat the underlying cause of illness. Furthermore, co-infections may alter the typical clinical course of each disease, potentially leading to more severe outcomes or unexpected complications.

Despite the growing recognition of Dengue Chikungunya co infections, there is limited data on their prevalence and impact on disease severity and patient outcomes.

This lack of information poses significant challenges for public health efforts, as misdiagnosis or delayed identification of severe cases can result in suboptimal patient management and increased morbidity. Understanding the seroprevalence of Dengue,

Chikungunya, and their co-infections is therefore essential for improving epidemiological surveillance. [5] By identifying trends in infection rates, seasonal variations, and population susceptibility, public health authorities can better predict and respond to outbreaks. Additionally, enhanced diagnostic capabilities are needed to differentiate between Dengue, Chikungunya, and co-infections based on laboratory and clinical findings. This would enable more accurate and timely diagnoses, ultimately leading to better patient outcomes. Finally, optimizing patient management strategies by tailoring treatments to the severity and complications of these infections is critical for reducing the burden of these diseases on affected communities. Through a combination of improved surveillance, diagnostics, and treatment approaches, it is possible to mitigate the impact of Dengue and Chikungunya and enhance the resilience of healthcare systems in endemic regions.

Methodology

Study Design and Setting: We conducted a retrospective observational study analyzing clinical and laboratory records of patients diagnosed with dengue virus (DENV) infection, chikungunya virus (CHIKV) infection, or co infection. The study was carried out across tertiary care hospitals in Western Maharashtra, India, over a period of three years between January 2022 and December 2024. These hospitals serve a broad and diverse population, representing varied geographic and demographic characteristics of the region.

Ethical approval for the study was obtained from the Institutional Ethical Committee. Given the retrospective nature of the study and the use of anonymized patient data, the requirement for written informed consent was waived.

Patient Selection: All consecutive patients of any age presenting with acute febrile illness suggestive of dengue or chikungunya infection (e.g., fever, arthralgia, rash) and who underwent serological testing during the study period were screened for inclusion.

Inclusion Criteria:

- Laboratory confirmation of DENV infection by positive non-structural protein 1 (NS1) antigen and/or anti DENV immunoglobulin M (IgM) antibody using enzyme linked immunosorbent assay (ELISA).
- Laboratory confirmation of CHIKV infection by positive anti CHIKV IgM antibody using ELISA.

Exclusion Criteria:

- Incomplete or missing medical records.
- Laboratory confirmed alternative causes of febrile illness (e.g., malaria, leptospirosis, or other infections).

Laboratory Diagnostics: Serological testing for dengue (NS1 antigen, IgM, and IgG antibodies)

and chikungunya (IgM antibodies) was performed using commercially available ELISA kits, (J Mitra & Co Private Limited, Delhi, India), following the World Health Organization (WHO) guidelines. Optical density cut off values were interpreted according to the manufacturer's instructions.

Routine laboratory investigations, including complete blood counts and biochemical parameters (liver and renal function tests), were conducted using automated analyzers (Coulter DXH 560 haematology analyser by Beckman Coulter, USA; and UNIKON 230 Fully Automatic Biochemistry Analyzer, by Vector Biotek, Navsari, India respectively) in ISO 15189 accredited laboratories, ensuring quality and standardization of results.

Data Collection: Data were systematically extracted from electronic medical records using a standardized case report form. The following variables were collected:

- Demographics: Age, sex, and geographical location/residence.
- Clinical Features: Presenting complaints, duration of illness prior to presentation, vital signs, and physical examination findings.
- Laboratory Indices: Dengue serological markers (NS1, IgM, IgG), CHIKV IgM serology, automated cell counts (platelets, hematocrit, leukocyte counts), and biochemical profiles (ALT, AST, serum creatinine, blood urea nitrogen).
- Clinical Outcomes: Length of hospital stay (days), severe disease manifestations (e.g., severe plasma leakage, dengue hemorrhagic fever, expanded dengue syndrome, persistent arthralgia, and circulatory shock), intensive care unit (ICU) admission, and discharge status (recovered/out of hospital mortality).

To ensure data accuracy and consistency, all records were reviewed and cross-validated by trained investigators.

Case Definitions: Patients were categorized into mutually exclusive diagnostic groups according to the following predefined criteria:

- DENV Mono infection: Positivity for DENV non-structural protein 1 (NS1) antigen and/or anti DENV immunoglobulin M (IgM) antibody by enzyme linked immunosorbent assay (ELISA), with negative anti CHIKV IgM. [6,7,8]
- CHIKV Mono infection: Positivity for anti CHIKV IgM antibody by ELISA, with negative DENV NS1 antigen and anti DENV IgM. [9,10]
- DENV CHIKV Co infection: Concurrent laboratory evidence of DENV infection (positive DENV NS1 antigen and/or anti DENV IgM) and CHIKV infection (positive anti CHIKV IgM). [6,7,8,9,10]
- Symptomatic dengue cases were classified as dengue (with or without warning signs) or severe dengue to facilitate dengue clinical management as per WHO guidelines. [11]

Statistical Analysis: Statistical analyses were performed using SPSS software version 26.0 (IBM Corp., Armonk, NY, USA). Continuous variables were summarized as mean ± standard deviation (SD) for normally distributed data or median with interquartile range (IQR) for non-normally distributed data, as assessed using the Shapiro Wilk test. Categorical variables were expressed as frequencies and percentages.

Differences across infection groups (DENV mono infection, CHIKV mono infection, and DENV CHIKV co infection) were evaluated as follows:

- Categorical Data: Compared using Pearson's chi square (χ^2) test or Fisher's exact test when expected cell frequencies were< 5. Output included test statistics, degrees of freedom (df), p values, and expected cell counts to evaluate independence (e.g., distribution of gender or clinical symptoms across infection categories).
- Continuous Data (2 Groups): Compared using the independent samples Student's t test for normally distributed parameters or the Mann Whitney U test for non-normally distributed parameters.
- Continuous Data (> 2 Groups): Evaluated using one way Analysis of Variance (ANOVA) followed by Tukey's Honestly Significant Difference (HSD) post hoc test for parametric data, or the Kruskal Wallis H test followed by Dunn's post hoc test with Bonferroni correction for non-parametric data.

A two-tailed p value of < 0.05 was considered statistically significant.

To identify independent predictors of severe disease and adverse clinical outcomes, multivariate logistic regression analysis was performed, adjusting for potential confounders including age, sex, and comorbidities. Adjusted odds ratios (ORs) with 95% confidence intervals (CIs) were reported.

Results

Diagnostic Distribution: Among 1,335 febrile patients tested during the study period, 766 (57.38%) had fever of other/undetermined cause, 289 (21.65%) were diagnosed with dengue, 183 (13.71%) with chikungunya, and 97 (7.26%) with dengue–chikungunya co-infection. Dengue, chikungunya, and co-infection together accounted for 569 patients (42.6% of the cohort). These findings are tabulated in table 1.

Table 1: Diagnostic distribution among 1,335 febrile hospital admissions, Jan 2022 – Dec 2024

Diagnostic category	n	% of cohort
Fever of other/undetermined cause	0766	057.38
Dengue (mono infection)	0289	021.65
Chikungunya (mono infection)	0183	013.71
Dengue + Chikungunya (coinfection)	0097	007.26
Total	1,335	100.0

Serological Test Results: Raw serological results (prior to case definition adjudication) are summarized below.

For dengue markers, 693 patients (51.91%) tested negative, 360 (26.97%) tested positive for anti-dengue IgM and/or NS1, 29 (2.17%) were confirmed by RT-PCR, 251 (18.8%) were indeterminate, and 2 (0.15%) were not tested. For chikungunya IgM, 826 patients (61.87%) tested negative, 281 (21.05%) tested positive, 226 (16.93%) were indeterminate, and 2 (0.15%) were not tested. These raw test-positivity rates are higher than the final diagnostic category counts in Table 1 because a positive dengue and a positive chikungunya result occurring in the same patient are counted separately here but combined into the single "coinfection" category in the case definitions above. These findings are shown in table 2.

Table 2: Distribution of raw serological/virological test results (N = 1,335)

Result	Anti-dengue marker, n (%)	Anti-chikungunya IgM, n (%)
Negative	693 (51.91%)	826 (61.87%)
Positive (IgM/NS1)	360 (26.97%)	281 (21.05%)
RT-PCR positive	029 (02.17%)	—
Indeterminate	251 (18.8%)	226 (16.93%)
Not done	002 (0.15%)	002 (0.15%)

Clinical context: Dengue IgM antibodies typically become detectable around fourth to fifth day of illness. Patients presenting early in the disease window (days 1 – 3) often fall into the equivocal optical density (OD) range. Dengue ELISAs can exhibit cross - reactivity with other circulating flaviviruses or secondary Dengue infections (where IgM levels are lower and IgG predominates). [12] Chikungunya IgM ELISAs generally have cleaner OD cutoffs and lower background cross - reactivity. [13]

Over half of the cohort tested negative for Chikungunya IgM (61.87%) and nearly half tested negative for Dengue IgM (51.91%).

Epidemiological context: A high proportion of negative acute febrile illness cases is standard in tertiary care screening. It suggests that a sizeable portion of febrile presentations stems from other etiologies (e.g., non arboviral infections, malaria, and bacterial sepsis) or patients who presented before antibody seroconversion occurred. [14]

Demographic Characteristics: The study population had a mean age of 33.6 ± 16.8 years (median 31 years, range 1 – 84 years; two records with unparseable age data were excluded from this calculation). Patients were predominantly female (814, 60.97%) compared with male (521, 39.03%). The proportion of female patients differed significantly across diagnostic categories (χ^2=15.89, df=3, p=0.001): 67.01% of co-infected patients were female, compared with 64.36% of the fever of other cause group, 57.92% of chikungunya patients, and 51.9% of dengue patients — a proportion close to parity.

Table 3: Sex distribution by diagnostic category (χ^2=15.89, df=3, p=0.001)

Diagnostic category	Female, n (%)	Male, n (%)	Total
Dengue	150 (51.9%)	139 (48.1%)	0289
Chikungunya	106 (57.92%)	077 (42.1%)	0183
Dengue + Chikungunya	065 (67.01%)	032 (33.0%)	0097
Fever, other/undetermined	493 (64.36%)	273 (35.6%)	0766
Total	814 (61.0%)	521 (39.0%)	1,335

Table 4: Age-group distribution by diagnostic category (columns may not sum exactly to Table 1 totals owing to a small number of missing age records)

Age group (years)	Dengue	Chikungunya	Co-infection	Fever, other cause
0–9	15	11	04	037
10–19	47	18	16	147
20–29	82	33	14	183
30–39	65	42	17	146
40–49	31	42	20	120
50–59	22	18	11	060
60–69	22	15	12	052
70–79	04	04	02	018
80–89	00	00	01	002

Seasonal Pattern: Cases showed a marked seasonal concentration. Aggregated across the three study years, monthly case counts were lowest from January to June (5 – 36 cases/month) and rose sharply from July, peaking in September (413 cases) before declining through December. Overall, 1,075 of 1,335 cases (80.52%) occurred between July and October, coinciding with the monsoon and post monsoon period in Pune. Considered by diagnosis, chikungunya and coinfection cases both peaked in September (55 and 37 cases, respectively), while dengue cases peaked one month later, in October (82 cases). These findings are presented in table 5; and figure 1.

Table 5: Monthly case counts, aggregated across January 2022 – December 2024, by diagnostic category (Fever of other cause column omitted for brevity; but is included in the column of total cases)

Month	Total cases	Dengue	Chikungunya	Coinfection
January	036	07	04	00
February	022	01	02	00
March	010	02	02	02
April	005	00	00	00
May	006	01	01	00
June	013	04	03	00
July	168	28	26	10
August	276	41	45	18
September	413	73	55	37
October	218	82	27	20
November	118	35	13	08
December	050	15	05	02

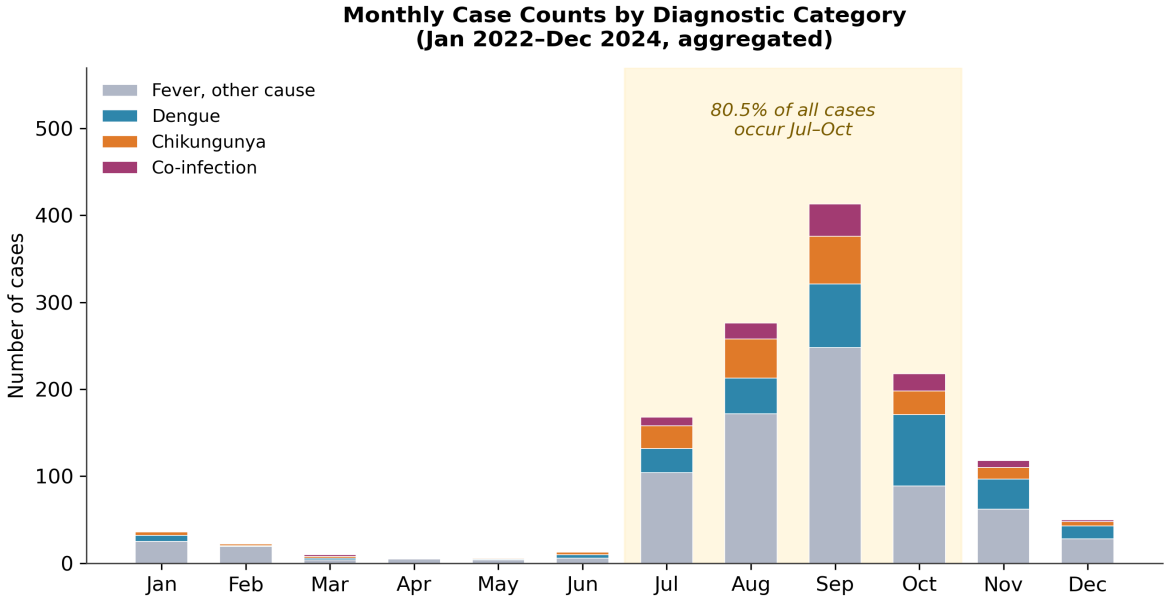

Figure 1: Monthly case counts by diagnostic category, aggregated across the study period. The shaded band marks the July–October window, which accounted for 80.52% of all cases

Length of Hospital Stay: Length of stay data were available for the 569 patients admitted with a confirmed vector borne diagnosis (dengue, chikungunya, or coinfection); length of stay was not recorded separately for patients classified with fever of other/undetermined cause. Overall mean length of stay among these 569 patients was 4.4 ± 0.9 days. Length of stay differed significantly across the three diagnostic categories (one way ANOVA, $F = 84.9$, $p < 0.001$): dengue patients had the shortest mean stay (4.0 ± 0.9 days), followed by chikungunya (4.8 ± 0.7 days) and coinfection (4.94 ± 0.81 days). Tukey's HSD post hoc test showed that coinfected patients stayed significantly longer than dengue mono infection patients (mean difference 0.97 days, $p < 0.001$) and that chikungunya patients also stayed significantly longer than dengue patients (mean difference 0.84 days, $p < 0.001$); the difference between chikungunya and coinfection was not statistically significant (mean difference 0.13 days, $p = 0.41$). When dengue and chikungunya mono infections were combined and compared with coinfection directly, coinfected patients (4.94 ± 0.81 days, n = 97) stayed significantly longer than mono infected patients (4.29 ± 0.91 days, n = 472; Welch's $t = 6.95$, $p < 0.001$). These findings are depicted in table 6; and figure 2.

Table 6: Length of hospital stay by diagnostic category (one-way ANOVA $F = 84.9$, $p < 0.001$; Tukey's HSD results in text)

Diagnostic category	n	Mean stay (days)	SD	Median	Range
Dengue	289	4.0	0.9	4	2 – 7
Chikungunya	183	4.8	0.7	5	4 – 7
Dengue + Chikungunya	097	4.94	0.81	5	3 – 7
All vector borne cases	569	4.4	0.9	4	2 – 7

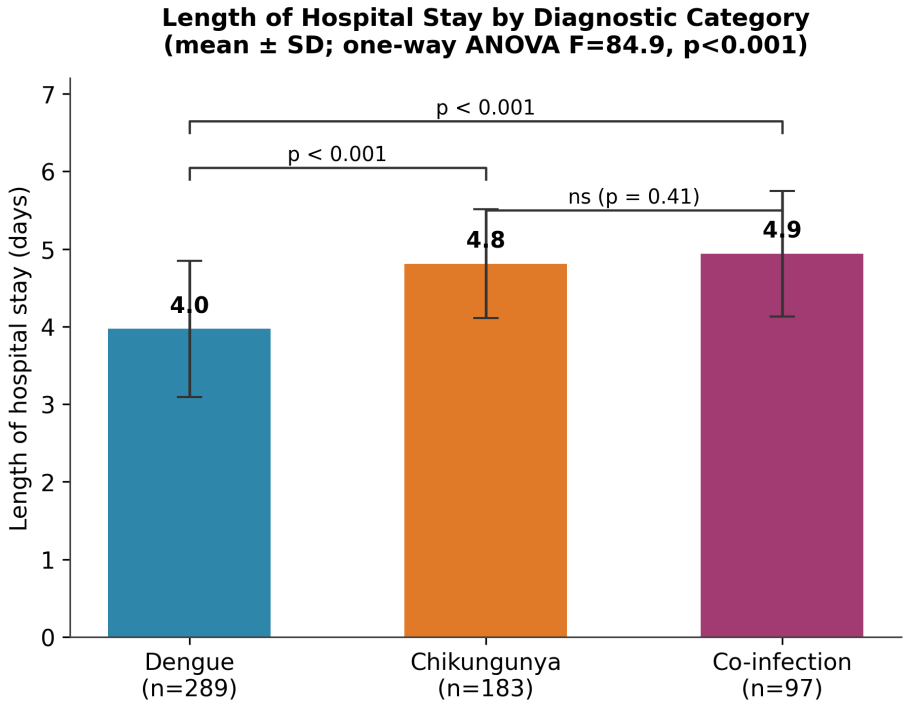

Figure 2: Length of hospital stay by diagnostic category (mean ± SD). Coinfected patients stayed significantly longer than dengue mono infection patients; the difference between chikungunya and coinfection was not significant

Patients with dengue infection (n = 360) predominantly presented with fever (98.61%), headache (87.22%), retro orbital pain (72.22%), myalgia (68.61%), and arthralgia (54.17%). Gastrointestinal symptoms including nausea, vomiting, and abdominal pain were observed in 63.61% of cases. Hemorrhagic manifestations such as petechiae, ecchymosis, gum bleeding, and epistaxis were noted in 28.33% of patients.

Laboratory findings in dengue patients revealed thrombocytopenia (platelet count < 150,000/mm³) in 68.89% of cases, with severe thrombocytopenia (< 50,000/mm³) in 23.61%. Leukopenia was observed in 57.22% of patients, and elevated liver enzymes (AST/ALT > 40 IU/L) in 62.5%. According to the WHO classification,[11] 76.39% of dengue cases were classified as dengue without warning signs, 18.33% as dengue with warning signs, and 5.28% as severe dengue.

Chikungunya patients (n = 281) typically presented with high grade fever (97.86%), severe arthralgia (94.30%), particularly affecting small joints of hands and feet, myalgia (79%), and characteristic maculopapular rash (67.62%). Headache was reported in 72.24% of cases, and gastrointestinal symptoms in 48.40%. Notably, 42.7% of patients reported persistent joint pain even after the resolution of other symptoms, with a median duration of 8 weeks (range: 2 - 24 weeks). Laboratory findings in chikungunya cases included lymphopenia in 63.70% of patients, elevated ESR in 82.21%, and mild to moderate elevation of liver enzymes in 43.06%. Unlike dengue, thrombocytopenia was less common in Chikungunya mono infection, observed in only 28.83% of cases.

Patients with coinfections (n = 97) exhibited a combination of symptoms characteristic of both diseases, often with increased severity. Fever (100%), severe headache (92.78%), arthralgia (95.88%), myalgia (88.66%), and gastrointestinal symptoms (77.32%) were the predominant manifestations. Notably, hemorrhagic complications were significantly higher in coinfected patients (41.24%) compared to dengue mono infection (28.33%, $p < 0.01$).

Laboratory parameters in coinfected patients showed a higher frequency of severe thrombocytopenia (37.11% vs. 23.61% in dengue mono infection, $p = 0.02$) and more pronounced elevation of liver enzymes. The mean duration of hospitalization was significantly longer in coinfected patients (4.94 ± 0.81 days) compared to those with mono infections (dengue mono infection patients, mean difference 0.94 days, $p < 0.001$). Chikungunya patients also stayed significantly longer than dengue patients (mean difference 0.8 days, $p < 0.001$)

Discussion

The clinical relevance of our findings is significant. In India, dengue burden has steadily increased over the past decades, with climatic factors such as rainfall and temperature influencing transmission dynamics [1]. Behavioral risk factors, including inadequate container management and poor personal protection, also contribute to sustained transmission [2]. In such settings, misdiagnosis of CHIKV as dengue is common, as both infections share vectors and clinical features. [5,6]

This retrospective study provides comprehensive data on the seroprevalence of dengue, chikungunya and their coinfections in India, particularly in Pune. The 21.65% rate for dengue and 13.71% rate for chikungunya, and 7.26% coinfection rate, highlight the ongoing risk of both the standalone infections and the elevated risks when both of these diseases occur together.

Environmental risk factors for dengue also vary widely across geographic settings. [15] The observed seroprevalence rates indicate endemic transmission of both viruses in Pune, with significant variations across different wards of the district. The higher prevalence in urban areas likely reflects the predominant breeding of Aedes mosquitoes in urban settings with inadequate water storage practices and waste management. [1,5] The seasonal pattern, with peak incidence during monsoon and post monsoon periods, aligns with previous reports from other parts of India and can be attributed to increased vector breeding during these seasons. [5] Similar to Maharashtra, high seroprevalence of Dengue has been reported in urban settings throughout India. Studies in Delhi found that around 25% of those living in urban regions have been infected with Dengue, a rate surprisingly comparable to our rate of 21.65% in Pune. [5] Dengue prevalence rates of upto 25% have also been reported from regions such as Delhi, Tamil Nadu, Orissa, Arunachal Pradesh; Kerala and Mizoram, but such local variations are determined by the timing of outbreaks and the competency of diagnostic surveillance systems. [1,5,16,17] Studies in Tamil Nadu, especially during epidemic periods like the years 2017 - 2018, showed that exposure to Dengue was nearly 50% in high risk urban settings. [18]

Chikungunya incidence in other regions has also suggested variations in prevalence between epidemic waves. Chikungunya was less common than Dengue in some studies, similar to this study. [17] In another study, the Chikungunya rate was seen in around 24.63% of cases, a rate much higher than our own rate of 13.71%. [19] Kaur et al also reported a very high incidence of Chikungunya of 58% in their study in Delhi in 2016, which is a far cry from our incidence of 13.71%. [20] Vijayakumar et al reported an unusually high incidence of 52.8% of Chikungunya during the 2007 epidemic. [21]

Literature exists wherein the incidence of dengue and chikungunya coinfection has been reported as ranging from a low of 0.3% to a moderate incidence of 2.5% to 3.3%; and a high of 25.33%. [14,17,20] These findings are in stark contrast to those of our study. Coinfections of CHIKV and DENV have been documented in Delhi and other regions, complicating clinical outcomes. [19] Cross-reactivity of IgM assays has been a persistent challenge, often leading to false assumptions of dual infection [5].

Previous researchers have also reported the incidence of dengue and chikungunya coinfection in India, as ranging from 17% to 35.29%. [5,19]

The findings of our present study wherein we have observed a dengue and chikungunya coinfection rate of 7.26% are not consistent with the findings of above previous literature on the subject.

The identification of specific risk factors for severe disease, particularly age > 60 years, comorbidities, and delayed presentation, provides valuable insights for clinical risk stratification and triage. These findings can guide healthcare providers in identifying high risk patients who may benefit from more intensive monitoring and early intervention. Concurrent infections present with overlapping clinical manifestations, including acute fever, joint pain, headache, and cutaneous eruptions. Standard clinical case definitions often lack sufficient discriminatory power because key symptoms like high fever, debilitating arthralgia, and rashes overlap substantially between CHIKV and DENV cases. Furthermore, non-specific constitutional features such as nausea, vomiting, myalgia, and fatigue obscure early clinical distinction. During epidemic spikes, relying solely on nonspecific clinical presentation frequently leads to underreporting or misdiagnosis of CHIKV as DENV, delaying appropriate supportive care and public health containment measures. [5,22]

From a public health perspective, the substantial burden of these vector borne diseases in Pune calls for enhanced surveillance, vector control measures, and public awareness campaigns. The district wise variations in seroprevalence can help in targeting interventions for high burden areas. Additionally, the documentation of persistent arthralgia in a significant proportion of chikungunya patients highlights the need for long term follow-up and management strategies for chronic manifestations.

Limitations

This study has several limitations that should be acknowledged. As a retrospective analysis, it relies on the accuracy and completeness of medical records, which may introduce information bias. The study was conducted in tertiary care hospitals, which may not represent the entire population of Pune, particularly those seeking care in private facilities.

The serological tests used for diagnosis, while standard, have known limitations in terms of sensitivity and specificity, especially in the context of coinfections. Additionally, viral serotyping and genotyping were not performed, which could have provided further insights into strain specific clinical manifestations.

Despite these limitations, this study provides valuable data on the burden and clinical characteristics of dengue, chikungunya, and their coinfections in Pune. The findings have important implications for clinical practice, public health interventions, and future research in this endemic region.

Conclusion

This retrospective study provides comprehensive data on the seroprevalence of dengue, chikungunya and their coinfections in India, particularly in Pune. The 21.65% rate for dengue and 13.71% rate for chikungunya, and 7.26% co-infection rate, highlight the ongoing risk of both the standalone infections and the elevated risks when both of these diseases occur together.

Our in depth retrospective analysis provides valuable insights into the seroprevalence and clinical characteristics of dengue, chikungunya, and their coinfections in Pune. The substantial burden of these diseases, with dengue seroprevalence of 21.65%, chikungunya 13.71%, and coinfections 7.26%, highlights the endemic nature of these vector borne diseases in the region.

The distinct clinical profiles documented for each infection type can aid clinicians in early recognition and appropriate management. The more severe manifestations observed in coinfected patients emphasize the need for comprehensive diagnostic approaches and heightened clinical vigilance in endemic areas where both viruses cocirculate.

The identification of specific risk factors for severe disease provides a basis for clinical risk stratification and targeted interventions. The findings highlight the need for enhanced surveillance, vector control measures, and clinical management protocols tailored to the local epidemiological context.

Future research should focus on prospective studies with larger sample sizes, more comprehensive diagnostic approaches including molecular techniques, and long term follow up to better understand the chronic manifestations, particularly of chikungunya. Additionally, studies on vector dynamics, virus strains, and host factors in this region would provide further insights into the epidemiology and pathogenesis of these infections.

In conclusion, dengue and chikungunya remain significant public health challenges in Pune, with coinfections presenting unique diagnostic and therapeutic challenges. A multifaceted approach involving clinical vigilance, laboratory strengthening, vector control, and public education is essential to reduce the burden of these diseases in this endemic region.

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