ISSN: 2320-9267

Indian Journal of Pharmaceutical and Biological Research (IJPBR)

Journal homepage: www.ijpbr.in

RESEARCH ARTICLE

Assessment of chikungunya co-infection in the lab confirmed dengue cases using NS1 antigen and IgM ELISA in western Uttar Pradesh

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ABSTRACT

Background: In tropical and subtropical areas, dengue and chikungunya are common viral illnesses spread by Aedes aegypti mosquitoes. Co-infection with both viruses can raise the burden of disease, change clinical symptoms, and delay diagnosis. Recent years have seen frequent outbreaks of both illnesses in Western Uttar Pradesh

Aim: To assess the prevalence and pattern of chikungunya co-infection among laboratory-confirmed dengue cases using NS1 antigen and IgM ELISA at Shaikh-Ul-Hind Maulana Mahmood Hasan Medical College.

Methods: The Department of Microbiology carried out this retrospective observational study between April 2024 and March 2026. Patients who had been tested for dengue and chikungunya had their laboratory data examined. IgM ELISA and NS1 antigen were used to confirm dengue infection, whereas IgM ELISA was used to confirm chikungunya infection. The Chi-square test was used to statistically analyse data on the total number of samples examined, positivity rates, and co-infection status; $p < 0.05$ was deemed significant.

Results: During 2024–2025, 3,127 samples were tested for dengue, of which 175 (5.6%) were positive. A total of 2,075 samples were tested for chikungunya, among which 192 (9.3%) were positive, while 26 patients showed co-infection. During 2025–2026, 3,760 dengue samples were tested and 103 (2.7%) were positive. Among 1,969 chikungunya samples, 119 (6.0%) were positive, and 16 cases demonstrated co-infection. Overall, the study identified 42 co-infected patients. Chikungunya positivity was significantly associated with dengue positivity ($p < 0.05$). A declining trend in dengue positivity was observed in the second year, whereas chikungunya prevalence remained comparatively high.

Conclusion: Dengue–chikungunya co-infection constitutes a significant public health concern in western Uttar Pradesh. Simultaneous testing for both arboviral infections should be encouraged in endemic regions to facilitate early diagnosis, appropriate management, and improved surveillance strategies.

Keywords: Dengue, Chikungunya, Arboviral infections, Surveillance strategies, Public health

Indian J. Pharm. Biol. Res. (2026): https://doi.org/10.30750/ijpbr.14.2.34

Introduction

Major arthropod-borne viral diseases like dengue fever and chikungunya fever have become serious public health issues in tropical and subtropical nations, especially in India. Aedes aegypti and Aedes albopictus mosquitoes, which flourish in heavily populated urban and semi-urban areas with poor sanitation and standing water collections, are the primary carriers of both diseases. Co-infections and simultaneous outbreaks are frequently caused by shared mosquito vectors, overlapping geographic distribution, and similar seasonal incidence. While chikungunya virus is an alphavirus that is a member of the Togaviridae family, dengue virus is a member of the Flaviviridae family(1). Differentiation is challenging in the early stages of the disease since both infections clinically manifest as severe febrile sickness accompanied by headache, myalgia, rash, nausea, and arthralgia. However, dengue can develop into hemorrhagic symptoms, plasma leakage, and shock syndrome, but chikungunya is more frequently linked to severe and protracted joint pain. Laboratory confirmation is necessary for precise diagnosis and treatment because of these overlapping symptoms(2).

Over the past 20 years, dengue and chikungunya outbreaks have frequently occurred in India, especially during the monsoon and post-monsoon seasons. Rapid urbanisation, population density, insufficient vector control techniques, and climate conditions conducive to mosquito breeding make Western Uttar Pradesh a vulnerable area. The likelihood of concurrent infections is enhanced when dengue and chikungunya viruses co-circulate. This might result in atypical clinical presentations, diagnostic uncertainty, treatment delays, and an increased healthcare burden. While chikungunya IgM ELISA is still a common diagnostic method for chikungunya virus infection,

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How to cite this article: Singh IM, Kumar A, Singh MK, Kansal R. Assessment of chikungunya co-infection in the lab confirmed dengue cases using NS1 antigen and IgM ELISA in western Uttar Pradesh. Indian J. Pharm. Biol. Res. 2026;14(2):194-198.

Source of support: Nil

Conflict of interest: None.

Received: 22/03/2026 **Revised:** 18/04/2026 **Accepted:** 28/05/2026 **Published:** 05/06/2026

laboratory diagnostics employing dengue NS1 antigen and IgM ELISA offers accurate early detection of dengue infection. In endemic locations, retrospective analysis of laboratory-confirmed cases might yield important epidemiological information about co-infection incidence, positive patterns, and illness trends(3).

In order to determine the prevalence of chikungunya co-infection among laboratory-confirmed dengue cases throughout a two-year period from April 2024 to March 2026, the current study was carried out at Shaikh-Ul-Hind Maulana Mahmood Hasan Medical College. The study also sought to highlight the significance of dual testing in endemic settings and examine yearly trends in dengue and chikungunya positivity(4).

Materials and Methods

Study Design

A retrospective observational study.

Study Setting

The study was conducted in the Department of Microbiology at Shaikh-Ul-Hind Maulana Mahmood Hasan Medical College.

Study Duration

April 2024 to March 2026 (2 years).

Study Population

All clinically suspected dengue and chikungunya cases whose samples were received in the microbiology laboratory during the study period were included.

Inclusion Criteria

- Patients clinically suspected of dengue fever and/or chikungunya fever.
- Samples tested using NS1 antigen and IgM ELISA.

Exclusion Criteria

- Incomplete laboratory records.
- Duplicate samples from the same patient.

Statistical Analysis

Microsoft Excel was used to enter the data, and SPSS software version 25.0 was used for analysis. Frequencies and percentages were used to express categorical variables. The chi-square test was used to compare the study years. Statistical significance was defined as a p-value of less than 0.05.

Results

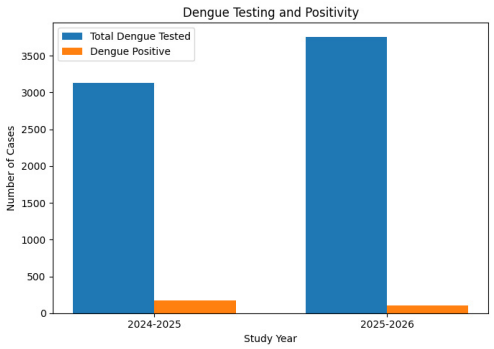

Figure 1: Dengue testing and positivity

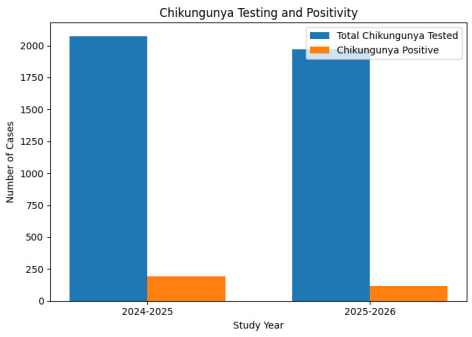

Figure 2: Chikungunya testing and positivity

Table 1: Year-wise Dengue Positivity Pattern

Study year	*Total dengue tested*	*Dengue positive*	*Positivity rate*	*p-value*
2024–2025	3127	175	5.6%	0.031*
2025–2026	3760	103	2.7%	0.031*

Table 2: Year-wise Chikungunya Positivity Pattern

Study year	*Total chikungunya tested*	*Chikungunya positive*	*Positivity rate*	*P-value*
2024–2025	2075	192	9.3%	0.042*
2025–2026	1969	119	6.0%	0.042*

Table 3: Dengue and Chikungunya Co-infection

Study year	*Dengue positive*	*Chikungunya positive*	*Both positive*	*Co-infection rate*	*P-value*
2024–2025	175	192	26	14.8%	0.021*
2025–2026	103	119	16	15.5%	0.021*

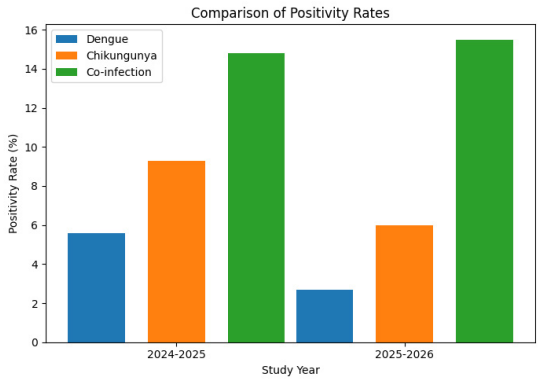

Figure 3: Comparison of positivity rates

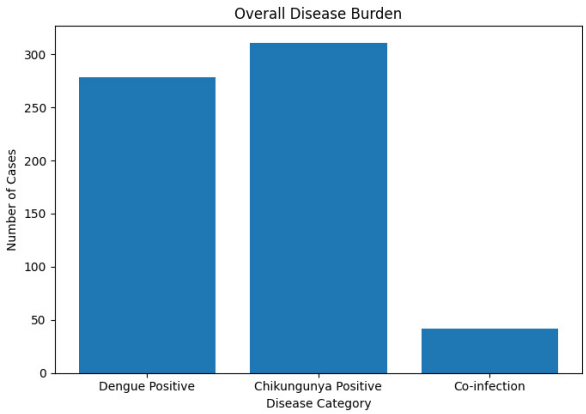

Figure 4: Overall disease burden

Table 4: Overall Laboratory Burden During Study Period

Parameter	*Total cases*
Total Dengue Tested	6887
Total Dengue Positive	278
Total Chikungunya Tested	4044
Total Chikungunya Positive	311
Total Co-infection Cases	42

Discussion

In India, dengue and chikungunya continue to be the most common vector-borne viral illnesses, especially in areas with tropical climates and ideal mosquito breeding grounds. Over the course of two years, the current retrospective study assessed the frequency of chikungunya co-infection among laboratory-confirmed dengue cases in western Uttar Pradesh. The results demonstrate the high prevalence of arboviral illnesses and the increasing significance of dual diagnostic testing in endemic areas(5). Dengue positive in the current study was 5.6% in 2024–2025 and dropped to 2.7% in 2025–2026. Seasonal fluctuations, enhanced public knowledge, better vector control techniques, and early intervention tactics used during succeeding epidemics could all contribute to this decrease. Previous studies conducted in India after increased surveillance and mosquito control initiatives have shown similar falling tendencies(6).

With rates of 9.3% and 6.0%, respectively, chikungunya positivity remained significantly higher than dengue positivity in both study years. Long-term virus

circulation in the community and underdiagnosis of cases of chronic arthralgia may be linked to persistent chikungunya transmission. The comparatively high positive also suggests that people in western Uttar Pradesh are still susceptible to contracting chikungunya. The co-infection of dengue and chikungunya was the study's most significant finding. Over the course of the trial, 42 individuals had laboratory-confirmed co-infection. Over the course of the two years, co-infection rates among dengue-positive cases were 14.8% and 15.5%, respectively. These results point to shared exposure to infected mosquito vectors and the simultaneous circulation of both viruses in the same geographic area(7).

Because fever, rash, headache, thrombocytopenia, and musculoskeletal complaints are common clinical signs of both diseases, co-infection presents a diagnostic problem. If thorough laboratory testing is not carried out, clinicians may misdiagnose one infection while the other is present. Co-infected patients may also have a protracted fever, excruciating joint pain, a heightened inflammatory response, and a slower rate of recovery(8). Even if the majority of cases still resolve on their own, early detection is crucial to avoid complications and guarantee proper supportive care. The usefulness of NS1 antigen testing and IgM ELISA in the diagnosis of arboviral infections is highlighted in this work. While IgM ELISA helps confirm recent infection, NS1 antigen detection enables early diagnosis of dengue during the acute fever phase. Combined serological testing makes epidemiological surveillance easier and improves diagnostic accuracy(9).

Due to its dense population, water stagnation, poor waste management, and climate that encourages mosquito reproduction, Western Uttar Pradesh is especially susceptible to arboviral outbreaks. Seasonal outbreaks typically occur during the monsoon and post-monsoon seasons, highlighting the importance of community involvement and integrated vector management(10). The study's retrospective design and the absence of a thorough clinical correlation were significant drawbacks. Due to resource constraints, molecular diagnostic methods like RT-PCR were excluded. Notwithstanding these drawbacks, the two-year research and huge sample size offer important epidemiological information about arboviral co-infection trends in this area(11).

Conclusion

The current study shows that among laboratory-confirmed dengue cases in western Uttar Pradesh, chikungunya co-infection is significantly more common. There is evidence of simultaneous virus circulation throughout the research period, and both dengue and chikungunya continue to significantly contribute to the regional burden of vector-borne infections. Chikungunya positivity and co-infection rates were significant during the second year, despite a downward trend in dengue positivity. Laboratory confirmation is crucial for precise diagnosis and efficient patient care because dengue and chikungunya have similar clinical presentations. In addition to chikungunya IgM ELISA, simultaneous testing with dengue NS1 antigen and IgM ELISA can enhance early co-infection detection and lower diagnostic mistakes. Clinicians can monitor issues and provide appropriate supportive treatment with the help of early detection.

The results of this study emphasise the significance of enhancing vector management strategies, bolstering arboviral surveillance programmes, and raising public awareness of mosquito-borne illnesses. Reducing disease transmission requires integrated methods such as rapid laboratory detection, community involvement, mosquito breeding site removal, and environmental sanitation. To further understand the epidemiology and clinical implications of dengue–chikungunya co-infection in endemic parts of India, more multicentric prospective studies including molecular diagnostic techniques and clinical outcome evaluation are advised.

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