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# Epidemiological characteristics and risk factors of a Chikungunya outbreak in Bantul, Indonesia (April-May 2024): a matched case-control study

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## Abstract

**Purpose:** The study aims to confirm the outbreak and identify associated risk factors of Chikungunya-like illnesses in the working area of Puskesmas Imogiri I, Bantul. **Methods:** A matched case-control design (1:1) using neighborhood control was conducted. Cases (n=86) were individuals with fever and arthralgia residing in Garjoyo and Karangtalun, and controls (n=86) were healthy individuals from the same area. Purposive sampling was conducted among 731 individuals identified as the population at risk within a 100-meter radius of confirmed cases. Data were collected using standardized questionnaires and Rapid Diagnostic Test (RDT) and analyzed using conditional logistic regression. **Results:** Multivariate analysis identified low income (aOR 8.49; 95% CI: 2.76-26.13), travel history to endemic areas (aOR 7.29; 95% CI: 1.19-44.54), and male sex (aOR 2.67; 95% CI:1.19-5.97) as significant risk factors. Paradoxically, the absence of larvivorous fish (aOR 0.13; 95% CI: 0.06-0.32) and lack of mosquito-repellent plants (aOR 0.06; 95% CI: 0.01-0.57) were associated with lower odds of infection, indicating a profound temporal bias following post-outbreak interventions. **Conclusion:** This localized outbreak was primarily driven by mobility-related viral importation and socioeconomic vulnerabilities. The findings underscore the limitations of reactive interventions and highlight the need for proactive, community-based larval control integrated with travel-aware surveillance to prevent future arboviral transmission.

**Keywords:** case-control study; chikungunya; outbreak response

## INTRODUCTION

Chikungunya is a viral illness caused by the chikungunya virus (CHIKV), primarily transmitted through the bites of *Aedes aegypti* and *Aedes albopictus* mosquitoes. The virus circulates through two primary cycles: a sylvatic cycle involving non-human primates and an urban cycle involving humans [1]. Over the past decades, chikungunya has caused significant outbreaks in Africa, Asia, Europe, and the Americas, driven by factors such as globalization, climate change, and genetic mutations in the virus, which enhance its adaptability [2,3]. Clinically, chikungunya presents in three stages: acute, post-acute, and chronic. The acute phase is marked by fever, arthralgia, myalgia, rash, and fatigue, while the chronic phase may include prolonged arthralgia or complications such as arthritis and neurological disorders [4]. These symptoms can significantly impact the quality of life, often disrupting daily activities. Diagnosis is typically confirmed through laboratory techniques like polymerase chain reaction (PCR) and serology. However, Rapid Diagnostic Tests

(RDTs) have emerged as practical tests for quickly identifying cases, especially outbreaks in resource-limited settings [1]. RDTs commonly used in Indonesia for chikungunya detection, detecting CHIKV IgM and IgG from several brands, have demonstrated a sensitivity of approximately 89.4% and a specificity of 94.4%, particularly effective during the acute phase of infection within the first five days of symptom onset [5].

Currently, there is no specific antiviral treatment or vaccine for chikungunya, and symptom management focuses on the use of nonsteroidal anti-inflammatory drugs (NSAIDs) and analgesics [6]. Prevention strategies rely on vector control methods, such as environmental management, insecticide application, Information, Education and Communication (IEC), and innovative techniques like modifying mosquito bacterial symbionts to reduce vector competence [7]. Despite these efforts, outbreaks continue to be a public health challenge, especially in endemic areas with socio-economic and environmental conditions that favor mosquito breeding and disease transmission [8].

While the global epidemiology of CHIKV is well-documented, localized outbreak dynamics particularly the complex interplay between socio-economic vulnerabilities, human mobility, and rapid behavioral shifts following reactive public health intervention remain underexplored in peri-urban Indonesian settings. By integrating epidemiological, socioeconomic, mobility, environmental, and post-intervention behavioral evidence collected during an active response, this investigation in Bantul provides locally relevant and actionable insights into transmission dynamics in peri-urban Imogiri. On 6 May 2024, Bantul District Health Office, in collaboration with Universitas Gadjah Mada Field Epidemiology Training Program (FETP), identified a cluster of suspected chikungunya cases in RT 03 Ngetal, Karangtalun Village, Imogiri Subdistrict, Bantul Regency. Residents presented symptoms such as fever, arthralgia, nausea, and vomiting, with some experiencing severe functional impairments including difficulty walking. An epidemiological investigation was launched on 7 May 2024, involving the Special Region of Yogyakarta Provincial Health Office, Bantul District Health Office, and Imogiri I Public Health Center. The investigation included a mosquito larval survey and screenings to confirm the outbreak and identify risk factors contributing to its spread.

This study aims to confirm the chikungunya outbreak in Imogiri using RDTs and to identify risk factors associated with the transmission. Specifically, this research examines socioeconomic, environmental, and behavioral factors that contribute to the persistence and spread of CHIKV in the community. The findings are expected to provide evidence-based recommendations for improving outbreak response strategies and implementing effective community-level prevention measures.

## METHODS

### Study design, setting, and participants

This study used a matched case-control design (1:1) with a neighborhood matching system to investigate the chikungunya outbreak in Karangtalun Village (RT 03) and Garjoyo Village (RT 01, RT 02, RT 03, and RT 04) in Imogiri Subdistrict, Bantul Regency. An operational case was a resident of an affected neighborhood in Garjoyo or Karangtalun who developed acute chikungunya-compatible illness during the outbreak period, defined as fever and/or arthralgia or myalgia, with or without rash, headache, joint swelling, nausea/vomiting, or difficulty walking; RDT reactivity supported the outbreak diagnosis but was not required for classification. A control was an asymptomatic resident of the same affected neighborhoods who reported no compatible illness during the outbreak period and remained asymptomatic at interview. Controls were selected solely based on being asymptomatic and were not tested using an RDT; therefore, they were not confirmed as RDT-negative. The study focused on a population at risk of 731 individuals living within a 100-meter radius of confirmed cases following the Indonesian Ministry of Health’s guidelines for the *Aedes* mosquito’s flight range. All 86 cases identified during the outbreak were enrolled using exhaustive (total) sampling. In addition, 86 neighborhood controls were selected from the same population at risk, yielding 172 participants. To minimize potential confounding effects, demographic variables such as sex and age were adjusted for in the multivariate conditional logistic regression model.

### Data collection

Trained investigators administered a structured electronic questionnaire and household observation checklist using KoboToolbox, an open-source platform for collecting and managing survey data. The electronic questionnaire was accessed on investigators’ mobile devices through KoboToolbox’s web-based interface, enabling responses to be recorded offline with built-in validation and uploaded to a centralized server when internet connectivity became available. Demographic information, clinical symptoms, treatment status, and environmental variables, including mosquito breeding sites, larval positivity, mosquito repellents, and proximity to symptomatic individuals, were collected. Suspected cases were tested during the field investigation using the STANDARD Q chikungunya IgM/IgG Test (SD BIOSENSOR, Inc.) with capillary whole-blood specimens. This qualitative immuno-chromatographic RDT detects anti-CHIKV IgM and IgG antibodies. The tests were administered by a medical team from Imogiri 1 Health Center, consisting of a medical doctor, nurses, and a medical laboratory technologist. Do not mention surveillance officers, since we do not know whether they are certified to perform the test procedure. Field implementation was supported by dengue program officers from the Special Region of Yogyakarta Provincial Health Office and Bantul District Health Office, a malaria program officer from Bantul District Health Office, and two Field Epidemiology Training Program trainees assigned to Bantul District Health Office.

Primary independent variables were operationalized as follows: low income was self-reported monthly income below the 2024 Bantul Regional Minimum Wage (IDR 2,216,463); recent travel was travel outside the neighborhood during the two weeks before symptom onset for cases or before interview for controls. Household environmental factors were assessed using the interviewer-administered questionnaire and observation checklist and coded separately as present or absent for larvae in inspected water-holding containers, intact screened ventilation, mosquito-repellent plants, and larvivorous fish; because these were binary indicators, no mean- or median-based environmental cut-off was applied. 3M-Plus preventive practice (the local health initiative comprising draining water containers, covering storage, and proper waste management, plus personal protection) was measured with nine yes/no items; each preventive response received one point (range 0–9), and scores of 6–9 were classified as good and 0–5 as less good using the prespecified two-thirds threshold rather than the sample mean or median.

**Data analysis**

The data were analyzed in three stages. First, univariate analysis was conducted to describe the distribution of variables related to person, place, time, and environment, with results presented in narrative, tables, and visual formats. Next, bivariate analysis using chi-square tests evaluated associations between independent variables and chikungunya cases, with a significance level set at $p < 0.05$. Multivariate analysis using conditional logistic regression was performed to account for the matched study design. This analysis identified significant risk factors with simultaneous effects on case occurrence, using a significance level of $p < 0.05$. This structured approach comprehensively explored the outbreak and supported the formulation of effective and targeted control strategies. The data were analyzed using STATA version 17.0. This epidemiological investigation was conducted as an emergency public health response to an active outbreak, officially mandated by the Bantul District Health Office, exempting it from formal Institutional Review Board (IRB) review. Informed consent was obtained from all participants prior to data collection. Furthermore, all authors have reviewed the final manuscript, agreed to their designated role, and confirmed that they meet the authorship criteria set forth by the International Committee of Medical Journal Editors (ICMJE) guidelines.

## RESULTS

Figure 1 shows participant flow and exclusions. Of the 731 residents in the population at risk, 88 were eligible operational cases; 86 were enrolled, and 86 of 643 asymptomatic residents were selected as controls. Two case submissions received after the data collection cut-off date were excluded, and no eligible case declined participation. The final analytic sample comprised 172 participants (86 cases and 86 controls). Among 23 symptomatic residents tested by RDT, 12 (52.17%) were reactive for anti-CHIKV IgM and/or IgG, supporting CHIKV circulation during the outbreak (Figure 1).

A total of 172 respondents, comprising 86 confirmed cases and 86 controls, were included in this study. Demographic characteristics showed that the majority of cases resided in RT 03 Karangtalun (72.1%), were female (53.5%), and belonged to the ≥60 age group (46.5%), as presented in Table 1. A large proportion of the cases reported a monthly income below the regional minimum wage (90.7%). Among the cases, the highest proportions had completed senior high school (34.9%) and worked as private-sector employees (25.6%) or housewives (19.8%). Most cases had health insurance coverage (95.3%) and no recent travel history (90.7%) (Table 1). Environmental and behavioral characteristics showed that most cases lacked larvivorous fish (53.5%) and mosquito-repellent plants (86.0%) in their households. Houses without screened ventilation were found in 66.3% of the cases. Additionally, a large proportion of the cases exhibited “less good” preventive measures (86.0%) during the outbreak investigation (Table 1).

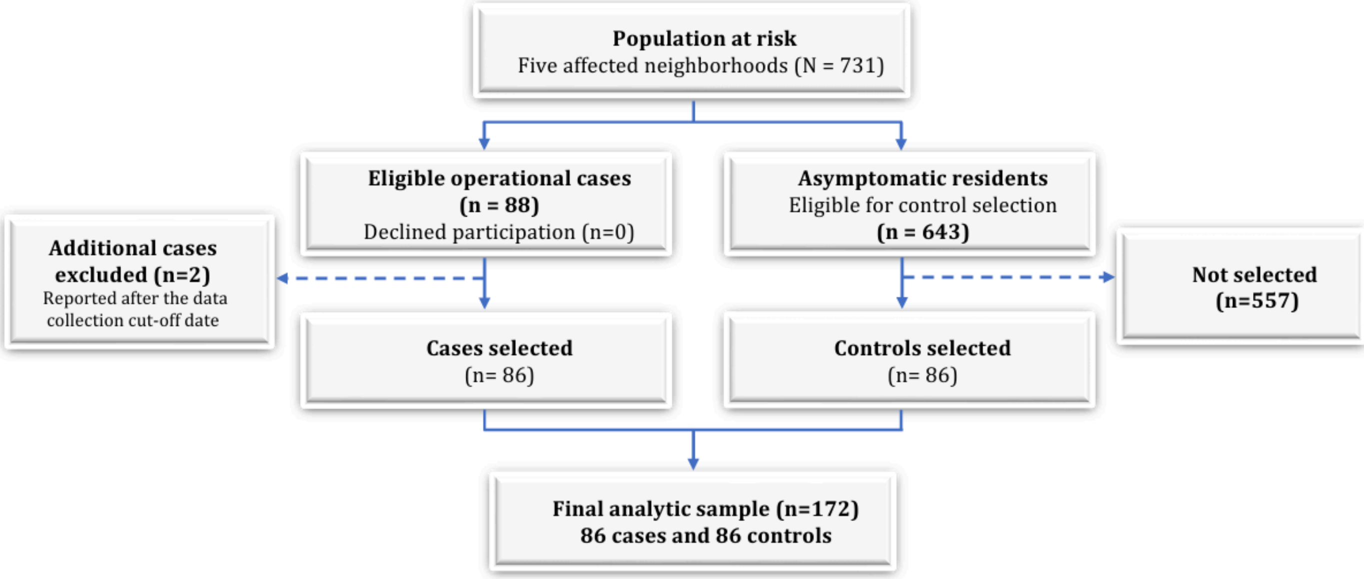


**Figure 1. Participant flow and analytic sample**

**Table 1. Respondent characteristics and relevant factors in Garjoyo and Karangtalun Villages (n=172)**

| Variable | n (%) | | |
|---|---|---|---|
| | Control (n=86) | Case (n=86) | Total (n=172) |
| **Address** | | | |
| RT 03 Karangtalun | 34 (39.5) | 62 (72.1) | 96 (55.8) |
| RT 01 Garjoyo | 8 (9.3) | 13 (15.1) | 21 (12.2) |
| RT 02 Garjoyo | 14 (16.3) | 6 (7.0) | 20 (11.6) |
| RT 03 Garjoyo | 12 (14.0) | 4 (4.7) | 16 (9.3) |
| RT 04 Garjoyo | 18 (20.9) | 1 (1.2) | 19 (11.0) |
| **Sex** | | | |
| Female | 59 (68.6) | 46 (53.5) | 105 (61.0) |
| Male | 27 (31.4) | 40 (46.5) | 67 (39.0) |
| **Age (years)** | | | |
| 0-4 | 1 (1.2) | 2 (2.3) | 3 (1.7) |
| 5-9 | 5 (5.8) | 2 (2.3) | 7 (4.1) |
| 10-17 | 6 (7.0) | 14 (16.3) | 20 (11.6) |
| 18-59 | 39 (45.3) | 28 (32.6) | 67 (39.0) |
| ≥60 | 35 (40.7) | 40 (46.5) | 75 (43.6) |
| **Educational level** | | | |
| No formal education | 3 (3.5) | 6 (7.0) | 9 (5.2) |
| Primary school | 21 (24.4) | 24 (27.9) | 45 (26.2) |
| Junior high school | 19 (22.1) | 18 (20.9) | 37 (21.5) |
| Senior high school | 33 (38.4) | 30 (34.9) | 63 (36.6) |
| Diploma/Bachelor’s degree | 10 (11.6) | 7 (8.1) | 17 (9.9) |
| Master’s/Doctorate degree | 0 (0.0) | 1 (1.2) | 1 (0.6) |
| **Occupation** | | | |
| Unemployed | 13 (15.1) | 13 (15.1) | 26 (15.1) |
| Housewife | 29 (33.7) | 17 (19.8) | 46 (26.7) |
| Farmer | 0 (0.0) | 2 (2.3) | 2 (1.2) |
| Private sector employee | 20 (23.3) | 22 (25.6) | 42 (24.4) |
| Entrepreneur | 21 (24.4) | 15 (17.4) | 36 (20.9) |
| Student | 2 (2.3) | 14 (16.3) | 16 (9.3) |
| Military/Police | 0 (0.0) | 1 (1.2) | 1 (0.6) |
| Civil servant | 1 (1.2) | 2 (2.3) | 3 (1.7) |
| **Income** | | | |
| ≥ Minimum wage (MW) | 23 (26.7) | 8 (9.3) | 31 (18.0) |
| < Minimum wage (MW) | 63 (73.3) | 78 (90.7) | 141 (82.0) |
| **Insurance** | | | |
| Yes | 78 (90.7) | 82 (95.3) | 160 (93.0) |
| No | 8 (9.3) | 4 (4.7) | 12 (7.0) |
| **Travel History** | | | |
| Yes | 2 (2.3) | 8 (9.3) | 10 (5.8) |
| No | 84 (97.7) | 78 (90.7) | 162 (94.2) |
| **Larvivorous fish presence** | | | |
| Yes | 14 (16.3) | 40 (46.5) | 54 (31.4) |
| No | 72 (83.7) | 46 (53.5) | 118 (68.6) |
| **Mosquito repellent plants** | | | |
| Yes | 1 (1.2) | 12 (14.0) | 13 (7.6) |
| No | 85 (98.8) | 74 (86.0) | 159 (92.4) |
| **Screened ventilation** | | | |
| Yes | 22 (25.6) | 29 (33.7) | 51 (29.7) |
| No | 64 (74.4) | 57 (66.3) | 121 (70.3) |
| **Preventive measures** | | | |
| Good | 4 (4.7) | 12 (14.0) | 16 (9.3) |
| Less good | 82 (95.3) | 74 (86.0) | 156 (90.7) |

**Table 2. Clinical symptoms of chikungunya cases in Garjoyo and Karangtalun Villages (n=86)**

| Symptoms | n (%) |
|---|---|
| **Fever** | |
| No | 7 (8.1) |
| Yes | 79 (91.9) |
| **Rash** | |
| No | 31 (36.0) |
| Yes | 55 (64.0) |
| **Joint pain** | |
| No | 7 (8.1) |
| Yes | 79 (91.9) |
| **Difficulty of walking** | |
| No | 30 (34.9) |
| Yes | 56 (65.1) |
| **Swelling** | |
| No | 50 (58.1) |
| Yes | 36 (41.9) |
| **Nosebleeds** | |
| No | 74 (86.0) |
| Yes | 12 (14.0) |
| **Nausea/vomiting** | |
| No | 50 (58.1) |
| Yes | 36 (41.9) |
| **Headache** | |
| No | 22 (25.6) |
| Yes | 64 (74.4) |
| **Itching from rash** | |
| No | 30 (34.9) |
| Yes | 56 (65.1 |

Table 2 shows that the most commonly reported symptoms during the chikungunya outbreak in Garjoyo and Karangtalun villages were fever (91.9%), joint pain (91.9%), and headache (74.4%). The spatial distribution of the outbreak shows a highly concentrated, localized transmission pattern. As illustrated in Figure 2, a dense geospatial cluster (hotspot) of chikungunya cases was identified primarily in RT 03 Karangtalun, with limited spread to adjacent areas of Garjoyo. Figure 3 illustrates an epidemiological curve with a propagated source pattern, indicating progressive community-level transmission. The outbreak persisted for approximately ten weeks. Field observations identified multiple mosquito breeding sites within household environments, including water storage tanks, buckets, and discarded containers around residences. Low *Angka Bebas Jentik (ABJ)* or Larval Free Index (LFI) was observed, particularly in RT 03 Karangtalun. An epidemiological linkage was identified between RT 03 Karangtalun and cases in Garjoyo village, suggesting connectivity between the two areas.

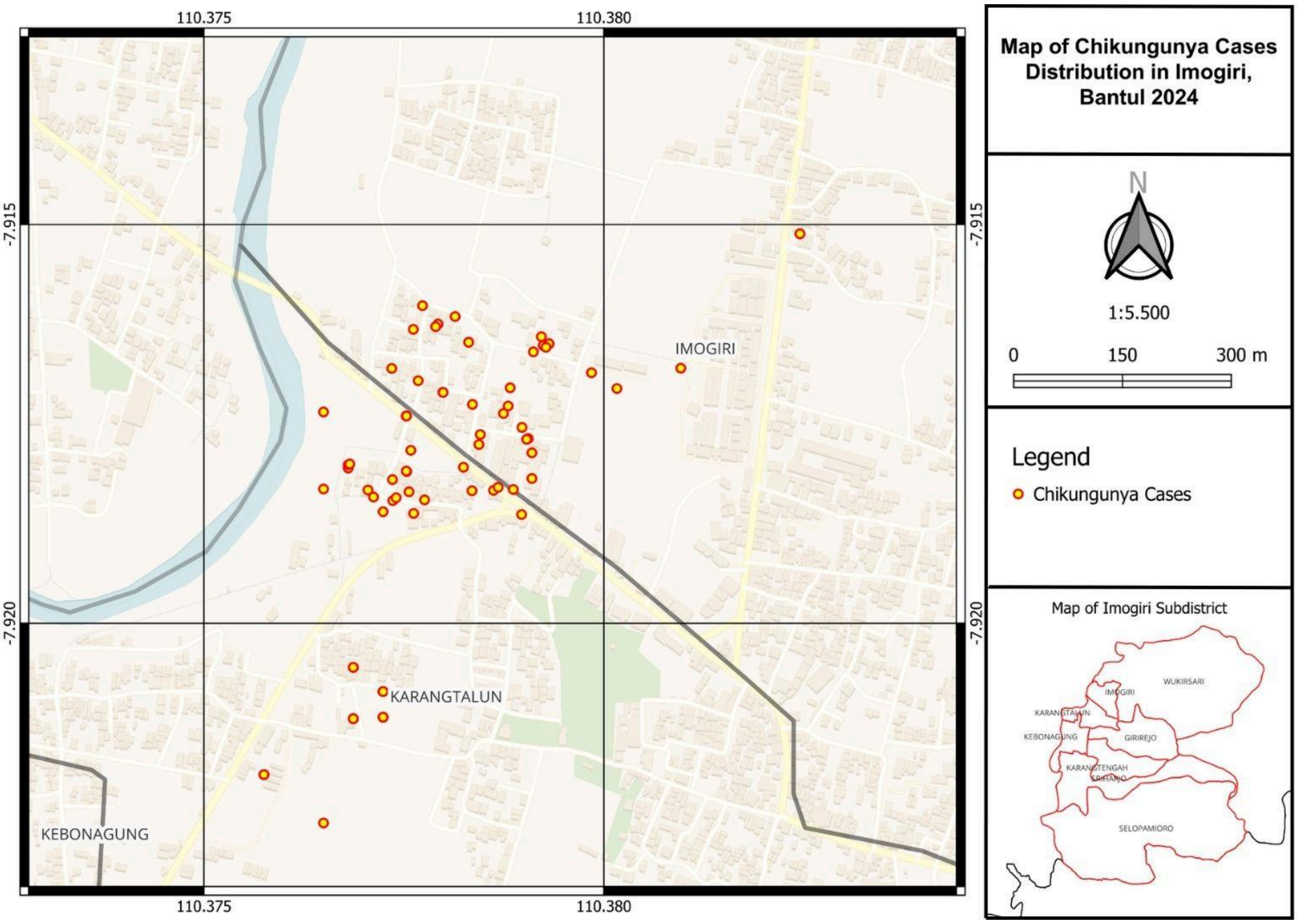


**Figure 2. Spatial distribution of chikungunya cases in Imogiri Subdistrict (April - May 2024)**

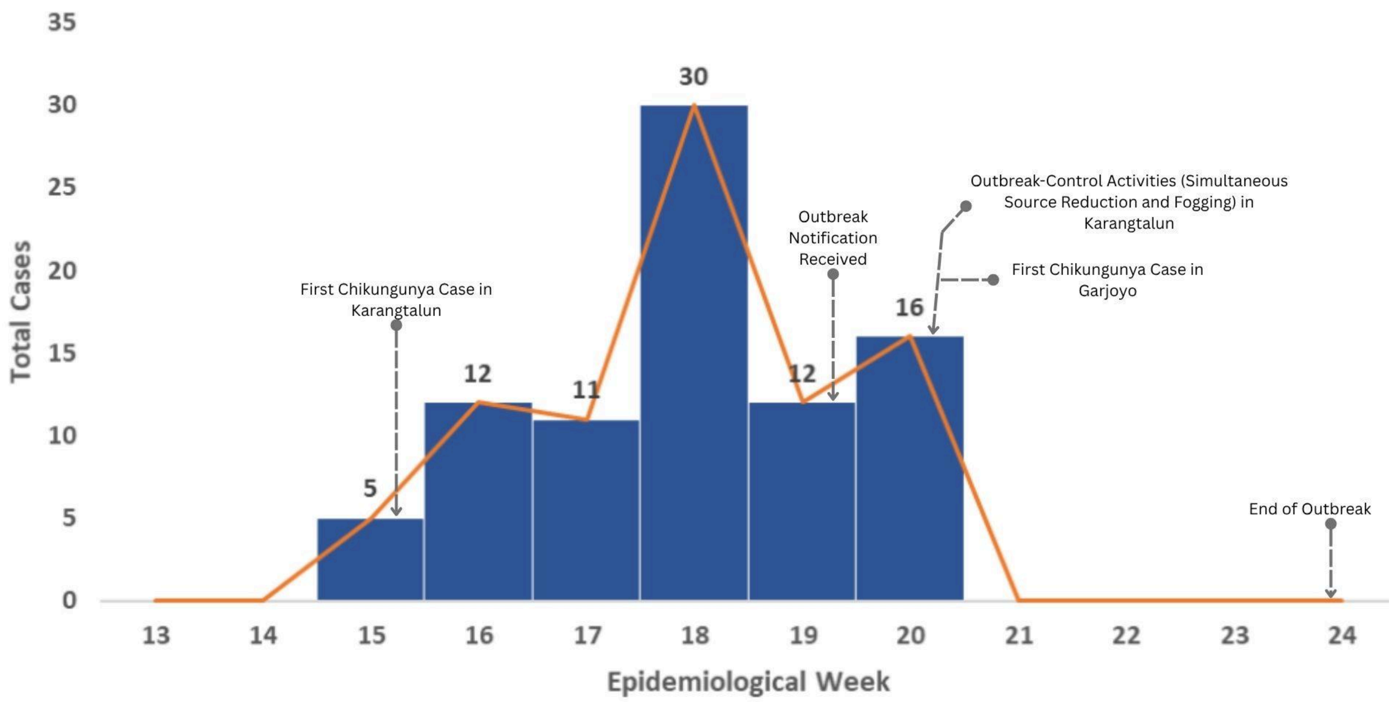


**Figure 3. The epidemiological curve of chikungunya cases in Karangtalun and Garjoyo Hamlets, Imogiri, Bantul (April - May 2024)**

**Table 3. Bivariate and multivariate analysis**

| Variable | OR | 95% CI | aOR | 95% CI |
|---|---|---|---|---|
| **Sex** | | | | |
| Male | 1.90 | (0.98–3.72) | 2.67* | (1.19–5.97) |
| Female | ref | | ref | |
| **Income** | | | | |
| < Minimum wage (MW) | 3.56** | (1.40-9.79) | 8.49*** | (2.76–26.13) |
| ≥ Minimum wage (MW) | ref | | ref | |
| **Travel history** | | | | |
| Yes | 4.31 | (0.82-42.53) | 7.29* | (1.19–44.54) |
| No | ref | | ref | |
| **Larvivorous fish presence** | | | | |
| No | 0.22*** | (0.10-0.47) | 0.13*** | (0.06–0.32) |
| Yes | ref | | ref | |
| **Mosquito repellent plants** | | | | |
| No | 0.07** | (0.00-0.52) | 0.06* | (0.01-0.57) |
| Yes | ref | | ref | |
| **Screened ventilation** | | | | |
| No | 0.68 | (0.33-1.37) | 0.54 | (0.24–1.21) |
| Yes | ref | | ref | |
| **Preventive measures** | | | | |
| Less good | 0.30* | (0.09-0.93) | 0.25* | (0.06–0.97) |
| Good | ref | | ref | |

**Notes:** P-value: *p < 0.05, **p < 0.01, ***p < 0.001, OR (Odds Ratio), aOR (Adjusted Odds Ratio), CI (Confidence Interval)

Table 3 presents the factors associated with chikungunya infection. The multivariate analysis identified sex, income, and travel history as significant risk factors. Males had a 2.67 times higher risk of infection compared to females (aOR 2.67; 95% CI 1.19-5.97). Respondents with a monthly income below the regional minimum wage were 8.49 times more likely to be infected than those with higher income (aOR 8.49; 95% CI 2.76-26.13). A positive history of travel was significantly associated with a 7.29-fold increase in the odds of infection (aOR 7.29; 95% CI 1.19-44.54). Inverse associations were observed for environmental and behavioral factors. Respondents without larvivorous fish (aOR 0.13; 95% CI 0.06-0.32), no mosquito-repellent plants (aOR 0.06; 95% CI 0.01-0.57), and "less good" preventive measures (aOR 0.25; 95% CI 0.06-0.97) had significantly lower odds of infection. The use of screened ventilation showed no statistically significant association with infection risk (aOR 0.54; 95% CI 0.24-1.21).

## DISCUSSION

This investigation elucidates the epidemiological dynamics of a chikungunya outbreak in Bantul Regency, highlighting a complex interplay of human mobility, socioeconomic vulnerability, and vector ecology. The findings reveal that while demographic and travel-related factors drove transmission, the rapid implementation of public health interventions induced significant behavioral shifts within the affected community, fundamentally altering the observable risk landscape. Contrary to literature suggesting a female predisposition to vector-borne disease [9,10], this study identified male sex as a significant risk factor (aOR 2.67). This divergence likely reflects specific local occupation patterns, where males experience prolonged outdoor exposure to diurnal *Aedes* vectors in peri-urban or agricultural settings. The high disease burden among the elderly (≥60 years) further suggests that age-related immunosenescence, coupled with increased time spent in indoor resting habitats of *Aedes aegypti,* amplifies infection risk [11].

Socioeconomic disparities fundamentally modulated outbreak vulnerability. Individual earnings below the regional minimum wage exhibited an 8.49-fold increased odds of infection. Poverty serves as a well-documented proxy for structural vulnerabilities, including substandard housing, inadequate water storage infrastructure, and limited access to personal repellent, which collectively sustain human-vector contact [11]. Although the majority of respondents possessed health insurance, economic constraints likely hindered effective environmental management at the household level, particularly in densely populated areas [12].

Furthermore, despite a moderate level of formal education within the cohort, baseline health literacy regarding arboviral prevention remained insufficient to avert transmission. This reinforces that formal education alone does not guarantee behavioral compliance prior to an outbreak, underscoring the need for targeted health education interventions [13,14]. Additionally, the relatively high proportion of private-sector employees among the cases suggests potential extra-domiciliary or occupational exposure, highlighting that vector control programs must extend beyond residential boundaries [15].

The predominance of fever and joint pain reflects the typical clinical presentation of chikungunya, a mosquito-borne viral disease transmitted mainly by *Aedes aegypti* and *Aedes albopictus*. These hallmark symptoms can significantly affect patients' quality of life and are important indicators for clinical diagnosis and case identification. In addition to fever and joint pain, chikungunya infection is often accompanied by other acute symptoms such as muscle pain, joint swelling, headache, nausea, fatigue, and rash, with varying intensity and duration [16]. Importantly, chronic manifestations, persistent polyarthralgia resembling autoimmune conditions, are also frequently reported. This debilitating pain commonly affects joints such as the knees, wrists, and feet, and can persist long after the acute phase of infection [17].

The proposed mechanism for these chronic symptoms involves the persistence of viral ribonucleic acid (RNA) in joint tissues, which may lead to prolonged inflammation and pain [18]. Additionally, chikungunya infection may trigger autoimmune responses, potentially exacerbating joint pain and increasing the risk of conditions such as rheumatoid arthritis in genetically predisposed individuals [19]. These findings highlight the importance of understanding both acute and chronic clinical manifestations of chikungunya to support effective patient management and long-term disease control strategies. Human mobility and spatial-environmental factors acted as primary catalysts for the sustained outbreak. A positive travel history emerged as a robust predictor of infection (aOR 7.29), consistent with the classical importation model of arboviral spread where an initial viral introduction by a viremic traveler is followed by rapid, localized autochthonous transmission [20].

The propagated nature of the epidemic curve and the tight spatial clustering in RT 03 Karangtalun perfectly reflect this dynamic [21]. This focal spread aligns with the restricted flight range of *Aedes* mosquitoes (typically <100 meters) [22], creating intense micro-clusters of transmission around unmanaged larval habitats. Furthermore, the prolonged duration of the outbreak (approximately ten weeks) and the historically low Larval Free Index (LFI) in the area reflect sustained community exposure to high vector densities. This demonstrates that active *Aedes* breeding, driven by poor baseline environmental management, maintains the transmission cycle and significantly increases the burden on public health systems [11].

While previous studies often highlight a female predominance driven by biological factors, such as estrogen-modulated immune responses [9], as well as behavioral factors like greater domestic exposure [10], our analysis identified males as having a significantly higher risk of infection (aOR 2.67). This epidemiological shift may be attributed to high occupational mobility and prolonged outdoor exposure in agricultural or peri-urban settings during the peak daytime biting hours of *the Aedes* vector, effectively overriding the traditional exposure risks typically associated with females.

A critical methodological finding of this study was the paradoxical inverse association between traditional protective behaviors and infection risk. The statistical model demonstrated that the absence of larvivorous fish, lack of repellent plants [23,24], and "less good" preventive measures were associated with lower odds of infection. Rather than indicating a biological protective effect of poor environmental management, these metrics expose a profound temporal bias and reverse causality. Data collection occurred concurrently with intensive post-outbreak public health intervention, including thermal fogging, larviciding, and community-based source reduction campaigns [25,26]. Consequently, affected households (cases) likely exhibited a hyperreactive behavioral shift, rapidly adopting rigorous preventive practices in response to the disease and targeted education, whereas control households maintained baseline behaviors. Similarly, the lack of significant association with screened ventilation may be due to improper installation, poor maintenance, or the dominance of extra-domiciliary transmission.

This study is subject to certain limitations. The reliance on self-reported data during an active, retrospective outbreak investigation inherently introduces recall bias, and as demonstrated, profound temporal bias regarding prior preventive practices. Additionally, the 100-meter sampling radius is entomologically justified by the *Aedes* flight range; however, purposive sampling within a single outbreak hotspot limits the generalizability of these findings to broader, non-endemic populations. Overall, the findings emphasize that chikungunya transmission is driven by a complex interplay of human mobility, socioeconomic vulnerability, and localized environmental factors. Reactive, post-outbreak interventions induce rapid behavioral changes but often fail to preempt propagated transmission. Comprehensive strategies that combine proactive community engagement, targeted travel-aware interventions, and sustainable vector control are essential to reduce the disease burden and prevent future outbreaks [27,28].

## CONCLUSION

In conclusion, the chikungunya outbreak in Imogiri Subdistrict was a highly localized, community-driven epidemiological event, with transmission primarily concentrated in the RT 03 Karangtalun hotspot. A combination of environmental and behavioral determinants significantly fueled the prolonged ten-week transmission cycle. Specifically, unmanaged domestic mosquito breeding sites, combined with socioeconomic vulnerabilities such as low income, severely restricted the community's baseline access to adequate preventive tools.

Furthermore, while male sex and a history of travel emerged as significant risk factors for infection, the seemingly high protective efficacy of environmental and behavioral variables actually exposed a profound temporal bias driven by intense post-outbreak interventions. To prevent recurrent arboviral outbreaks and reduce the strain on local health systems, public health authorities must strategically pivot from reactive measures to proactive, community-led vector management. Programmatically, it is imperative to integrate continuous larval source reduction into routine neighborhood sanitation campaigns *(Pemberantasan Sarang Nyamuk/PSN)*. This approach must be coupled with targeted health education tailored for vulnerable demographic groups, particularly low-income households and individuals with high occupational mobility. By institutionalizing these comprehensive, community-based interventions, the local health office can significantly strengthen local preparedness, optimize resource allocation, and protect public health security against future vector-borne disease threats.

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**Authors' contribution**
N.S.R.: Conceptualization, Methodology, Investigation, Formal analysis, Writing—original draft; M.R.F. & M.I.U. : Investigation, Data curation; S.A.: Resources, Project Administrator; S.A.W. & M.N.: Validation, Writing—review & editing; B.S.W.: Conceptualization, Methodology, Supervision, Writing—review & editing. All authors read and approved the final manuscript.

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**Data availability**
The epidemiological datasets generated and analyzed during this outbreak investigation are not publicly available due to patient confidentiality and public health data protection regulations. Still, they are available from the corresponding author upon reasonable request and with permission from the Bantul District Health Office.

**Ethics statement**

This outbreak investigation was classified as a non-research public health surveillance practice officially authorized by the Bantul District Health Office, which waives the requirement for formal ethical clearance. Nevertheless, all field procedures strictly adhered to the ethical principles of the Declaration of Helsinki. All personal identifiers were completely anonymized to ensure strict data confidentiality and respondent protection throughout the investigation and publication process.

**Conflicts of interest**

The authors declare no conflicts of interest regarding the publication of this article.

**Use of artificial intelligence (AI)**

Portions of this manuscript, specifically within the Discussion and Conclusion sections, were assisted by Google Gemini (Large Language Model) strictly for English language editing, grammatical correction, and structural narrative refinement. The AI tool was not used for data fabrication, scientific analysis, or result interpretation. All core intellectual contributions, field investigations, spatial and statistical analyses, data interpretations, and public health policy recommendations were entirely conceived and executed by the human authors. The authors meticulously reviewed, revised, and validated all AI-assisted language to ensure strict epidemiological accuracy and scientific integrity.

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