

Climate Teleconnections and Chikungunya Epidemic Peaks in Indonesia: A Decadal Analysis of ENSO Impacts, 2012–2023

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Received: 30-06-2026

e-ISSN : 2987-9140

Accepted: 28-08-2026

Volume : 4 No. 2, (2026)

Published: 01-10-2026

Page : 55-64

DOI: <https://doi.org/10.26740/ijgsme.v4n2.p55-64>

Abstract

This study evaluates the macro-climatic teleconnections between Pacific sea surface temperature anomalies—measured via the Oceanic Niño Index (ONI)—and Chikungunya transmission dynamics in Indonesia across the decadal horizon of 2012–2023. To preserve statistical integrity and avoid synthetic temporal autocorrelation, the analysis is maintained at the original annual temporal resolution ($n = 12$). Shapiro-Wilk normality testing confirmed that while the annual mean ONI is normally distributed, annual Chikungunya cases depart significantly from normality ($W = 0.8073, p = 0.0113$), justifying non-parametric Spearman rank correlation and local polynomial regression (LOESS) smoothing. The longitudinal dataset reveals a prominent double-peak epidemic pattern anchored by major surges in 2013 (15,324 cases) and 2023 (6,049 cases). Bivariate Spearman modeling demonstrated a weak, statistically non-significant positive correlation ($\rho = 0.2168, p = 0.4986$) between annual mean ONI and aggregate cases. The non-monotonic LOESS trajectory indicates that extreme outbreaks, such as the 2013 peak (unfolding at a weak ONI of -0.2417°C), occur independently of high positive ONI thresholds. These findings prove that global climate signals do not drive Chikungunya burden through direct linear pathways. Instead, the teleconnection is non-linearly mediated by local vector ecology, drought-induced domestic water storage, and multi-year herd immunity decay. Consequently, public health surveillance must transition toward integrated, multi-factorial frameworks combining climate indices, vector metrics, and population immunity tracking.

Keywords: Chikungunya virus; Oceanic Niño Index (ONI); Macro-climatic teleconnections

1. INTRODUCTION

Chikungunya virus (CHIKV) a mosquito-borne alphavirus transmitted primarily by *Aedes aegypti* and *Aedes albopictus* remains a major global public health threat capable of causing explosive, debilitating epidemics across tropical and subtropical environments (Rao et al., 2026; Houatthongkham & Kim, 2026). In hyper-endemic equatorial countries such as Indonesia, the transmission dynamics of arboviral diseases are governed by intricate interactions among environmental baselines, host population susceptibility, and vector ecology (De Souza & Weaver, 2024; Linthicum et al., 2010; Linthicum et al., 2016). Large-scale ocean-atmospheric oscillations, most notably the El Niño-Southern Oscillation (ENSO), drive planetary climate variability by shifting sea surface temperatures (SST) in the central and eastern Pacific Ocean. When evaluated via the Oceanic Niño Index (ONI), these macro-climatic shifts significantly alter precipitation patterns, relative humidity, and ambient temperature thresholds across the Indonesian archipelago.

At the local biological scale, thermal anomalies and hydrometeorological fluctuations directly alter vector competence, accelerate extrinsic incubation periods (EIP), and modulate mosquito biting frequencies (De Souza & Weaver, 2024; Mokhtar et al., 2024; Bellone & Failloux, 2020). Conversely, during periods of climate-induced drought or prolonged dry spells, altered

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human behavioral responses such as increased domestic water storage inadvertently create abundant artificial breeding sites for peri-domestic *Aedes* mosquitoes (Pirani et al., 2024). This complex interplay frequently triggers explosive local transmission spikes that coincide with or follow global climate shifts (Bastos et al., 2024; Pramanik et al., 2020). However, because these local micro-environmental triggers operate within localized eco-immunological limits, broad climate indices often exhibit non-linear patterns when compared against national epidemiological metrics (Pirani et al., 2024; Linthicum et al., 2010).

In Southeast Asia, atmospheric teleconnections and arboviral transmission display pronounced spatiotemporal non-stationarity, phase shifts, and transient cross-coherence (Tian et al., 2025; Tipayamongkholgul et al., 2009; Houatthongkham & Kim, 2026). In archipelagic landscapes like Indonesia, local climate dynamics are heavily modulated by surrounding maritime conditions and regional atmospheric processes (Azad & Lio, 2014; Cazelles et al., 2005). The archipelago's complex geography creates micro-climates where global climate signals interact non-linearly with host susceptibility and multi-year herd immunity decay (Van Panhuis et al., 2015; Wirasatriya et al., 2020). Consequently, aggregate national epidemic peaks such as Indonesia's decadal Chikungunya surge of 15,324 cases in 2013 during neutral-to-weak Pacific SST conditions ($ONI = -0.2417^{\circ}C$), or the decay during the severe 2015 El Niño ($ONI = +1.5583^{\circ}C$)—highlight the limitations of simple, direct-forcing climate models.

To evaluate these complex climate-disease relationships, longitudinal epidemiological registries require rigorous analytical approaches that account for non-normal distributions and temporal structures (Ehelepola et al., 2021; Zhang et al., 2026). Time-series data often exhibit secular trends and internal autocorrelation that can induce spurious statistical correlations if left unaddressed. To evaluate these complex, non-linear climate-disease relationships without introducing temporal autocorrelation or artificial variance inflation, longitudinal epidemiological registries must be analyzed at their original, un-interpolated temporal resolutions. Applying robust non-parametric bivariate frameworks specifically Spearman's rank correlation coupled with local polynomial regression (LOESS) smoothing allows for the isolation of macro-environmental signals and the evaluation of threshold-dependent, non-monotonic epidemic dynamics without assuming strict linear causal pathways (Barrera et al., 2023; Hutter et al., 2018; Shackleton et al., 2023; Zheng et al., 2020).

This study directly fills a critical scientific gap by establishing a rigid analytical framework to evaluate the teleconnection between the global ONI and local Chikungunya transmission in Indonesia over a comprehensive longitudinal horizon spanning twelve years (2012–2023). To preserve statistical integrity and avoid synthetic temporal autocorrelation artifacts, data were analyzed at their original annual temporal resolution ($n = 12$). We applied non-parametric Spearman rank correlation and local polynomial regression (LOESS) smoothing to isolate pure environmental signals and evaluate non-linear dynamics (Liao et al., 2015; Sánchez et al., 2025).

2. METHOD

Research Design

This study adopts a quantitative framework utilizing a longitudinal associative design to investigate inter-annual teleconnections. Specifically, the research evaluates the long-distance

relationship between macro-climatic global anomalies and the temporal dynamics of local Chikungunya epidemiological cycles in Indonesia over a decadal horizon (2012–2023). By assessing these macro-environmental drivers, the design isolates how large-scale ocean-atmospheric oscillations influence nationwide disease burdens over extended temporal scales.

Data and Data Sources

The data utilized in this study consist of annual aggregate secondary records spanning from January 2012 to December 2023 ($n = 12$ years). The variables under investigation are defined as follows:

1. **Dependent Variable (Health Metric):** The historical annual aggregate count of recorded Chikungunya cases in Indonesia. This dataset was retrieved from the official epidemiological surveillance reports compiled by the Directorate General of Disease Prevention and Control (Ditjen P2P), Ministry of Health of the Republic of Indonesia.
2. **Independent Variable (Macro-Climate Index):** The annual mean of the Oceanic Niño Index (ONI), sourced from the Climate Prediction Center of the National Oceanic and Atmospheric Administration (NOAA). The annual index was computed by calculating the arithmetic mean of the monthly ONI values for each respective calendar year, serving as a proxy for the dominant phase of the El Niño-Southern Oscillation (ENSO) cycle (El Niño, La Niña, or Neutral).

Data Preprocessing and Structuring

Data synchronization and structural formatting were executed within the R Studio statistical environment. To preserve the statistical integrity of the dataset and mitigate the risk of artificial variance inflation, the data were maintained at their original annual temporal resolution. Restructuring the annual macro-level records into synthetic monthly increments was intentionally avoided to prevent temporal autocorrelation artifacts and replication bias. The final longitudinal dataframe systematically pairs the total annual disease burden directly against the synchronized mean intensity of Pacific sea surface temperature (SST) anomalies

Statistical Analysis Stages

The statistical evaluation was deployed in three sequential stages to ensure robust inference:

Stage 1: Distributional Normality Assessment. To determine the appropriate analytical paradigm (parametric vs. non-parametric) for the longitudinal time-series dataset ($n = 12$), the distributional properties of both variables—annual mean ONI and aggregate Chikungunya cases—were evaluated using the Shapiro-Wilk normality test. The test statistic (W) is mathematically calculated as:

$$W = \frac{(\sum_{i=1}^n a_i x_{(i)})^2}{\sum_{i=1}^n (x_i - \bar{x})^2}$$

Where

$x_{(i)}$ represents the i -th order statistic (the i -th smallest value in the sample),

$\bar{x}$ is the sample mean ($\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$),

a_i are calculated weights derived from the covariances, variances, and means of the order statistics from a normal distribution.

The test evaluates the null hypothesis (H_0) that the data conform to a Gaussian distribution. Obtaining a p -value < 0.05 indicates a significant departure from normality, thereby establishing the empirical justification for non-parametric correlational modeling.

Stage 2: Teleconnection Rank Correlation Modeling. Following the rejection of distributional normality for the disease metric ($p = 0.0113$), a non-parametric Spearman's rank correlation model was executed to quantify the strength, direction, and statistical significance of the synchronous teleconnection. The Spearman rank correlation coefficient (ρ) is computed as:

$$\rho = 1 - \frac{6 \sum_{i=1}^n d_i^2}{n(n^2 - 1)}$$

Where

$d_i = R(X_i) - R(Y_i)$ is the difference between the ranks of corresponding values of the annual mean ONI (X_i) and aggregate Chikungunya cases (Y_i) for year i ,

n is the total number of paired annual observations ($n = 12$).

To test the statistical significance of ρ , the test statistic t is derived using the Student's t -distribution approximation with $n - 2$ degrees of freedom:

$$t = \rho \sqrt{\frac{n - 2}{1 - \rho^2}}$$

Given the annual temporal resolution constraint—which precludes the application of multi-month lag structures via Cross-Correlation Functions (CCF)—this synchronized rank formulation serves as the primary rigorous measure of immediate inter-annual macro-climatic forcing.

Stage 3: Categorical Analysis of Decadal Epidemic Peaks. Complementing the inferential rank correlation, a categorical assessment was integrated to contextualize the historical epidemic peaks of 2013 ($Y_{2013} = 15,324$) and 2023 ($Y_{2023} = 6,049$). against dominant ENSO states. These explosive epidemiological anomalies were systematically cross-referenced against the synchronized mean ENSO thermal intensity ($\bar{X}_{\text{ONI}}$) to evaluate whether nationwide resurgences coincide with positive Pacific SST forcing ($\bar{X}_{\text{ONI}} > +0.5^\circ\text{C}$) or function through non-linear eco-immunological thresholds.

3. RESULTS AND DISCUSSION

Result

The annual temporal progression of macro-climatic forcing and nationwide Chikungunya disease burden across Indonesia over the 12-year observational window reveals an epidemiological profile characterized by distinct, highly explosive outbreak waves separated by prolonged periods of endemic quiescence (Figure 1). The longitudinal dataset highlights a pronounced double-peak epidemic pattern anchored by major outbreaks in 2013 and 2023. Following a minor baseline elevation in 2012 ($Y_{2012} = 2,602$), nationwide transmission surged exponentially to reach a decadal maximum of 15,324 cases in 2013 (Y_{2013}). Crucially,

this primary nationwide epidemic unfolded during a neutral-to-weak Pacific thermal state, where the annual mean Oceanic Niño Index was slightly negative ($\bar{X}_{\text{ONI}} = -0.2417^{\circ}\text{C}$). Over the subsequent multi-year period, case reports decayed progressively, reaching an all-time decadal trough in 2018 ($Y_{2018} = 97$ cases). Notably, even during the severe, canonical El Niño event of 2015 ($\bar{X}_{\text{ONI}} = +1.5583^{\circ}\text{C}$), Chikungunya incidence continued its downward trajectory ($Y_{2015} = 2,282$), indicating that strong global thermal forcing alone was insufficient to sustain transmission.

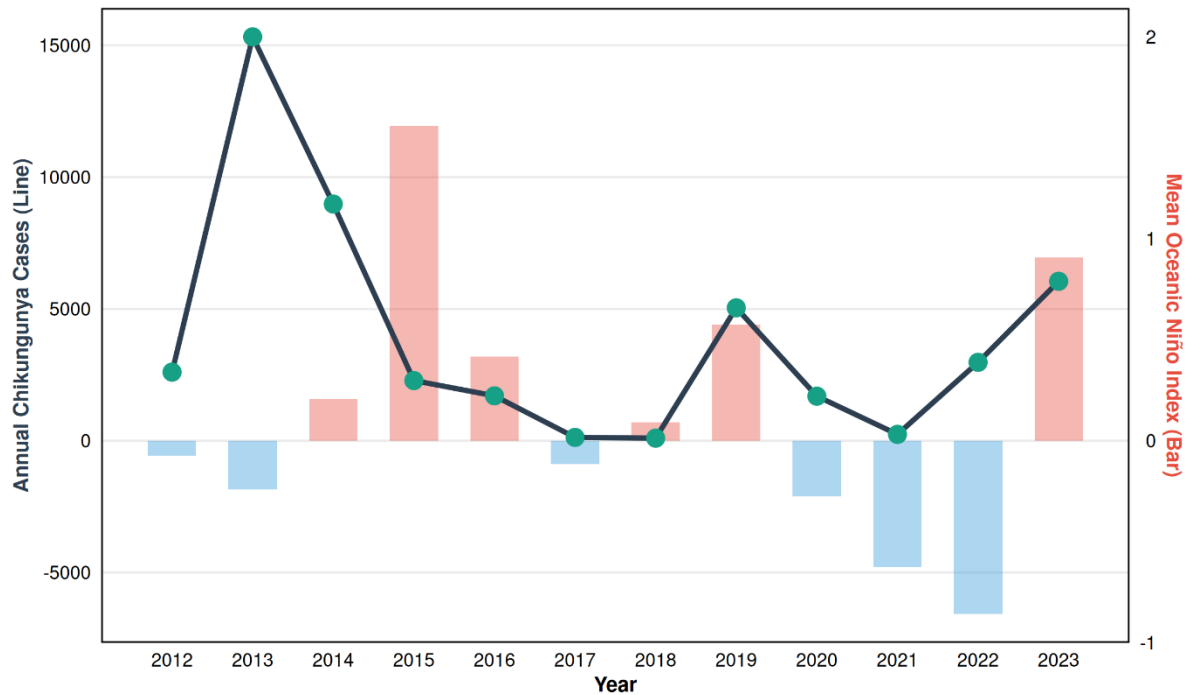


Figure 1 Inter-annual temporal dynamics of nationwide Chikungunya incidence and Oceanic Niño Index (ONI) anomalies in Indonesia (2012–2023)

Following this extended period of low-level endemic persistence, disease incidence experienced a major secondary resurgence between 2022 and 2023. Transmission escalated from 2,974 cases in 2022 to 6,049 cases in 2023 (Y_{2023}), coinciding with the re-emergence of positive Pacific Sea Surface Temperature anomalies ($\bar{X}_{\text{ONI}} = +0.9083^{\circ}\text{C}$). To evaluate whether this synchronous alignment reflected a direct macro-climatic driver, non-parametric rank correlation modeling and local regression smoothing were executed (Figure 2). The bivariate scatterplot demonstrates widespread dispersion of annual observations across the coordinate space. The Spearman rank correlation yielded a weak positive monotonic coefficient ($\rho = 0.2168$) that was statistically non-significant ($p = 0.4986$), confirming that synchronous inter-annual fluctuations in ONI do not share a direct, statistically meaningful linear relationship with nationwide disease burden.

The underlying non-linear dynamic is further emphasized by the non-parametric LOESS regression curve in Figure 2, which displays a non-monotonic trajectory rather than a uniform upward slope. The local smoothing trajectory indicates that severe nationwide epidemic spikes, such as the 2013 anomaly, occur independently of high positive ONI thresholds. Conversely, years marked by intense El Niño forcing did not systematically translate into heightened epidemiological risk. Taken together, these empirical findings demonstrate that annual nationwide Chikungunya dynamics in Indonesia are not governed by a simple direct-

forcing macro-climatic mechanism. Instead, the teleconnection operates within a complex, non-linear framework, suggesting that global climate indices act primarily as background environmental modulators whose impacts are mediated by local eco-immunological factors, including multi-year herd immunity decay.

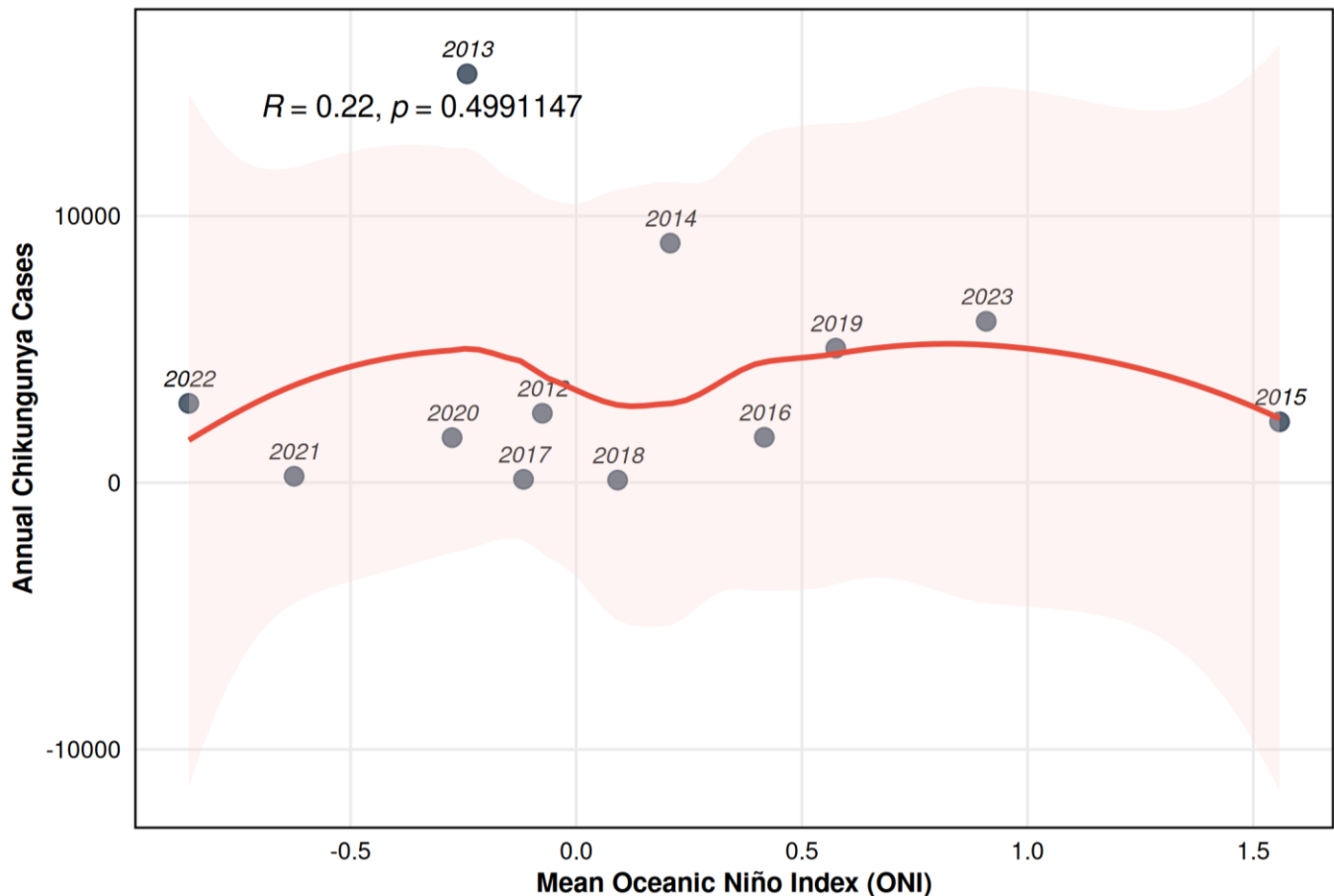


Figure 2 Bivariate Spearman rank correlation scatterplot and LOESS regression between annual mean ONI and Chikungunya cases (2012–2023)

Discussion

The empirical evaluation of annual nationwide Chikungunya transmission and Pacific Sea Surface Temperature anomalies across Indonesia from 2012 to 2023 reveals a complex, non-linear interaction between macro-climatic drivers and regional disease burden (**Figure 1**). Statistical diagnostic testing via the Shapiro-Wilk test confirmed that while annual mean ONI values exhibited a normal distribution ($W = 0.9656, p = 0.8593$), annual Chikungunya case counts departed significantly from normality ($W = 0.8073, p = 0.0113$). This non-normal epidemiological distribution justified the implementation of non-parametric bivariate analysis, which yielded a weak positive Spearman rank correlation coefficient ($\rho = 0.2168$) that was statistically non-significant ($p = 0.4986$) at the aggregated annual scale (**Figure 2**). The non-monotonic LOESS local regression smoothing curve further highlights that explosive nationwide epidemic surges—most notably the decadal peak of 15,324 cases in 2013—occurred independently of high positive ONI thresholds, whereas the canonical El Niño of 2015 ($\bar{X}_{\text{ONI}} = +1.5583^{\circ}\text{C}$) coincided with a continued decline in disease incidence.

The absence of a statistically significant linear correlation at the annual aggregate level does not imply that macro-climatic forcing plays no role in Chikungunya dynamics across the Indonesian archipelago. Instead, it demonstrates that macro-climatic indices operate non-linearly and are strongly mediated by localized eco-immunological factors. From an entomological perspective, climate fluctuations alter vector competence and extrinsic incubation period (EIP) thresholds for *Aedes aegypti* and *Aedes albopictus* within optimal biological ranges (Rao et al., 2026; Kakarla et al., 2019). However, when climate data are aggregated into broad annual averages, short-term seasonal dynamics and immediate environmental triggers become smoothed out. Furthermore, large-scale outbreaks, such as the major surge in 2013, are heavily driven by human behavioral responses—such as domestic water storage during dry spells (Linthicum et al., 2016)—and multi-year population immunity cycles, which can obscure direct annual climate-disease synchronization.

These findings mirror the transient and non-monotonic patterns documented in arboviral climate studies across Southeast Asia. As highlighted by Yuan et al. (2025) and Huang et al. (2019), atmospheric teleconnections and disease transmission often display phase shifts and non-linear responses depending on localized transmission contexts and environmental baselines. Rather than following a direct, synchronous linear pathway, global ocean thermal signals act as background modulators whose actual impact on localized transmission intensity depends heavily on vector density thresholds, local micro-climates, and susceptibility within the human host population.

For public health administration and epidemiological surveillance in Indonesia, these results provide critical practical insights. Relying solely on raw, unadjusted annual climate metrics like the ONI is insufficient for predicting nationwide Chikungunya outbreak intensity. Instead, integrated surveillance frameworks must combine global climate indicators with local meteorological data, vector density metrics, and population immunity tracking (Huitts et al., 2025). Transitioning from a simplistic linear climate-response model toward a multi-factor epidemiological framework will enable public health authorities to better anticipate resurgence risks and deploy proactive mitigation strategies before localized transmission reaches severe epidemic thresholds.

The primary limitation of this study lies in its dependency on national-level aggregated annual records (n=12 years), which was necessitated by the lack of verified, continuous monthly epidemiological surveillance data at the sub-national scale. While maintaining the analysis at this coarse temporal resolution preserves statistical validity and prevents artificial replication bias, it inevitably smooths out short-term seasonal dynamics, localized meteorological variations, and immediate environmental triggers (e.g., weekly rainfall spikes or temperature anomalies). Consequently, future research should prioritize the establishment of high-resolution, sub-national spatio-temporal datasets. Integrating regional meteorology, vector density indices (such as Container Indices), and age-stratified seroprevalence data will enable the construction of multi-factorial, predictive early warning systems that surpass the limitations of global macro-climatic indices

4. CONCLUSION

An empirical evaluation of nationwide Chikungunya transmission and ENSO macro-climatic variability (ONI) in Indonesia from 2012 to 2023 revealed that annual case counts departed

significantly from a normal distribution ($W = 0.8073, p = 0.0113$) and exhibited a weak, statistically non-significant positive Spearman correlation ($\rho = 0.2168, p = 0.4986$), with non-linear LOESS regression confirming that the decadal epidemic peak in 2013 (15,324 cases) occurred independently of high El Niño thresholds. These findings demonstrate that global macro-climatic signals do not drive Chikungunya burden through a simple linear pathway, but instead operate within a complex, non-linear framework mediated by local vector ecology (*Aedes aegypti/albopictus*), human water-storage behaviors during dry spells, and multi-year host immunity dynamics. Consequently, public health authorities in Indonesia must transition from simplistic linear climate-response assumptions toward integrated, multi-factorial surveillance frameworks that combine climate indicators, vector density metrics, and population immunity tracking to strengthen proactive outbreak prevention.

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