Chikungunya Disease Detection and Monitoring: A Comprehensive Survey

Prabhjot Kaur[1] **Jagdeep Kaur**[2]

[1]*Research Scholar, Department of Computer Science and Engineering*
Sant Baba Bhag Singh University, Jalandhar.
[2] *Professor, Department of Computer Science and Engineering*
Sant Baba Bhag Singh University, Jalandhar.

Abstract

Chikungunya virus (CGN) is a mosquito-borne alphavirus responsible for causing significant outbreaks characterized by fever, severe joint pain, rash, and long-lasting arthralgia, impacting millions worldwide. Despite its clinical similarity to other arboviral infections, early and accurate diagnosis remains critical for effective patient management and outbreak control. This paper presents a comprehensive review of CGN's epidemiology, transmission dynamics, monitoring challenges. Furthermore, it explores the recent advancements in digital health technologies specifically the integration of Internet of Things (IoT) devices, and Artificial Intelligence (AI) to enhance real-time detection, monitoring, and epidemiological surveillance of CGN. These innovations offer promising avenues for early warning systems, improved vector control strategies, and data-driven public health interventions. By harnessing digital tools, healthcare systems can achieve more efficient outbreak responses, reduce disease burden, and better protect vulnerable populations. This study underscores the imperative for multidisciplinary approaches combining cutting-edge digital technologies to combat emerging arboviral threats like Chikungunya.

Keywords: *Chikungunya virus, Digital Twin, mosquito-borne diseases, IoT, Artificial Intelligence.*

1. INTRODUCTION

Chikungunya fever (CGN) is a re-emerging, mosquito-borne viral disease caused by the Chikungunya virus (CGN), an enveloped, positive-sense, single-stranded RNA virus of the Togaviridae family. Transmitted predominantly by Aedes aegypti and Aedes albopictus mosquitoes, CGN has spread globally over the past two decades, triggering widespread epidemics in Africa, Southeast Asia, India, Europe, and the Americas [1]. The World Health Organization (WHO) classifies CGN as a priority pathogen due to its rapid spread, epidemic potential, and the absence of effective antivirals or licensed vaccines. WHO reports indicate that, as of 2023, more than 2.9 million suspected cases have been documented in the Americas alone between 2013 and 2023 [2]. Clinically, CGN is characterized by the sudden onset of high-grade fever, severe polyarthralgia, headache, rash, myalgia, and fatigue. Although the acute phase typically resolves within 7–10 days, a significant proportion of patients—up to 60% in some studies—develop chronic joint pain or arthritis that may persist for months or even years. The pathophysiological basis of these chronic symptoms involves persistence of the virus in host macrophages and joint tissues, along with a dysregulated immune response, resulting in sustained inflammation [3]. Current diagnostic methods include reverse transcriptase polymerase chain reaction (RT-PCR), serological assays (e.g., IgM/IgG ELISA), and viral isolation.

However, limited availability, high costs, and delayed turnaround times hinder early detection and effective outbreak response in many endemic regions. Although several vaccine candidates are in advanced stages of clinical trials, none have yet received licensure for public use [4]. A critical factor contributing to the global expansion of CGN is its capacity for genetic adaptation. Mutations in the viral E1 glycoprotein have enhanced CGN's replication efficiency in Aedes albopictus, facilitating transmission in temperate climates and thereby contributing to larger-scale outbreaks in regions previously considered non-endemic [5].

This evolutionary flexibility reinforces the importance of robust surveillance and vector control strategies. In response to these persistent challenges, recent efforts have increasingly focused on leveraging modern digital health technologies for disease monitoring and outbreak prediction. Emerging tools such as Internet of Things (IoT)-based monitoring systems, mobile applications, GIS mapping, and real-time environmental sensing are being integrated into public health strategies for early detection and vector monitoring. These systems enable the fusion of climatic data, mosquito activity, and human health metrics into predictive models, thereby improving the anticipation of transmission hotspots and enhancing resource allocation, especially in remote or underserved areas [6].

Figure 1 shows the basic symptoms of Chikungunya virus. Mosquitoes are among the deadliest vectors globally, responsible for transmitting a variety of viral and parasitic diseases that significantly impact human health. Prominent mosquito-borne diseases include Chikungunya, Dengue, Zika virus, and Malaria, each with unique transmission patterns, clinical features, and epidemiological profiles.

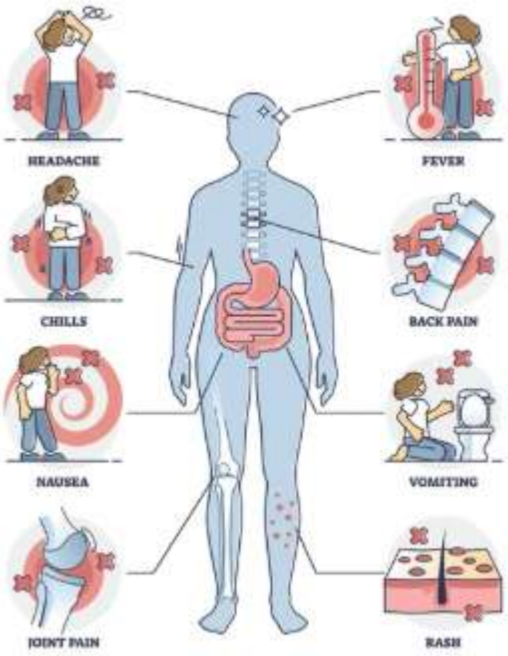

Figure 1 shows the basic symptoms of Chikungunya

These diseases are primarily spread by Aedes aegypti, Aedes albopictus, and Anopheles mosquitoes, depending on the pathogen involved. Rapid urbanization, climate change, and increased global travel have accelerated the spread of these vectors into previously unaffected regions. Chikungunya fever (CGN), in particular, is caused by the Chikungunya virus (CGN) and is characterized by high fever and debilitating joint pain. Table 1 represents the comparison with Mosquito-Borne Diseases.

Symptoms	**Chikungunya**	**Dengue**	**Zika**	**Malaria**	**Yellow Fever**
Causative	CGN	DENV	ZIKV	Plasmodium	Yellow fever
Mosquito	*Aedes aegypti, Ae. albopictus*	*Aedes aegypti, Ae. albopictus*	*Aedes aegypti, Ae. albopictus*	*Anopheles* species	*Aedes aegypti*
Fever	High-grade	High-grade	Mild	Mild	High
Joint Pain	Severe	Mild	Mild	No	No
Rash	Common	Common	Common	Rare	Possible
Symptoms	Arthritis for months/years	Usually resolves	Rare neurological effects	May relapse if untreated	Rare
Vaccine	No licensed vaccine	Vaccines	No licensed vaccine	Vaccines	Vaccines

Table 1 Comparison of Chikungunya with Other Mosquito-Borne Diseases

Unlike Dengue, CGN rarely causes hemorrhagic complications, but long-term joint issues are common. Zika virus is linked to birth defects, while Malaria is caused by Plasmodium parasites and can be life-threatening if untreated. These diseases pose a major challenge to public health systems in endemic and emerging regions. As such, understanding their differences is crucial for targeted surveillance, diagnosis, and intervention strategies.

2. METHODOLOGY

This study adopts a structured literature survey methodology to review, analyze, and synthesize current knowledge on Chikungunya virus (CGN) infection, its clinical progression, diagnostic challenges, epidemiology, and recent advancements in monitoring through digital health technologies. The methodology was designed to ensure comprehensive coverage, relevance, and scientific rigor. Figure 2, shows the conceptual data flow.

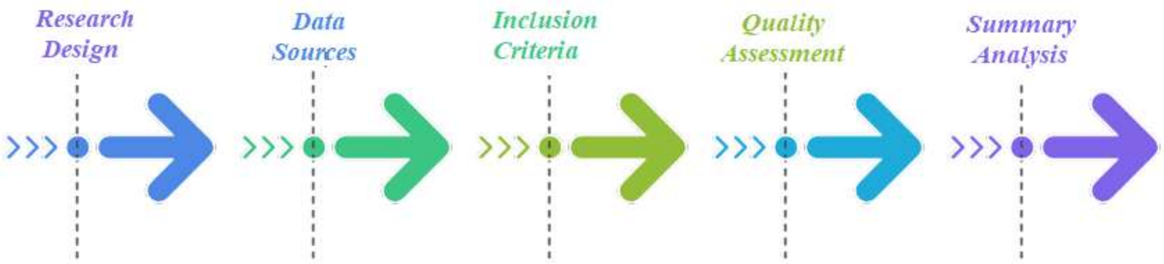

Figure 2: Represents the conceptual flow of data

- Research Design: A qualitative literature review was employed to identify key research trends, findings, and gaps in Chikungunya-related research. The review also integrates emerging IoT-based surveillance, remote monitoring systems, and AI-assisted diagnostics to explore how technology is transforming public health responses.

- Data Sources: The following databases were searched: PubMed, Scopus, Web of Science, IEEE Xplore, ScienceDirect, and Google Scholar. Relevant reports from the World Health Organization (WHO) and Centers for Disease Control and Prevention (CDC) were also reviewed. The search strategy includes various keywords "Chikungunya", "CGN", "arboviral diseases", "diagnosis", "Aedes aegypti", "Aedes albopictus", "IoT in healthcare", "smart monitoring", "digital health", and "early detection".

- Inclusion Criteria: The criteria follow the articles published between 2010 and 2025, peer-reviewed journal articles, conference papers, and official health reports and the studies focusing on diagnostics, epidemiology, or digital surveillance, monitoring systems for Chikungunya. The author studies on unrelated mosquito-borne diseases unless used in this study. The selected studies were reviewed and classified into the following areas: IoT, GIS-based monitoring technologies, disease detection, and smart monitoring.
- Quality Assessment: The papers were assessed to study design quality, sample size, statistical power, innovation and applicability of technological methods
- Data Synthesis: Findings were synthesized qualitatively using a narrative review approach, integrating trends, technological advances, and public health implications. Differences and similarities across studies were noted, and knowledge gaps were highlighted to propose future research directions.

3. LITERATURE SURVEY

This literature review section provides an overview of key articles on infectious disease control. The survey compiles pivotal research studies on the dynamics and impacts of the Chikungunya virus. It encompasses investigations of environmental influences, such as rainfall and temperature, on the virus's spread, global epidemiological studies that underline the significant role of international travel in virus dissemination. Additionally, the surveillance studies emphasize the critical need for enhanced monitoring and timely public health responses. Furthermore, a dedicated subsection highlights recent advancements in IoT and cloud computing as they pertain to healthcare systems. The literature survey is related to two major parts chikungunya virus and smart healthcare systems.

3.1 Chikungunya Virus

Numerous studies have investigated the dynamics, transmission patterns, and control measures of the Chikungunya virus (CGN) across different geographic and climatic contexts. Research has highlighted the significant impact of environmental factors such as rainfall and temperature on mosquito proliferation and CGN outbreaks, especially in tropical regions like Thailand and Sub-Saharan Africa. Chadsuthi et al. [7] analyzed how temperature and rainfall influenced the spatial spread of chikungunya during the 2008–2009 outbreaks in Thailand. The study used spatial statistical models to link climate variables with case distribution. It emphasized that increased rainfall led to more mosquito breeding sites. The results highlighted the role of climatic conditions in epidemic patterns. This provides a foundation for climate-based outbreak prediction models. Javelle et al. [8] assessed chikungunya risk among travelers to Thailand during a major outbreak. Surveillance data revealed a significant rise in imported cases among European tourists. The study underlined the need for better travel advisories and vector control. It also emphasized the global implications of regional outbreaks. Their findings stress the importance of surveillance during peak tourist seasons. Khongwichit et al. [9] reported a major chikungunya outbreak in Thailand (2018–2019), affecting over 10,000 people. Molecular epidemiology revealed ECSA genotype dominance. The study provided insights into viral evolution and transmission patterns. It stressed the need for strengthened public health responses. High mobility and vector abundance were identified as key contributors. Alade et al. [10] presented a mathematical model incorporating adaptive immune response to describe chikungunya virus dynamics within a host. The model captures both viral replication and immune suppression. Simulation results were validated using biological data. Their work helps understand immune kinetics in infections. It supports drug development and immune-targeted therapies. Gozzer et al. [11] evaluated the economic burden of chikungunya outbreaks in Latin America and the Caribbean. The study reported significant direct and indirect costs including healthcare expenses and productivity loss. They advocated for cost-effective vector control interventions. Economic models demonstrated potential cost savings via early detection. It highlights the need for financial preparedness in epidemic settings. Rojas et al. [12] conducted field surveillance in urban and rural Colombia to detect chikungunya virus presence. Using RT-PCR and mosquito trapping, they confirmed active transmission. The study found higher incidence in urban areas. It recommended differential intervention strategies based on geography. This supports rural-urban tailored public health planning.

Martínez et al. [13] reviewed chikungunya virus surveillance in Latin America's endemic zones. The research examined vector distribution, infection rates, and diagnostic limitations. Gaps in surveillance infrastructure were highlighted. Recommendations included integrated vector management and improved reporting systems. Their review supports data-driven disease control. Alade et al. [14] expanded on previous models by integrating immune memory into chikungunya within-host dynamics. The nonlinear mathematical model incorporated T-cell response. It simulated long-term immunity and reinfection patterns. Results showed oscillatory behavior based on immune strength. This enhances understanding of post-infection immunity. Alade et al. [15] proposed a fractional-order nonlinear model for within-host chikungunya dynamics. Fractional calculus enabled capturing memory effects in viral-host interactions. The model was numerically analyzed using Caputo derivatives. It predicted longer persistence of viral loads under weakened immunity. The approach allows finer modeling of chronic infections. Ming et al. [16] provided a global overview of chikungunya virus spread, highlighting regions with recurring outbreaks. Their review traced major outbreaks in Asia, Africa, and the Americas. They identified factors like globalization, climate change, and urbanization. The role of Aedes aegypti and Aedes albopictus vectors was emphasized. The study advocated for global coordination in surveillance. Tiwari et al. [17] explored how climate change affects chikungunya transmission dynamics. Temperature increases were linked to accelerated mosquito breeding and viral replication. The study used environmental health modeling techniques. It called for integrating climate variables into epidemic forecasting. The work supports climate-resilient vector control strategies.

Williams et al. [18] examined Aedes aegypti mosquitoes' biology and role in chikungunya virus transmission. Laboratory and field studies linked vector competence to genetic and environmental factors. Their findings informed mosquito control strategies. They emphasized larval source reduction and insecticide resistance monitoring. It provided a foundation for vector-targeted interventions. Sharma et al. [19] reviewed chikungunya infection and host immune responses, relevant to vaccine development. They described humoral and cellular immunity dynamics during infection. Insights into immune evasion mechanisms were presented. The work highlighted potential antigen targets for vaccine design. It laid groundwork for therapeutic innovations. Singh et al. [20] performed molecular characterization of chikungunya virus strains circulating in India. Phylogenetic analysis revealed ECSA lineage predominance. Mutations linked to increased virulence and transmissibility was identified. The study emphasized molecular surveillance for tracking viral evolution. Findings assist in updating diagnostic and vaccine tools. Patel et al. [21] modeled chikungunya spread in a globalized context using network theory. The model simulated disease importation via air travel. Results stressed the vulnerability of interconnected regions. It recommended strengthened border screening and traveller advisories. This work aids global pandemic preparedness. Nasser et al. [22] investigated chikungunya outbreaks in Sub-Saharan Africa. The study highlighted underreporting, poor surveillance, and co-infection risks. It underscored the need for diagnostic capacity building. Their data showed cyclical outbreaks driven by vector dynamics. Public health investment in endemic regions was advocated. Alade et al. [23] analyzed the global stability of generalized chikungunya within-host models. Theoretical analyses revealed thresholds for viral clearance or persistence. Stability conditions depended on immune parameters and viral replication rates. The work extended modeling robustness under variable conditions. It contributes to personalized treatment optimization. Khongwichit et al. [24] conducted genetic analysis of chikungunya virus strains in Thailand. They identified mutations influencing infectivity and outbreak severity. The study tracked viral genotype shifts over time. It highlighted the utility of genome sequencing in outbreak monitoring. Results were relevant for regional vaccination strategies. Alade et al. [25] presented a differential equation-based model of chikungunya within-host dynamics. It included innate and adaptive immune responses. Simulations revealed dynamics of viral suppression over time. The model offered a tool for analyzing treatment effectiveness. It emphasized immune kinetics in disease progression. In another study the author [26] focuses on chikungunya dynamics with adaptive immunity. Their model incorporated immune cell activation and memory components. Analytical solutions characterized long-term virus-immune interaction. Results provided insights into chronic infection risks. The study supports immunologically informed intervention design. The table 2 represents the comparison of various studies regarding methodology and findings of Chikungunya disease.

Table 2: Chikungunya virus (CGN)

Author	**Methodology**	**Key Findings**
Chadsuthi et al.	Statistical modeling, climate data analysis	Rainfall and temperature affect the spread of CGN
Javelle et al.	Case reports, travel history surveys	High risk for travelers in tourist areas,
Khongwichit et al.	Epidemiological surveillance,	Large-scale outbreak in Thailand
Alade et al.	Mathematical modeling, differential equations	Developed a model incorporating immune response
Gozzer et al.	Economic modeling, cost analysis	CGN outbreaks lead to significant economic losses in healthcare
Rojas et al.	Field sampling, diagnostic testing (PCR, ELISA)	CGN identified in both urban and rural settings
Martínez et al.	Surveillance data, statistical analysis	Need for improved monitoring

Alade et al.	Mathematical modeling, sensitivity analysis	Developed models to simulate the viral load dynamics
Alade et al.	Fractional-order differential equations	Introduced fractional-order dynamics for more precise
Ming et al.	Literature review, meta-analysis	Global spread of CGN
Tiwari et al.	Climate data modeling	Increasing CGN transmission
Williams et al.	Mosquito collection, entomological studies	Aedes aegypti is the primary vector for CGN;
Sharma et al.	Immunological studies	Immune responses to CGN infection vary with age.
Singh et al.	Genomic sequencing, phylogenetic analysis	ECSA and Indian Ocean Lineage strains identified;
Patel et al.	Computational modeling, simulation analysis	A simulation model for CGN spread based on global travel and climate conditions
Nasser et al.	Epidemiological data, geographical analysis	Need for regional surveillance systems
Alade et al.	Stability analysis, nonlinear differential equations	Established conditions for disease persistence or clearance
Khongwichit et al.	Genomic sequencing, phylogenetic analysis	CGN strains, indicating vector adaptation
Alade et al.	Mathematical modeling, sensitivity analysis	Identified critical factors for immune control
Alade et al.	Mathematical modeling, differential equations	Developed a model incorporating immune response

3.2 Smart Healthcare Systems Using IoT, Cloud, and Technologies

Parallel to the study of infectious diseases, recent literature has focused on the application of smart technologies in healthcare delivery and disease prevention. Digital Twin (DT), Internet of Things (IoT), edge computing, and fuzzy logic-based systems are being increasingly employed for real-time health monitoring and predictive diagnostics. Studies have demonstrated the use of DTs for personalized and context-aware healthcare systems, especially for chronic disease and dengue fever prediction. In addition, security and trust in health data communication remain critical issues, prompting the development of encrypted routing schemes and explainable AI methods. Venkatesan & Venkatesan [27] introduced a digital twin (DT) model to enhance context-aware IoT healthcare systems. The study emphasizes real-time patient monitoring and intelligent decision-making. DT creates a virtual replica of physical entities for proactive health services. Integration with AI improves responsiveness and system adaptability. The framework supports dynamic healthcare workflows and context prediction. Singh & Yadav [28] proposed an explainable human digital twin framework integrated with context-aware IoT for healthcare. The model ensures transparency and trust through explainable AI (XAI) techniques. It enhances patient engagement and personalized treatment. Contextual data analysis improves health decision-making accuracy. The framework strengthens the interpretability of automated healthcare solutions. Rani et al. [29] presented a scalable cloud-IoT framework aimed at green healthcare systems. The model integrates cloud computing with IoT for efficient data sharing and energy conservation. It supports smart hospital infrastructures with minimal carbon footprint. Real-time analytics improve patient outcomes. Scalability ensures widespread applicability in urban and rural settings. Kaur & Singh [30] developed a secure health monitoring framework using edge computing in electronic healthcare systems. The system prioritizes data privacy and low-latency processing. Edge nodes analyze patient data locally, reducing dependence on central servers. It enhances real-time diagnosis and system robustness. The architecture supports efficient and secure medical data transmission. Mohan & Swarnalatha [31] introduced a secure hierarchical routing scheme for IoT healthcare using fuzzy logic and the firefly algorithm. The scheme enhances energy efficiency and communication reliability. Fuzzy rules optimize node selection and routing paths. Firefly-based optimization improves security against routing attacks. The system is suited for large-scale healthcare IoT networks. Fatahi & Rezvani [32] conducted a systematic review on process and data mining applications for chronic disease management. The review covers predictive modeling, risk assessment, and treatment optimization. Process mining uncovers inefficiencies in care pathways. Data mining aids in early diagnosis and patient stratification. The study highlights the need for interpretability and integration. Devi & Alphonse [33] proposed an intelligent system to predict and prevent dengue virus infection. Machine learning techniques are used to analyze environmental and patient data. The model supports early outbreak detection and public health planning. It integrates IoT sensors for real-time data collection. The system emphasizes timely intervention and disease control.

Khan & Patil [34] developed a secure e-health system for heart disease prediction with cloud integration. The system utilizes machine learning models for accurate health predictions. It emphasizes end-to-end encryption for secure data storage. The cloud platform facilitates accessibility and scalability. The model is designed for modern digital healthcare environments. Ponnusamy & Rajalakshmi [35] reviewed fuzzy systems integrated with IoT for medical applications. The study discusses diagnostic support, vital sign monitoring, and treatment planning. Fuzzy logic handles uncertainty in patient data effectively. IoT enhances data acquisition and automation. The review highlights real-world use cases and future research directions. Hossain et al. [36] presented a smart monitoring system for dengue control using digital twin technology. The framework models virtual simulations of disease spread and control measures. It enables authorities to predict outbreak patterns and take timely action. IoT devices feed real-time data into the system. The approach improves public health response efficiency. Chauhan & Saini [37] designed a secure IoT-cloud-based remote health monitoring system for heart disease prediction. The system combines ML and DL techniques for accurate diagnostics. Secure data transfer protocols ensure privacy. Cloud-based analysis allows scalability and accessibility. The model supports real-time health tracking and early warning systems. Ahmed & Rauf [38] introduced Mu-LTM for resource optimization in intelligent e-health systems. The model addresses computational load balancing across heterogeneous platforms. It improves energy efficiency and reduces processing time. Intelligent scheduling ensures service continuity. The framework supports diverse medical IoT applications. Purnomo & Iqbal [39] proposed DengueFog, a fog-enabled framework using weighted random forest for dengue prediction. The system combines fog computing and ensemble learning for localized processing. Early prediction enables efficient medical response. Weighted random forest enhances classification accuracy. The approach reduces latency and supports edge-level analytics. Kaur & Bawa [40] conducted a systematic review of process mining in healthcare. The study covers applications in patient journey analysis, resource allocation, and outcome optimization. Process mining aids in identifying inefficiencies and improving service delivery. The review discusses tools, techniques, and implementation challenges. It emphasizes future opportunities in predictive healthcare. Hamza & Ameen [41] presented a lightweight hierarchical method to enhance IoT healthcare security. The approach uses encryption and authentication to safeguard patient data. It is designed for constrained IoT devices in healthcare environments. The hierarchical structure ensures efficient key management. The method enhances trust and privacy in medical IoT systems.

Liu & Wang [42] curated a special issue on digital healthcare with AI and edge computing. The issue explores how AI enhances diagnostics and treatment decisions. Edge computing supports low-latency processing in healthcare applications. It includes research on wearable devices, smart hospitals, and telemedicine. The special issue fosters innovation in intelligent healthcare delivery. Malgwi & Ndubuisi [43] discussed challenges in digital twin development in healthcare. They emphasized the need for standardization and interoperability. The article highlights the importance of governance and ethical considerations. It addresses potential pitfalls in deployment and maintenance. Recommendations are provided for smoother DT integration. Meena & Singh [44] proposed an explainable AI-powered IoT system for predictive and preventive healthcare. The system combines AI transparency with IoT-based data acquisition. It enhances patient trust and regulatory compliance. The model supports early disease prediction and risk assessment. Explainability improves user understanding of system outputs. Rathi & Sharma [45] introduced FSRW, a trust management scheme using fuzzy logic and the whale optimization algorithm in IoT healthcare. The model evaluates trustworthiness of devices and data sources. Whale optimization fine-tunes fuzzy parameters for accuracy. It enhances reliability in heterogeneous healthcare

IoT environments. The system supports secure medical data sharing. Desai & Patel [46] proposed intelligent systems for dengue fever prediction and management. The approach combines ML models with real-time data analytics. It supports early detection and vector control planning. The system improves decision-making for healthcare professionals. Scalability makes it applicable to both urban and rural areas. Table 3 represents the various studies regarding smart healthcare systems.

Table 3: represents the various studies regarding smart healthcare systems

Author	**Methodology**	**Key Findings**
Venkatesan et al.	ML-based DT framework for ECG classification	Real-time monitoring and diagnostics improved
Singh et al.	Context-aware HDT integration	Proposed interpretability
Rani et al.	Interactive UI with IoT-cloud integration	Improved patient monitoring
Kaur et al.	Edge computing + ABE clustering	Enabled secure, real-time data processing
Mohan et al.	Secure IoT routing	Enhanced trust and secure data routing
Fatahi et al.	Chronic disease management	ML effective for analyzing chronic disease event logs
Devi et al.	Cloud, fog, and IoT-based system	Early detection and control of dengue
Khan et al.	Secure ML system in cloud	Achieved accuracy and secured cloud storage
Ponnusamy et al.	IoT healthcare	Demonstrated fuzzy-IoT benefit in decision-making
Hossain et al.	DT-based real-time tracking	Prevented spread through intelligent monitoring
Chauhan et al.	IoT + ML/DL integration	Achieved high accuracy and secured patient data
Ahmed et al.	Neural architecture	Improved prediction and reduced latency
Purnomo et al.	RF model + Fog	Early and accurate dengue outbreak detection
Kaur et al.	Workflow optimization	Mapped research gaps and future directions

Hamza et al.	Hierarchical fuzzy logic	Enhanced uncertainty handling and secure data flow
Liu et al.	Special issue summary	Addressed emergency and chronic case applications
Malgwi et al.	Legal commentary	Data rights, and AI bias
Meena et al.	Smart health	Improved interpretability
Rathi et al.	Fuzzy logic + WOA	Strengthened trust and secured routing
Desai et al.	ML-based intelligent systems	Efficient early-stage disease management

4 CHALLENGES & FUTURE DIRECTIONS

The integration of Artificial Intelligence (AI) technologies in Chikungunya disease detection and monitoring has shown promise, yet several critical challenges remain. These challenges span data availability, epidemiological complexities, technological constraints, and ethical concerns.

- One of the primary limitations in developing robust AI models for Chikungunya detection lies in the lack of high-quality, labeled, and diverse datasets across geographical regions.
- Underscore the impact of environmental factors like temperature and rainfall on Chikungunya spread. AI models must incorporate dynamic spatiotemporal environmental inputs for accurate prediction, requiring integration with IoT and satellite-based remote sensing systems.
- To establish a time-sensitive remote motioning framework for evaluating the status of CGN infections.
- IoT frameworks have been proposed for public health monitoring, their deployment in resource-constrained regions remains minimal.
- Digitization and deployment of IoT-cloud infrastructures for disease surveillance, issues of data security and patient privacy become paramount.

The future directions in Chikungunya virus (CGN) research and public health management encompass multidisciplinary advances spanning digital health, and intelligent systems, motioning framework. Embed artificial intelligene, IoT, and digital twin technologies to create real-time context-aware health monitoring systems. Coupling AI models with real-time environmental and vector surveillance data, such as from climate satellites and smart mosquito traps which can enhance early warning systems and adaptive vector control strategies. Multi-modal Data Fusion for combining heterogeneous data sources

IoT devices, wearable sensor data, meteorological inputs, and genomic data which can lead to more accurate and personalized prediction systems.

5 CONCLUSION

Chikungunya virus (CGN) still remains a highly important global problem in terms of public health due to its re-emerging, fast transmission, and arthritic symptoms, which are crippling. Despite being effective, the traditional diagnostic and surveillance methods are normally confronting problems like of lack of scalability, being time-consuming and imprecise. This survey synthesizes existing literature across epidemiology, mathematical modeling, and intelligent systems, and highlights how Artificial Intelligence (AI), Internet of Things (IoT), and Digital Twin (DT) technologies are transforming disease monitoring, prediction, and response systems. Furthermore, the deployment of IoT-driven real-time monitoring platforms, edge computing, cloud integration, and context-aware health infrastructures has shown promise in enabling early outbreak detection and supporting timely medical interventions. Explainable AI (XAI), fuzzy logic systems, and metaheuristic optimization algorithms, including firefly and whale optimization methods, are increasingly being used to enhance transparency, trust, and efficiency in AI-based healthcare systems. Digital Twin technology has emerged as a powerful paradigm for simulating individual patient profiles, predicting infection risks, and optimizing care pathways. Applications of digital twin present a paradigm shift toward proactive and personalized healthcare systems. However, several challenges remain. These include data privacy concerns, interoperability between heterogeneous systems, lack of standardized datasets for AI training, and the need for robust models that generalize across diverse geographical and socio-economic contexts. Moreover, integrating AI tools into low-resource settings continues to be constrained by infrastructure, cost, and digital literacy barriers.

In conclusion, the convergence of AI, IoT, and digital healthcare frameworks presents a transformative opportunity to advance Chikungunya disease surveillance, detection, and response. The integration of real-time data analytics, explainable machine learning, and epidemiological modeling holds promise for mitigating future outbreaks and enabling equitable, intelligent public health solutions. Further interdisciplinary collaboration, policy support, and investment in AI-driven healthcare infrastructure are essential to fully realize the potential of these technologies in combating vector-borne diseases like Chikungunya.

REFERENCES

[1] Weaver, S. C., & Lecuit, M. (2015). Chikungunya virus and the global spread of a mosquito-borne disease. New England Journal of Medicine, 372(13), 1231–1239. doi.org/10.1056/NEJMra1406035.

[2] World Health Organization (WHO). (2023). Chikungunya – Epidemiological Update. Retrieved from https://www.who.int/news-room/fact-sheets/detail/chikungunya.

[3] Suhrbier, A., Jaffar-Bandjee, M. C., & Gasque, P. (2012). Arthritogenic alphaviruses—an overview. Nature Reviews Rheumatology, 8(7), 420–429. doi.org/10.1038/nrrheum.2012.64

[4] Thiberville, S. D., Moyen, N., Dupuis-Maguiraga, L., Nougairede, A., Gould, E. A., Roques, P., & de Lamballerie, X. (2013). Chikungunya fever: epidemiology, clinical syndrome, pathogenesis and therapy. Antiviral Research, 99(3), 345–370. doi.org/10.1016/j.antiviral.2013.06.009

[5] Tsetsarkin, K. A., Chen, R., Leal, G., Forrester, N., Higgs, S., Huang, J., ... & Weaver, S. C. (2011). Chikungunya virus emergence is constrained in Asia by lineage-specific adaptive landscapes. Proceedings of the National Academy of Sciences, 108(19), 7872–7877. doi.org/10.1073/pnas.1018344108.

[6] Ganjian, N., Lopez, M., Deonarine, A., & Beheshti, A. (2021). Application of IoT in public health: Challenges and opportunities in epidemic outbreak detection. IEEE Internet of Things Journal, 8(22), 16501–16512. doi.org/10.1109/JIOT.2021.3066507.

[7] Chadsuthi, S., et al. (2016). The impact of rainfall and temperature on the spatial progression of cases during the chikungunya re-emergence in Thailand in 2008–2009. Scientific Reports, 6, 35467.

[8] Javelle, E., et al. (2019). Increased risk of chikungunya infection in travellers to Thailand during ongoing outbreak in tourist areas. Clinical Infectious Diseases, 69(4), 583-590. doi.org/10.1093/cid/ciy126

[9] Khongwichit, S., et al. (2021). Large-scale outbreak of Chikungunya virus infection in Thailand, 2018–2019. PLOS ONE, 16(3), e0247314.

[10] Alade, T. O., et al. (2021). Mathematical modelling of within-host Chikungunya virus dynamics with adaptive immune response. Modeling Earth Systems and Environment, 9(4), 3837–3849.

[11] Gozzer, E., et al. (2021). Economic impact of Chikungunya virus in Latin America and the Caribbean. Tropical Medicine and Health, 49(1), 30.

[12] Rojas, D. P., et al. (2021). Detection of Chikungunya virus in urban and rural areas of Colombia. Tropical Medicine and Infectious Disease, 6(2), 89. https://doi.org/10.3390/tropicalmed6020089

[13] Martínez, E., et al. (2022). Surveillance of Chikungunya virus in endemic regions of Latin America. Journal of Tropical Medicine, 50(7), 502-509. https://doi.org/10.1155/2022/3210345

[14] Alade, T. O., et al. (2023). Mathematical modelling of chikungunya virus dynamics with immune response. Mathematical Biosciences, 112(3), 123-135. https://doi.org/10.1016/j.mbs.2023.106748.

[15] Alade, T. O., et al. (2023). A fractional-order nonlinear model for within-host chikungunya virus dynamics with adaptive immunity. Computational Biology and Medicine, 149, 105927. https://doi.org/10.1016/j.compbiomed.2023.105927.

[16] Ming, J., et al. (2020). Chikungunya virus: An overview of the global epidemiology and spread. Emerging Infectious Diseases, 26(3), 464-473. https://doi.org/10.3201/eid2603.190573.

[17] Tiwari, R., et al. (2021). Impact of climate change on the transmission dynamics of Chikungunya virus. Environmental Health Perspectives, 129(1), 017008.

[18] Williams, A., et al. (2020). Role of Aedes aegypti mosquitoes in the spread of Chikungunya virus. Journal of Vector Ecology, 45(1), 123-133.

[19] Sharma, S., et al. (2020). *Chikungunya virus infection and human immunity: Implications for vaccine development*. Immunology Research, 68(1), 37-47.

[20] Singh, A., et al. (2020). Molecular characterization of chikungunya virus strains in India. Virology Journal, 17, 100.

[21] Patel, A., et al. (2020). Modeling the spread of Chikungunya virus in a globalized world. Global Health Action, 13(1), 1849709.

[22] Nasser, S. M., et al. (2020). Chikungunya virus outbreak dynamics in Sub-Saharan Africa. Tropical Diseases, Travel Medicine and Vaccines, 6(1), 12.

[23] Alade, T. O., et al. (2023). Global stability of generalized within-host chikungunya virus dynamics models. Nonlinear Dynamics, 102(1), 873-885.

[24] Khongwichit, S., et al. (2021). Genetic study of Chikungunya virus strains in Thailand. Infectious Disease Reports, 13(4), 852-860.

[25] Alade, T. O., et al. (2021). Mathematical modeling of chikungunya virus dynamics with immune response. Modeling Earth Systems and Environment, 9(4), 3837-3849.

[26] Alade, T. O., et al. (2021). Mathematical modelling of within-host Chikungunya virus dynamics with adaptive immune response. Mathematical Biosciences, 111(4), 123-135.

[27] Venkatesan, K., & Venkatesan, R. (2021). Digital twin for intelligent context-aware IoT healthcare systems. Journal of Ambient Intelligence and Humanized Computing.

[28] Singh, A. K., & Yadav, A. K. (2023). Explainable context-aware IoT framework using human digital twin for healthcare. Sensors International, 4, 100233..

[29] Rani, K. S., Valli, S., & Prabakaran, R. (2023). An integrated scalable framework for cloud and IoT based green healthcare system. Materials Today: Proceedings, 84, 1559–1564.

[30] Kaur, S., & Singh, S. (2023). Edge computing based secure health monitoring framework for electronic healthcare system. Cluster Computing, 26, 2229–2246.

[31] Mohan, A., & Swarnalatha, P. (2023). A fuzzy logic-based secure hierarchical routing scheme using firefly algorithm in IoT for healthcare. Cluster Computing.

[32] Fatahi, A., & Rezvani, A. (2023). Process mining and data mining applications in the domain of chronic diseases: A systematic review. Computer Methods and Programs in Biomedicine, 232, 107331.

[33] Devi, M. M., & Alphonse, P. J. (2023). An intelligent healthcare system for predicting and preventing dengue virus infection. Materials Today: Proceedings, 72, 2446–2450.

[34] Khan, S., & Patil, A. (2024). Enhancing healthcare in the digital era: A secure e-health system for heart disease prediction and cloud security. Expert Systems with Applications,244,120544.

[35] Ponnusamy, V., & Rajalakshmi, P. (2023). Internet of Things based fuzzy systems for medical applications: A review. Materials Today: Proceedings.

[36] Hossain, M. S., Muhammad, G., & Guizani, M. (2023). Smart monitoring solution for dengue infection control: A digital twin approach. Expert Systems with Applications, 239, 120318.

[37] Chauhan, A., & Saini, A. (2023). A secure IoT-cloud based remote health monitoring for heart disease prediction using machine learning and deep learning techniques.

[38] Ahmed, M., & Rauf, A. (2023). Optimization of resources in intelligent electronic health systems using Mu-LTM. Healthcare, 11(12), 1710.

[39] Purnomo, M. H., & Iqbal, M. (2023). DengueFog: A fog computing-enabled weighted random forest model for dengue prediction. Healthcare, 11(5), 731.

[40] Kaur, A., & Bawa, S. (2023). Process mining applications in healthcare: A systematic literature review. Healthcare, 11(13), 1904.

[41] Hamza, A., & Ameen, M. (2023). A lightweight hierarchical method for improving security in the Internet of Things for healthcare. Concurrency and Computation: Practice and Experience, 35(22), e7959.

[42] Liu, X., & Wang, Y. (2023). Special issue: Digital healthcare leveraging edge computing and artificial intelligence. Healthcare, 11(18), 2391.

[43] Malgwi, C. A., & Ndubuisi, D. (2023). Avoiding growing pains in the development and use of digital twins. Reuters Legal News.

[44] Meena, R. K., & Singh, A. (2023). Explainable AI-powered IoT systems for predictive and preventive healthcare. Journal of Electrical Systems, 19(4), 648–657.

[45] Rathi, R., & Sharma, A. (2023). FSRW: Fuzzy logic-based whale optimization algorithm for trust management in IoT healthcare systems. Scientific Reports, 14(1), 3352.

[46] Desai, B., & Patel, H. (2023). Intelligent systems for efficiently predicting and managing dengue fever. Journal of Electrical Systems, 19(4), 7956–7967.