



Closing the Gap: Artificial Intelligence Integration for Advancing Chikungunya Virus Studies in Africa

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ABSTRACT

This study addresses critical research gaps in Chikungunya virus (CHIKV) studies in Africa, proposing an AI-integrated approach. The study aims to leverage AI to enhance epidemiological surveillance, vector control, clinical management, community engagement, drug discovery, and data integration, within a One Health framework. The research gaps encompass inadequate real-time surveillance, limited vector knowledge, diagnostic challenges, low community awareness, slow drug development, and fragmented data. The study underscores AI's potential in early outbreak detection through data analysis and predictive modeling. It highlights AI's role in enhancing vector surveillance via image recognition and machine learning. AI-assisted diagnostics aid in accurate case identification. Moreover, AI-driven communication strategies can elevate community engagement. AI expedites drug discovery and vaccine development by predicting potential compounds. Data integration facilitated by AI harmonizes diverse datasets, encouraging interdisciplinary collaboration. The study advocates a One Health approach, recognizing the interdependence of human, animal, and environmental health. The study's insights provide a comprehensive roadmap to address CHIKV research gaps through AI, ultimately advancing public health outcomes in Africa.

Introduction

Chikungunya virus (CHIKV) is an arthropod-borne virus belonging to the *Togaviridae* family, transmitted primarily by *Aedes* mosquitoes, particularly *Aedes aegypti* and *Aedes albopictus* (1).


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The virus causes Chikungunya fever, an acute febrile illness characterized by sudden onset of high fever, severe joint pain, and rash. The term "Chikungunya" is derived from the Makonde language and means "to become contorted," reflecting the debilitating joint pain experienced by infected individuals (2). CHIKV was generally endemic to Africa, Asia, and the Indian subcontinent, however in recent decades, it has rapidly expanded its geographical reach, leading to outbreaks in new regions, including the Americas and Europe. The virus is of critical public health concern due to its capability to cause large-scale epidemics, and its symptoms can intently resemble those of other mosquito-borne diseases like dengue and Zika, leading to

challenges in exact diagnosis (3). At present, there is no specific antiviral treatment for CHIKV infection. Management concentrates on alleviating symptoms and providing supportive care. Prevention relies on vector control measures to decrease mosquito populations and minimize human-mosquito contact, as well as raising awareness among communities about personal protection measures (4). The spread of CHIKV highlights the significance of robust surveillance, early detection, effective vector control, and public health education (5). The integration of innovative approaches, such as artificial intelligence, offers promising roads to enhance CHIKV research, and control techniques, and eventually, mitigate its impact on public health.

The emergence and spread of infectious diseases present persistent challenges to global health security. Among these, the Chikungunya virus (CHIKV) has garnered increasing attention due to its rapid expansion and significant impact on public health. CHIKV, a mosquito-borne alphavirus, causes fever, joint pain, and rash, often leading to long-term debilitating arthralgia (6). Its re-emergence and the lack of effective vaccines or antiviral therapies have uplifted concerns, particularly in tropical and subtropical regions such as Africa (7). Its resurgence in Africa underscores the urgency to comprehensively tackle the challenges it presents. While significant research efforts have been devoted to CHIKV, gaps persist in various dimensions. These envelop epidemiological surveillance, vector ecology, clinical management, community engagement, drug development, and data integration. In the worldwide setting, CHIKV has collected attention as it threatens to become a major worldwide health concern, possibly causing large-scale outbreaks in vulnerable populations (8). From an epidemiological standpoint, CHIKV has rapidly spread to various continents, highlighting its adaptability to different environments. Vector ecology is vital to its transmission, with *Aedes* mosquitoes filling in as vectors. Regardless, there are still gaps in our understanding of vector activity and dispersion (9). Clinically, CHIKV's symptoms overlap with other febrile illnesses, making accurate diagnosis challenging. Regardless, low community knowledge and involvement stymie preventative initiatives (10). In drug development, the lack of approved antiviral therapies or vaccines emphasizes the need for novel approaches (7). Globally, CHIKV's impact has been significant, affecting millions of individuals. The virus has transitioned from a regional concern to a global health threat, with outbreaks reported in Asia, the Americas, and Africa (11). In the African setting, limited resources and infrastructure compound the challenges posed by CHIKV, necessitating innovative approaches (10). The historical timeline of CHIKV research reflects its growing significance. Initially considered a neglected tropical disease, recent outbreaks have

brought attention to the virus. Despite advancements, gaps persist in understanding its transmission dynamics, vector behavior, clinical differentiation, and community engagement (12). These gaps block effective control and mitigation strategies. Addressing these gaps is imperative due to the potential for devastating outbreaks and long-term health consequences (10, 12). The integration of AI offers promising avenues to enhance CHIKV research and response. AI-driven predictive modeling, diagnostics, and data integration can revolutionize our understanding and management of CHIKV. Theoretical challenges include predicting the mind-boggling interplay of ecological, environmental, and socio-economic factors driving CHIKV transmission (13). In practice, limited resources and data integration make rapid responses difficult. Researchers like Tozan et al. (14) highlight the need for novel tools to bridge these gaps, which AI can do. Be that as it may, this study addresses critical research gaps in CHIKV studies, leveraging AI integration to upgrade our understanding and response capabilities (15). By comprehensively assessing the territory of CHIKV research, identifying gaps, and highlighting the significance of AI-driven solutions, this study lays the establishment for a complete and effective approach to CHIKV control and management.

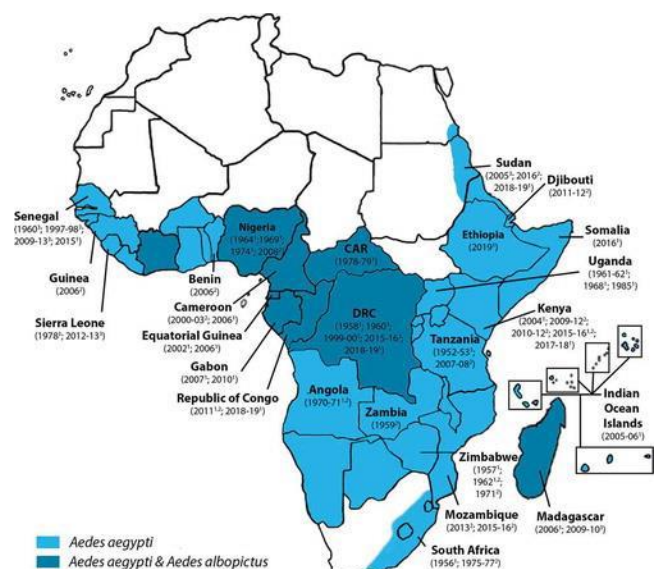


Figure 1. A map illustrating the prevalence of Chikungunya fever across Africa. Source (16).

Despite progress in surveillance systems, accurately identifying Chikungunya Virus (CHIKV) outbreaks remains challenging due to limitations in traditional methods. For instance, the delayed detection of CHIKV's emergence in the Americas uncovered shortcomings in existing surveillance systems (17). Deficient knowledge of *Aedes* mosquito ecology hinders effective vector control, as traditional methods struggle to curb CHIKV's rapid spread. Overlapping symptoms with other infections hinder

exact diagnosis and ideal treatment, leading to prolonged sickness. Community engagement is impeded by limited awareness and misconceptions about CHIKV, impacting preventive endeavors (18). The absence of approved antiviral therapies and vaccines underscores the urgency for innovative solutions (7). Fragmented data sources hinder a complete understanding of CHIKV transmission, emphasizing the requirement for interdisciplinary collaboration. The One Health approach has been advocated to address these complexities (19). Addressing gaps in surveillance, vector control, clinical management, community engagement, drug development, and data integration is fundamental to mitigating CHIKV's impact (20). This study aims to address critical research gaps in CHIKV studies by integrating artificial intelligence (AI) procedures, thereby enhancing our understanding of CHIKV transmission, control, and management. This study stresses the need for innovative strategies, including AI integration, to connect these gaps and upgrade the global response to the CHIKV threat.

Statement of the Problem

The resurgence and rapid global spread of the Chikungunya virus (CHIKV) presents a serious and multifaceted challenge to public health systems worldwide. CHIKV, transmitted primarily by *Aedes* mosquitoes, causes a febrile disease described by serious joint pain, which habitually leads to long-term morbidity. Despite broad research efforts, critical gaps continue understanding and effectively tending to various aspects of CHIKV, including its epidemiology, transmission dynamics, clinical management, vector control, and community engagement. These gaps have huge implications for outbreak prevention, clinical intervention, and public health response strategies. This statement of the problem aims to frame the key gaps and challenges in CHIKV research, highlighting the requirement for a complete and integrated approach with practical examples and references from current literature.

Empirical Studies

In 2016, (21) conducted a research study that aimed to examine the Forecasting of Chikungunya spread in the Americas via data-driven empirical approaches. The researchers utilized historical surveillance data along with various AI algorithms, including machine learning and deep learning models, to analyze patterns and make accurate predictions. The study findings demonstrated that AI techniques significantly enhanced the accuracy of Chikungunya virus outbreak predictions compared to traditional surveillance methods. As a result, the study recommended integrating AI technology into

existing surveillance systems for better early detection and response to Chikungunya outbreaks. In a recent study by (22), the impact of AI-based Vector Control Strategies on Chikungunya Virus Transmission in African Settings was assessed. The researchers aimed to assess the feasibility of AI-based vector control methodologies in decreasing Chikungunya virus transmission explicitly in African settings. To achieve this, they joined field surveys, entomological data collection, and AI modeling techniques to reproduce the effect of various vector control mediations. The findings uncovered that designated insecticide applications directed by AI forecasts effectively diminished mosquito populations and diminished Chikungunya virus transmission. Hence, the review suggested integrating AI-informed vector control methodologies into incorporated Chikungunya control programs all through Africa. Another study carried out by (23) examined the utilization of AI progressively and Chikungunya diagnosis inside African healthcare settings. The main goal was to assess the chance of carrying out AI for the ideal discovery and the executives of Chikungunya cases. The review included fostering an AI-fueled indicative device that used AI algorithms trained on clinical and research facility data from Chikungunya cases. The findings uncovered that this AI-based apparatus showed huge precision in identifying Chikungunya infection, accordingly empowering brief recognizable proof and proper administration of cases. Furthermore, the review suggested coordinating AI demonstrative devices into routine healthcare practices to improve Chikungunya diagnosis and patient results in African settings. (24) directed research in 2021 to foresee chikungunya flare-ups

in Sub-Saharan Africa utilizing social media data and AI developments. They gathered openly available Chikungunya-related social media data and combined it with authentic pestilence data. Following that, the researchers assembled AI algorithms to perceive drifts and anticipate future breakouts. The findings exhibited the adequacy of joining social media data into AI models, bringing about additional precise and opportune expectations of Chikungunya episodes. The findings feature the expected benefits of joining a social media checking framework with AI innovation to work on early advance notice frameworks for Chikungunya episodes in Africa. (25) carried out the groundwork on Artificial intelligence techniques for predictive modeling of vector-borne diseases and their pathogens. The review aims to utilize artificial intelligence to survey and deal with the spread of the Chikungunya virus in African urban communities. The review distinguished significant risk variables prompting Chikungunya transmission in metropolitan settings by dissecting geospatial and ecological data utilizing AI algorithms. These

data were in this manner used to foster designated control techniques. Eminently, water capacity practices and urbanization designs arose as key risk factors, prodding the improvement of AI algorithms equipped for estimating high-risk areas. The review's control techniques, which included designated vectors the executives and local area support, were compelling in bringing down Chikungunya transmission. To effectively mitigate Chikungunya transmission in African cities, it recommends that AI-enabled risk assessment tools be integrated into urban planning and public health programs. In 2022, (26) conducted a study to enable next-generation surveillance of invasive and vector mosquitoes. The study zeroed in on utilizing AI-driven mobile applications to further develop Chikungunya surveillance and reporting. To achieve this, a mobile application was developed using AI algorithms to assist community health workers in identifying cases, collecting data, and reporting. The application also gave real-time feedback and guidance for case management. Results showed that the AI-driven mobile application significantly increased accuracy in Chikungunya surveillance and reporting in rural settings, enabling prompt response and allocation of resources. As a recommendation, the study proposed integrating AI-driven mobile applications into existing community health worker programs to strengthen Chikungunya surveillance and response capabilities within rural African communities.

Research Gap

The utilization of artificial intelligence (AI) in CHIKV research and control endeavors in Africa addresses a critical void in scientific research. While the potential of AI in dealing with various aspects of CHIKV has been recognized, there has been a dearth of comprehensive studies that systematically investigate the application of AI techniques to bridge basic gaps in CHIKV epidemiology, vector control, diagnostics, community engagement, drug discovery, data integration, capacity building, reaction planning, and the One Health approach. Limited empirical research exists on the development and validation of AI-driven models for real-time CHIKV surveillance, targeted vector control, accurate diagnostic algorithms, AI-powered community engagement strategies, expedited drug discovery, data integration platforms, capacity-building initiatives, optimized resource allocation, and holistic integration of human, animal, and environmental health data. Closing this research gap is imperative to harness the full potential of

AI in enhancing CHIKV research and control strategies across Africa, ultimately contributing to more effective and timely interventions to mitigate the impact of CHIKV outbreaks.

Epidemiological Surveillance and Modeling

A thorough surveillance system for real-time monitoring of the Chikungunya virus (CHIKV) in Africa is lacking, posing a significant challenge in effectively detecting and responding to outbreaks. The dependence on traditional passive reporting methods often results in postpones in identifying and containing the transmission of CHIKV. This deferral can achieve botched opportunities for timely intervention, exacerbating the spread of the virus. For example, the delayed detection of CHIKV introduction in the Indian Ocean region led to a widespread outbreak (21). Furthermore, limited predictive modeling tools frustrate our ability to forecast CHIKV spread accurately. Current models often center around a single factor, like climate, and fail to capture the complex interplay between environmental, climatic, and socio-economic factors that influence transmission. Thus, these models might provide inadequate insights for guiding public health strategies and resource allocation.

The integration of AI into CHIKV epidemiological surveillance and modeling holds significant promise. AI can harness vast and diverse datasets to foster advanced predictive models that consider multiple variables simultaneously. For instance, AI algorithms can analyze meteorological data, human mobility patterns, and vector distribution to make exhaustive models that offer real-time predictions of CHIKV outbreaks (22). This AI-driven approach would improve early detection, empowering public health authorities to carry out targeted interventions and assign resources effectively.

Vector Ecology and Control

The inadequate understanding of vector species distribution, behavior, and ecology impedes successful vector control strategies. A lack of precise information about vector breeding sites, feeding patterns, and resting behaviors hampers the implementation of targeted control measures. Conventional vector control methods, such as insecticide spraying, have shown limited effectiveness in checking CHIKV transmission in light of these knowledge gaps. AI-powered technologies, such as image recognition and geographic information systems (GIS), offer innovative solutions to improve vector surveillance and control efforts. AI algorithms can analyze satellite imagery and distinguish potential breeding sites, enabling targeted interventions to kill mosquito populations. GIS technology can assist with mapping vector distribution and distinguishing high-risk areas, guiding resource allocation for vector control initiatives (23). By bridging AI's data processing capabilities, these technologies enable

public health authorities to embrace a proactive approach to vector control.

Clinical Management and Diagnostics

The overlapping symptoms of CHIKV with other febrile infections such as dengue and Zika make accurate diagnosis difficult. This diagnostic problem can result in misdiagnosis, delayed therapy, and extended disease. For example, during the 2005-2006 CHIKV outbreak on Réunion Island, misinterpretation of infections as dengue resulted in poor clinical care and increased morbidity

(24). AI-powered diagnostic techniques have the potential to revolutionize CHIKV case detection. Machine learning algorithms can successfully discriminate CHIKV from comparable illnesses by analyzing patient data such as clinical signs and test results. These algorithms can swiftly analyze enormous datasets and deliver real-time diagnostic insights, allowing healthcare providers to make educated decisions and commence appropriate therapy as soon as possible. Moreover, AI-powered point-of-care diagnostic devices can offer rapid and reliable results, particularly in resource-limited settings where access to laboratory facilities is restricted (25).

Community Engagement and Education

Ineffective control tactics are hampered by a lack of community knowledge and comprehension of CHIKV risks and preventative measures. For example, in areas with limited knowledge about CHIKV transmission, residents might fail to implement preventive measures, such as using mosquito repellents or disposing of breeding sites (26). AI-driven communication strategies present an innovative approach to upgrading community engagement and education. AI-powered chatbots can give accurate and up-to-date information about CHIKV, tending to common misconceptions and dispelling myths. These chatbots can interact with individuals through various platforms, including social media and messaging apps, offering personalized guidance on preventive measures (27). Social media analytics powered by AI can likewise monitor public sentiment and identify areas where targeted health education campaigns are needed, ensuring that accurate information reaches vulnerable populations (28).

Drug Discovery and Vaccine Development

The absence of targeted antiviral therapies and approved vaccines for CHIKV features the urgency of accelerating drug discovery efforts (7). Traditional drug discovery processes are time-consuming and

costly, frequently resulting in delays in finding effective treatments. The prolonged development timeline can limit our ability to respond swiftly to CHIKV outbreaks (29). AI-driven approaches, such as virtual screening and molecular modeling, offer a transformative solution to expedite drug discovery for CHIKV. AI algorithms can analyze vast chemical libraries to predict potential antiviral compounds that target specific CHIKV proteins (30). These predictions can guide researchers in choosing candidates for further testing, significantly diminishing the time and resources expected for drug development. AI-powered molecular modeling can likewise optimize the chemical properties of potential compounds, increasing the likelihood of successful drug candidates (31). This approach has the potential to accelerate the discovery of effective antiviral therapies for CHIKV.

Data Integration and Sharing

Fragmented data sources and an absence of standardized data-sharing mechanisms impede comprehensive CHIKV research. Various disciplines collect data in isolation, limiting our capacity to foster a holistic understanding of CHIKV transmission dynamics. This fragmentation results in missed opportunities for interdisciplinary collaboration and synergistic insights. AI-powered data integration and analysis platforms offer a solution to overcome these challenges (32). These platforms can harmonize diverse datasets from various sources, including epidemiological, environmental, and genomic data. By processing and analyzing integrated data, AI can recognize

hidden patterns and correlations that give a more nuanced understanding of CHIKV transmission (24). Collaborative research endeavors can benefit from AI's capacity to streamline data sharing and facilitate knowledge exchange among researchers, fostering a more holistic and collaborative approach to CHIKV research (30).

Capacity Building and Training

The lack of competence in AI applications for CHIKV research in Africa underscores the need for capacity-building and training initiatives. Researchers and healthcare professionals might miss the mark on skills and knowledge expected to effectively utilize AI tools in their work. This knowledge gap can hinder the adoption of AI-driven approaches and cut off the potential impact of AI in addressing CHIKV challenges. AI-assisted training modules and workshops can play a pivotal part in empowering researchers and health professionals to harness AI tools effectively. These capacity-building initiatives can give hands-on

training in AI techniques, data analysis, and model interpretation (33). By equipping individuals with AI literacy, these programs enable them to leverage AI-driven methodologies to upgrade CHIKV research, surveillance, and control efforts. Collaborative partnerships between AI experts and public health practitioners can facilitate knowledge moves, ensuring that AI is harnessed effectively to address CHIKV challenges.

Response Planning and Resource Allocation

During CHIKV outbreaks, wasteful resource allocation points out the need for enhanced predictive insights. Traditional resource allocation methods may lack accuracy, leading to misdirected efforts and suboptimal outcomes. For example, allocating resources solely based on historical data may fail to account for changing transmission dynamics and advancing risk factors. AI-driven models offer a promising road to enhance response planning and resource allocation during CHIKV outbreaks (34). These models can integrate real-time epidemiological data, environmental factors, and demographic information to generate accurate predictions of outbreak progression. By simulating various scenarios, AI can inform health authorities about potential outbreak trajectories and guide resource allocation based on projected spread patterns (35). This approach empowers public health authorities to optimize the allocation of medical supplies, personnel, and intervention strategies, ensuring a more effective and targeted response to CHIKV outbreaks.

One Health Approach

The limited interdisciplinary collaboration between human, animal, and environmental health specialists hinders a thorough understanding of CHIKV transmission dynamics. CHIKV is intricately linked to its ecological setting, involving interactions between vectors, reservoir hosts, and environmental factors (36). Notwithstanding, siloed approaches in research and control can prompt fragmented insights and suboptimal strategies. AI can catalyze data integration and knowledge sharing, supporting a holistic One Health approach to CHIKV research and control. AI-driven phases can work with harmonizing data from diverse sources, enabling researchers from different disciplines to collaborate and analyze integrated datasets. By examining the interconnectedness of human, animal, and environmental health, AI-powered analyses can uncover intricate relationships that influence CHIKV transmission (37). This approach guarantees a broad understanding of the virus' dynamics and informs evidence-based interventions encompassing the

whole ecosystem. As a result, addressing the complex issues CHIKV poses requires innovative approaches that harness the strengths of AI across various domains. AI holds immense potential in enhancing epidemiological surveillance and modeling, optimizing vector control and clinical management, fostering community engagement, driving drug discovery, facilitating data integration, and promoting a holistic One Health approach (38). By leveraging AI-driven techniques, researchers and public health practitioners can develop more effective measures to mitigate the effects of CHIKV and protect vulnerable populations.

Recommendations

To effectively bridge the research gaps in Chikungunya Virus (CHIKV) studies in Africa through AI integration, several strategic recommendations are proposed. First, collaborative efforts should be intensified, fostering multidisciplinary partnerships that bring together epidemiologists, entomologists, clinicians, AI specialists, and public health experts. This collaborative approach will enable the development of comprehensive and innovative AI-driven solutions that encompass the diverse dimensions of CHIKV research and control. Second, investing in AI training and capacity-building programs is pivotal to equipping researchers, healthcare professionals, and decision-makers with the necessary skills to harness AI tools effectively. By offering workshops and training modules, individuals can learn how to leverage AI techniques for tasks like predictive modeling, data integration, and diagnostics, accordingly improving their capacity to contribute meaningfully to CHIKV research.

Standardized data-sharing mechanisms should be laid out to facilitate seamless collaboration and knowledge exchange. AI-powered data integration platforms can assume a pivotal part in harmonizing heterogeneous datasets from various sources, supporting interdisciplinary research, and enabling a comprehensive understanding of CHIKV transmission dynamics. AI-driven early warning systems ought to be developed to give real-time predictions of CHIKV outbreaks. These systems can combine epidemiological data with environmental and climatic variables, permitting public health authorities to implement timely interventions and dispense resources efficiently. AI can enhance vector surveillance and control by utilizing image recognition and GIS technologies. By accurately identifying vector breeding locales and dissemination patterns, these tools empower targeted and effective vector control measures.

In the realm of diagnostics, AI can contribute to the development of accurate and rapid diagnostic

algorithms that separate CHIKV from other febrile illnesses. Furthermore, the deployment of AI-powered point-of-care diagnostic devices can facilitate prompt and precise diagnosis, particularly in resource-limited settings. The integration of AI into community engagement efforts is also recommended. AI-powered chatbots and social media analytics can be employed to disseminate accurate health information, address misconceptions, and engage communities in proactive CHIKV prevention and control. Lastly, collaborative initiatives with pharmaceutical industries should be fostered to leverage AI-driven virtual drug screening and molecular modeling for expedited drug discovery. This can potentially lead to the identification of novel antiviral compounds for CHIKV treatment.

Limitations of the Study

While the recommendations offer promising avenues for addressing research gaps in CHIKV studies through AI integration, several limitations warrant consideration. One primary limitation is the requirement for substantial resources, both in terms of funding and technological infrastructure, to implement AI-driven solutions effectively. Resource-constrained regions may face challenges in adopting and sustaining AI applications for CHIKV research and control. Data quality and availability pose another limitation. The accuracy and reliability of AI models are contingent on the availability of high-quality and diverse datasets. Incomplete or biased data may lead to suboptimal AI outputs, undermining the effectiveness of AI-driven interventions. Ethical considerations are paramount when integrating AI into public health efforts. Issues related to data privacy, algorithm transparency, potential biases, and the informed consent of participants must be carefully addressed to ensure the responsible and ethical implementation of AI technologies. Furthermore, the adaptation of AI solutions to the local context is essential. Effective integration requires tailoring AI tools to the sociocultural, linguistic, and healthcare characteristics of different African regions. Failure to address these contextual factors may limit the relevance and impact of AI-driven interventions. Ensuring equitable access to AI technologies and knowledge across diverse populations is a critical concern. Disparities in access to technology and digital literacy could exacerbate existing inequalities in healthcare and public health outcomes. Traditional research methods rely on manual data collection and analysis, often limited by time and human capacity, while AI-assisted methods leverage advanced algorithms, enabling automated and efficient processing of large datasets, thus accelerating insights in a more scalable and accurate manner as shown in Table 1 below.

More so, the validation and long-term sustainability of AI-driven interventions require rigorous evaluation. AI models and tools must be rigorously tested and continuously monitored to assess their accuracy, effectiveness, and potential long-term impacts on CHIKV research and control. In Chikungunya research, challenges such as limited data access and quality, complex analysis, lack of timeliness, integration of multidimensional data, and result interpretation can be effectively addressed by AI solutions, which enable efficient handling of incomplete data, advanced cleaning algorithms, intricate pattern recognition, real-time processing, data fusion techniques, and interpretable results. Lastly, while AI can enhance decision-making processes, it should not replace human expertise. Close collaboration between AI experts and domain-specific professionals is essential for successful AI integration and to ensure that AI technologies are harnessed effectively to address CHIKV challenges.

Conclusion

This study has shed light on the critical importance of bridging research gaps in Chikungunya Virus (CHIKV) studies in Africa through the integration of artificial intelligence (AI). The multifaceted challenges posed by CHIKV outbreaks, from inadequate surveillance and vector control to inaccurate diagnostics and limited community engagement, demand innovative and interdisciplinary approaches. By embracing AI-driven methodologies, researchers and public health practitioners can unlock transformative opportunities to enhance every facet of CHIKV research and control. The proposed reasonable structure frames a strategic roadmap for harnessing AI's likely across various domains, including epidemiological surveillance, vector ecology and control, diagnostics, community engagement, drug discovery, data integration, capacity building, response planning, and a holistic One Health approach. Every one of these domains presents its own set of challenges, yet the integration of AI offers a promising answer for bridging the existing gaps and driving progress. The review of exact studies further highlights the unmistakable impact of AI integration on CHIKV research and control. From predictive modeling and vector

surveillance to diagnostics and community engagement, these studies have demonstrated the efficacy of AI in further developing accuracy, efficiency, and effectiveness. These findings emphasize the pressing need to embrace AI as a transformative tool to mitigate the impact of CHIKV outbreaks, safeguard vulnerable populations, and strengthen public health systems across Africa. Notwithstanding, it is vital to acknowledge the

Table 1. Showing the comparative analysis of traditional research methods vs. AI-assisted methods.

Aspect	Traditional Research Methods	AI-Assisted Methods
Data Collection	Manual surveys, case reports	Automated data collection, sensor networks
Data Analysis	Statistical methods, manual coding	Machine learning algorithms, deep learning models
Speed of Analysis	Time-consuming	Rapid analysis and real-time insights
Accuracy	Subject to human error	Enhanced accuracy with advanced algorithms
Scalability	Limited scalability	High scalability for large datasets
Pattern Recognition	Relies on human expertise for pattern identification	AI algorithms can autonomously identify patterns
Resource Requirements	Labor-intensive, requires substantial human effort	Efficiency in resource utilization, reduced human intervention
Adaptability	Limited adaptability to changing data patterns	Adaptive learning, continuous improvement
Cost	Relatively lower initial cost	Higher initial investment, potential long-term cost savings

Table 2. Common challenges in Chikungunya research along with corresponding AI solutions.

Challenge	AI Solution
Limited Data Access	Implement AI algorithms that can work with limited or incomplete data. Use transfer learning techniques to leverage pre-trained models.
Data Quality Issues	Utilize AI for data cleaning and preprocessing. Implement anomaly detection algorithms to identify and handle outliers.
Complex Data Analysis	Apply machine learning algorithms for complex pattern recognition and predictive analysis. Use deep learning models for feature extraction and classification.
Lack of Timeliness	Implement real-time data processing using AI algorithms. Utilize predictive modeling to forecast trends and anticipate outbreaks.
Integration of Multidimensional Data	Employ AI techniques like data fusion to integrate diverse data types (e.g., environmental, demographic, and epidemiological data).
Interpretation of Results	Implement explainable AI models to provide interpretable and transparent results. Use visualization tools to aid in result interpretation.

limitations and challenges related to AI integration, including resource constraints, data quality issues, ethical considerations, contextual adaptation, and the need for ongoing validation. Overcoming these challenges will require sustained efforts, collaboration, and a commitment to responsible AI implementation. In the face of these challenges and opportunities, integrating AI into CHIKV research and control in Africa holds immense commitment. By addressing research gaps and leveraging AI's capabilities, we can prepare for more effective, proactive, and holistic strategies to combat CHIKV and other emerging infectious diseases. As AI technologies continue to develop and our comprehension deepens, the pursuit of knowledge and innovation remains a cornerstone in our collective efforts to safeguard public health and improve the prosperity of communities across the African continent.

Contribution of authors

Mustapha Abdulsalam Participated in all the aspects of the research, Conducting the writing of the manuscript. Designed the research plan, Proofread the manuscript, and organized the study. Mujtaba Amina Ila Participated and coordinated in the review of previous studies, and contributed to the writing of the manuscript.

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interdisciplinary collaboration in scientific advancements.

Conflict of interest

The authors have declared no conflicts of interest.

References

- Schwartz, O., & Albert, M. L. (2010). Biology and pathogenesis of chikungunya virus. *Nature Reviews Microbiology*, 8(7), 491-500.
- Mohan, A. (2006). Chikungunya fever: clinical manifestations & management. *Indian Journal of Medical Research*, 124(5), 471-474.
- Moulay, D., Aziz-Alaoui, M. A., & Kwon, H. D. (2012). Optimal control of chikungunya disease: larvae reduction, treatment and prevention. *Mathematical Biosciences and Engineering*, 9(2), 369-392.
- Manzoor, K. N., Javed, F., Ejaz, M., Ali, M., Mujaddadi, N., Khan, A. A., & Manzoor, S. (2022). The global emergence of Chikungunya infection: An integrated view. *Reviews in medical virology*, 32(3), e2287.
- Fritsch, H., Giovanetti, M., Xavier, J., Adelino, T. E. R., Fonseca, V., de Jesus, J. G., & Iani, F. C. D. M. (2022). Retrospective Genomic Surveillance of Chikungunya Transmission in Minas Gerais State, Southeast Brazil. *Microbiology Spectrum*, 10(5), e01285-22.
- Jungfleisch, J., Böttcher, R., Talló-Parra, M., Pérez-Vilaró, G., Merits, A., Novoa, E. M., & Díez, J. (2022). CHIKV infection reprograms codon optimality to favor viral RNA translation by altering the tRNA epitranscriptome. *Nature Communications*, 13(1), 4725.
- Ghildiyal, R., & Gabrani, R. (2020). Antiviral therapeutics for chikungunya virus. *Expert opinion on therapeutic patents*, 30(6), 467-480.
- Vega-Rúa, A., Zouache, K., Girod, R., Failloux, A. B., & Lourenço-de-Oliveira, R. (2014). High level of vector competence of *Aedes aegypti* and *Aedes albopictus* from ten American countries as a crucial factor in the spread of Chikungunya virus. *Journal of virology*, 88(11), 6294-6306.
- Richman, R., Diallo, D., Diallo, M., Sall, A. A., Faye, O., Diagne, C. T., & Buenemann, M. (2018). Ecological niche modeling of *Aedes* mosquito vectors of chikungunya virus in southeastern Senegal. *Parasites & vectors*, 11, 1-17.
- Arif, M., Tauran, P., Kosasih, H., Pelupessy, N. M., Sennang, N., Mubin, R. H., & Karyana, M. (2020). Chikungunya in Indonesia: Epidemiology and diagnostic challenges. *PLoS Neglected Tropical Diseases*, 14(6), e0008355.
- Davies, S. E. (2019). *Containing contagion: The politics of disease outbreaks in Southeast Asia*. Johns Hopkins University Press.
- Mehta, R., Soares, C. N., Medialdea-Carrera, R., Ellul, M., da Silva, M. T. T., Rosala-Hallas, A., & Solomon, T. (2018). The spectrum of neurological disease associated with Zika and chikungunya viruses in adults in Rio de Janeiro, Brazil: A case series. *PLoS Neglected Tropical Diseases*, 12(2), e0006212.
- Kohnert, D. (2021). On the socio-economic impact of pandemics in Africa- Lessons learned from COVID-19, Trypanosomiasis, HIV, Yellow Fever, and Cholera. *Trypanosomiasis, HIV, Yellow Fever, and Cholera (May 6, 2021)*.
- Tozan, Y., Sjödin, H., Muñoz, Á. G., & Rocklöv, J. (2020). Transmission dynamics of dengue and chikungunya in a changing climate: Do we understand the eco-evolutionary response? *Expert Review of Anti-infective Therapy*, 18(12), 1187-1193.
- Wong, F., de la Fuente-Nunez, C., & Collins, J. J. (2023). Leveraging artificial intelligence in the fight against infectious diseases. *Science*, 381(6654), 164-170.
- Russo, G., Subissi, L., & Rezza, G. (2020). Chikungunya fever in Africa: a systematic review. *Pathogens and Global Health*, 114(3), 111-119.
- Bettis, A. A., L'Azou Jackson, M., Yoon, I. K., Breugelmans, J. G., Goios, A., Gubler, D. J., & Powers, A. M. (2022). The global epidemiology of chikungunya from 1999 to 2020: A systematic literature review to inform the development and introduction of vaccines. *PLoS Neglected Tropical Diseases*, 16(1), e0010069.
- Espinal, M. A., Andrus, J. K., Jauregui, B., Waterman, S. H., Morens, D. M., Santos, J. I., & Olson, D. (2019). Emerging and reemerging *Aedes*-transmitted arbovirus infections in the region of the Americas: implications for health policy. *American journal of public health*, 109(3), 387-392.
- Vairo, F., Aimè Coussoud-Mavoungou, M. P., Ntoumi, F., Castilletti, C., Kitembo, L., Haider, N., ... & Pandora-ID-NET Consortium Chikungunya Outbreak Group Taskforce. (2020). Chikungunya outbreak in the Republic of the Congo, 2019–Epidemiological, virological and entomological findings of a South-North Multidisciplinary Taskforce Investigation. *Viruses*, 12(9), 1020.
- da Silva, S. J. R., de Magalhães, J. J. F., & Pena, L. (2021). Simultaneous circulation of DENV, CHIKV, ZIKV, and SARS-CoV-2 in Brazil: an inconvenient truth. *One Health*, 12, 100205.
- Escobar, L. E., Qiao, H., & Peterson, A. T. (2016). Forecasting Chikungunya spread in

- the Americas via data-driven empirical approaches. *Parasites & Vectors*, 9(1), 1-12.
22. Abboubakar, H., Guidzavai, A. K., Yangla, J., Damakoa, I., & Mouangue, R. (2021). Mathematical modeling and projections of a vector-borne disease with optimal control strategies: A case study of the Chikungunya in Chad. *Chaos, Solitons & Fractals*, 150, 111197.
 23. Witt, C. J., Richards, A. L., Masuoka, P. M., Foley, D. H., Buczak, A. L., Musila, L. A., & AFHSC-GEIS Predictive Surveillance Writing Group. (2011). The AFHSC-Division of GEIS Operations Predictive Surveillance Program: a multidisciplinary approach for the early detection and response to disease outbreaks. *BMC Public Health*, 11, 1-16.
 24. Pley, C., Evans, M., Lowe, R., Montgomery, H., & Yacoub, S. (2021). Digital and technological innovation in vector-borne disease surveillance to predict, detect, and control climate-driven outbreaks. *The Lancet Planetary Health*, 5(10), e739-e745.
 25. Kaur, I., Sandhu, A. K., & Kumar, Y. (2022). Artificial intelligence techniques for predictive modeling of vector-borne diseases and its pathogens: a systematic review. *Archives of Computational Methods in Engineering*, 29(6), 3741-3771.
 26. Carney, R. M., Mapes, C., Low, R. D., Long, A., Bowser, A., Durieux, D., ... & Palmer, J. R. (2022). Integrating global citizen science platforms to enable next-generation surveillance of invasive and vector mosquitoes. *Insects*, 13(8), 675.
 27. Santosh, K. C., & Gaur, L. (2022). *Artificial intelligence and machine learning in public healthcare: Opportunities and societal impact*. Springer Nature.
 28. Saheed, Y. K., Balogun, B. F., Odunayo, B. J., & Abdulsalam, M. (2023). Microarray Gene Expression Data Classification Via Wilcoxon Sign Rank Sum and Novel Grey Wolf Optimized Ensemble Learning Models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*.
 29. Pérez-Pérez, M. J., Delang, L., Ng, L. F., & Priego, E. M. (2019). Chikungunya virus drug discovery: still a long way to go? *Expert opinion on drug discovery*, 14(9), 855-866.
 30. Chaudhary, M., & Sehgal, D. (2022). In silico identification of natural antiviral compounds as a potential inhibitor of chikungunya virus non-structural protein 3 macrodomain. *Journal of Biomolecular Structure and Dynamics*, 40(22), 11560-11570.
 31. Sharma, P., Sharma, G., Singh, M., Sharma, K., Kour, N., & Chadha, P. (2022). Applications of Artificial Intelligence in Modern Health Care and Its Future Scope. In *Society 5.0 and the Future of Emerging Computational Technologies* (pp. 97-122). CRC Press.
 32. Rocklöv, J., Tozan, Y., Ramadona, A., Sewe, M. O., Sudre, B., Garrido, J., ... & Semenza, J. C. (2019). Using big data to monitor the introduction and spread of Chikungunya, Europe, 2017. *Emerging infectious diseases*, 25(6), 1041.
 33. Braack, L., Wulandhari, S. A., Chanda, E., Fouque, F., Merle, C. S., Nwangwu, U., ... & Clarke, S. E. (2023). Developing African arbovirus networks and capacity strengthening in arbovirus surveillance and response: findings from a virtual workshop.
 34. Cauchemez, S., Ledrans, M., Poletto, C., Quénel, P., De Valk, H., Colizza, V., & Boëlle, P. Y. (2014). Local and regional spread of chikungunya fever in the Americas. *Eurosurveillance*, 19(28), 20854.
 35. Jiao, Z., Ji, H., Yan, J., & Qi, X. (2023). Application of big data and artificial intelligence in epidemic surveillance and containment. *Intelligent Medicine*, 3(1), 36-43.
 36. Wesula Olivia, L., Obanda, V., Bucht, G., Mosomtai, G., Otieno, V., Ahlm, C., & Evander, M. (2015). Global emergence of Alphaviruses that cause arthritis in humans. *Infection ecology & epidemiology*, 5(1), 29853.
 37. Socha, W., Kwasnik, M., Larska, M., Rola, J., & Rozek, W. (2022). Vector-borne viral diseases as a current threat for human and animal health—One Health perspective. *Journal of Clinical Medicine*, 11(11), 3026.
 38. Ellwanger, J. H., Veiga, A. B. G. D., Kaminski, V. D. L., Valverde-Villegas, J. M., Freitas, A. W. Q. D., & Chies, J. A. B. (2021). Control and prevention of infectious diseases from a One Health perspective. *Genetics and Molecular Biology*, 44.