Chikungunya resurgence highlights gaps in *Aedes* surveillance and control in South America

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Over the past decade, chikungunya has re-emerged as a major public health concern in the Americas.[1] In 2025 alone, more than 313,000 cases and 170 deaths were reported across 18 countries, according to the Pan American Health Organization (PAHO). Transmission continued to expand in 2026, particularly in Suriname, Bolivia, Brazil, and Argentina (Fig. 1). Although promising results have recently been obtained with chikungunya vaccines, several challenges still impede large-scale implementation, including the absence of WHO recommendations, safety concerns in certain populations, manufacturing and supply constraints, and limited data regarding efficacy, long-term protection, and optimal vaccination strategies for endemic areas and high-risk populations.[2] In addition, climate and environmental changes are reshaping the genomic diversity and bionomics of *Aedes* vectors, influencing population dynamics, vector competence, and resistance patterns, and potentially facilitating arbovirus expansion into previously unsuitable areas.[3] While PAHO recently issued an epidemiological alert regarding the risk of sustained transmission and large-scale epidemics,[4] the current chikungunya situation once again highlights the persistent weaknesses of vector surveillance and control systems in the region, which remain largely reactive rather than proactive.

As highlighted during the annual assembly of the WINSA network[5] held in Bogotá in March 2026, with participation from representatives of 13 countries and territories, a paradigm shift is required from passive entomological monitoring toward an operational, decision-oriented surveillance system capable of

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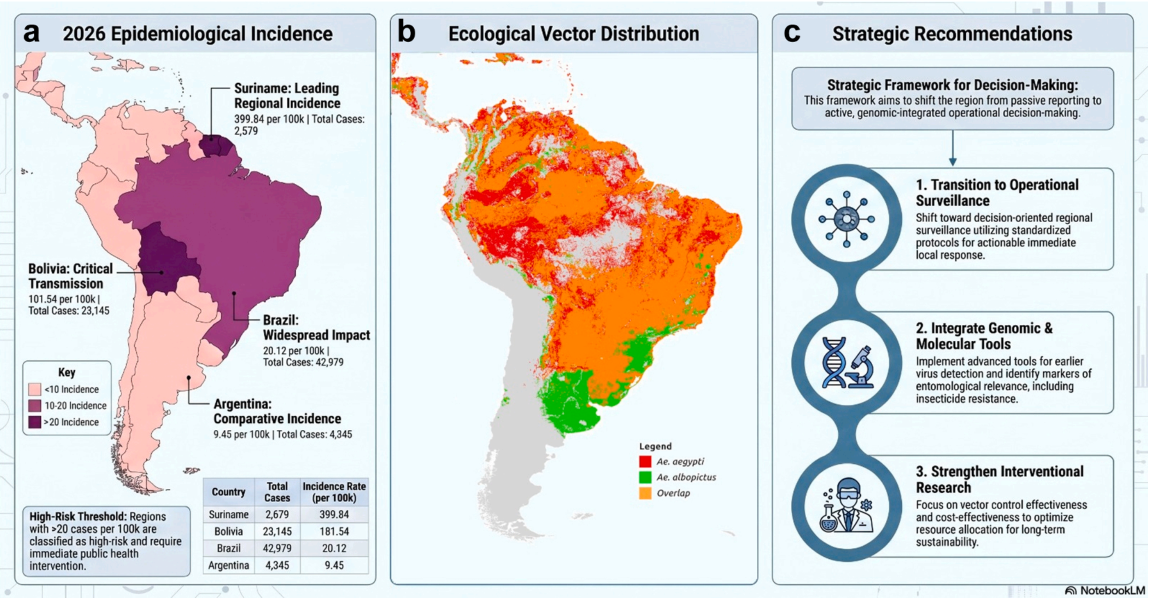

High-Risk Threshold: Regions with >20 cases per 100k are classified as high-risk and require immediate public health intervention.

Country	Total Cases	Incidence Rate (per 100k)
Suriname	2,679	399.84
Bolivia	23,145	181.54
Brazil	42,979	20.12
Argentina	4,345	9.45

Strategic Framework for Decision-Making: This framework aims to shift the region from passive reporting to active, genomic-integrated operational decision-making.

1. Transition to Operational Surveillance
Shift toward decision-oriented regional surveillance utilizing standardized protocols for actionable immediate local response.

2. Integrate Genomic & Molecular Tools
Implement advanced tools for earlier virus detection and identify markers of entomological relevance, including insecticide resistance.

3. Strengthen Interventional Research
Focus on vector control effectiveness and cost-effectiveness to optimize resource allocation for long-term sustainability.

Fig. 1: **Chikungunya in South America, 2026: epidemiological status, estimated vector distribution, and components of an improved regional strategic response.** (A) Incidence of Chikungunya cases per 100,000 inhabitants in 2026, according to PAHO (source: Integrated Arbovirus Platform; open access: https://www.paho.org/en/arbo-portal). (B) Predicted distribution of *Aedes spp.* in South America, based on *Ae. Aegypti* and *Ae. Albopictus* global distribution estimates, provided by Kramer et al. (2015)[6]; green indicates areas where habitat suitability for *Ae. albopictus* is >0.5; red indicates areas where habitat suitability for *Ae. aegypti* is >0.5; orange indicates areas where habitat suitability for both species exceeds 0.5. (C) Proposed strategic framework shifting from passive surveillance to active, genomics-informed decision-making.

delivering rapid, graded, and context-specific preventive and outbreak response measures. First, a harmonized regional surveillance system based on standardized protocols, methods, indicators, and data reporting is needed to ensure comparability and improve the capacity to guide vector control efforts. Second, integrating molecular and genomic tools into entomo-virological surveillance would enable earlier detection of circulating viruses and relevant entomological genetic markers (e.g., insecticide resistance, population genetics, and vector competence), thereby strengthening early warning systems and enhancing predictive capacity. Recent advances in high-throughput genomic technologies, including next-generation sequencing and metabarcoding, could provide faster, more standardized, and cost-effective approaches for pathogen detection and vector characterization, facilitating large-scale surveillance while limiting unnecessary operational costs. Third, interventional research must be strengthened to generate robust evidence on vector control, including the comparative effectiveness and cost-effectiveness of chemical and non-chemical approaches in various transmission settings, to better inform policy and optimize resource allocation. Recent advances in vector control innovation, including next-generation traps, genetic approaches (e.g., RIDL, SIT, and enhanced SIT), and biological strategies such as *Wolbachia*, offer promising alternative tools that could deliver substantial public health benefits while reducing selection pressure associated with conventional insecticide-based interventions.

A coordinated regional approach is urgently needed to address these challenges and reduce the burden of *Aedes*-borne diseases in South America. Regional initiatives such as the WINSA network provide a unique framework to fill knowledge gaps in vector biology and control, foster collaboration, harmonize surveillance systems, and strengthen research and training efforts across the region. It aims to support countries in developing more efficient surveillance systems and sustainable vector control strategies, while contributing to the achievement of the Sustainable Development Goals related to health and well-being in South America.

Contributors

Conceptualization (VC, AJM), Data curation (ER), Investigation (VC, MA, TB, KDR, LSD, JBD, SD, LF, CRG, NGB, LH, AL, JBPL, RL, DM, MLQP, ER, MPS, GW, AJM), Methodology (VC, AJM), Visualization (VC, SD, ER), Writing - original draft (VC, AJM), Writing – review & editing (VC, MA, TB, KDR, LSD, JBD, SD, LF, CRG, NGB, LH, AL, JBPL, RL, DM, MLQP, ER, MPS, GW, AJM).

Declaration of generative AI and AI-assisted technologies

During the preparation of this work, the author used NotebookLM to prepare the figure and ChatGPT to review the English. After using these tools, the authors reviewed and edited the content as needed and, therefore, take full responsibility for the content of the published correspondence.

Editor note

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Declaration of interests

The authors (VC, MA, TB, KDR, LSD, JBD, SD, LF, CRG, NGB, LH, AL, JBPL, RL, DM, MLQP, ER, MPS, GW, AJM) declare no competing interests. All authors have a volunteer (unpaid) position in the Worldwide Insecticide Resistance Network (WINSA).

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