

Arbovirus researchers unite: expanding genomic surveillance for an urgent global need



Arthropod-borne viruses (arboviruses) are transmitted by arthropod vectors to humans, leading to disease outbreaks mainly in tropical regions of the world.¹ Although many arboviruses are known, three *Aedes*-spp-borne viruses are particularly concerning for humans at a global scale due to recurring large and expanding epidemic outbreaks of dengue virus, Zika virus, and chikungunya virus. These viruses cause a heavy disease burden with mild to potentially life-threatening symptoms, resulting in substantial short-term and long-term morbidity and mortality.² Epidemiological estimates underscore the impact of these viruses, with half of the world population at risk of dengue virus infection and around 100–400 million cases and 20 000 deaths reported each year.³ In addition to worsening outbreaks in tropical areas, there has been an increase in disease in subtropical and temperate regions, driven by the expansion of the main vectors *Aedes aegypti* and *Aedes albopictus* to new areas associated with urbanisation, globalisation, human mobility, and climate change.⁴ An additional 100 million people are estimated to be at risk of infection owing to wider transmission seasons in high-altitude areas and temperate regions of the world in the next 50 years.⁵ To strengthen the mitigation of epidemics of these arboviruses, WHO launched the Global Arbovirus Initiative in March, 2022, to build a coalition of key stakeholders to improve surveillance and prevention.⁶

Molecular surveillance of arboviruses is crucial to assess lineage prevalence and evaluate the impact of these viruses on human populations. For instance, genomic data and meaningful epidemiological metadata are essential for early warning of virus outbreaks; understanding epidemic potential of endemic and newly introduced virus strains; early introduction of new strains into naive populations; detection of emergence of more virulent lineages and virus lineages resistant to interventions such as vaccines, antiviral drugs, and various vector control interventions (eg, *Wolbachia*-spp-infected mosquito strategies); evaluation of intervention effectiveness; characterisation of the transmission network between vertebrates, including humans, and vector species; and detection of genomic

variants that could affect molecular assays. Following the implementation of genomic surveillance in most countries around the world for monitoring of SARS-CoV-2 lineages, there is now an opportunity to implement routine and sustainable large-scale genomic surveillance for high-impact arboviruses with substantial human disease burden.

However, comprehensive epidemiological and risk assessment analyses are only possible through rapid genomic data sharing associated with relevant metadata and data aggregation. Despite various well intentioned efforts to establish databases and standardise arbovirus genomic data, the available information is highly heterogeneous geographically and over time and is littered with inconsistent metadata.^{7,8} Normally, such data only become available after peer reviewed publication, which hinders or delays genomic epidemiology inferences and outbreak response and intervention. Therefore, new high-quality curated databases and data sharing solutions are needed to augment the efforts to tackle arbovirus outbreaks across the globe.

The COVID-19 pandemic has shown not only that worldwide genomic surveillance is possible, but also that equitable data sharing systems and cross-border collaboration are important to tackle pathogen threats. The Global Data Science Initiative (GISAID) is an important data science initiative that allows timely data sharing and aggregate data analysis for public health intervention, while also stimulating collaborative studies and protecting sensitive data and data generator authorship. With the goal of effectively implementing global genomic surveillance for arboviruses with substantial public health impact, we encourage public health researchers working on molecular surveillance of arboviruses to contribute and share data through EpiArbo, a new data sharing platform with an initial focus on dengue virus and chikungunya virus, and expanding to Zika virus, built on the success of GISAID's EpiFlu and EpiCov databases. This new implementation has many features that incorporate the complexity of arbovirus transmission and allows the integrated assessment of genetic, pharmacological, and vector

Published Online
August 1, 2023
[https://doi.org/10.1016/S2214-109X\(23\)00325-X](https://doi.org/10.1016/S2214-109X(23)00325-X)

For the GISAID initiative and the EpiFlu, EpiCov, and EpiArbo databases see <https://gisaid.org/>

interventions. Moreover, this database can be easily expanded to cover other arboviruses of concern, such as West Nile virus, yellow fever virus, and Japanese encephalitis virus.

As humanity recovers from the worst phase of the COVID-19 pandemic, molecular surveillance continues to be crucial for monitoring SARS-CoV-2 evolution and other epidemic-prone and difficult-to-control viruses with high public health impact. Engagement of the global community will be crucial to maximise the benefits from aggregated genomic epidemiology to tackle the increasing arbovirus burden across the planet.^{9,10}

A full list of researchers that endorse this initiative can be found in the appendix.

This work was supported by the Alexander von Humboldt and the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior and was partly supported by the Centers for Research in Emerging Infectious Diseases and the Coordinating Research on Emerging Arboviral Threats Encompassing the Neotropics grant (U01 AI151807) from the US National Institutes of Health. We declare no competing interests.

Copyright © 2023 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY 4.0 license.

*Gabriel Luz Wallau, Global Arbovirus Researchers United
gabriel.wallau@fiocruz.br

Entomology Department and Bioinformatic Core Facility, Aggeu Magalhães Institute, Fundação Oswaldo Cruz, Recife 50.740-465, Brazil

- 1 Weaver SC, Charlier C, Vasilakis N, Lecuit M. Zika, chikungunya, and other emerging vector-borne viral diseases. *Annu Rev Med* 2018; **69**: 395–408.
- 2 Labeaud AD, Bashir F, King CH. Measuring the burden of arboviral diseases: the spectrum of morbidity and mortality from four prevalent infections. *Popul Health Metr* 2011; **9**: 1.
- 3 Bhatt S, Gething PW, Brady OJ, et al. The global distribution and burden of dengue. *Nature* 2013; **496**: 504–07.
- 4 Kraemer MUG, Reiner RC Jr, Brady OJ, et al. Past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. *Nat Microbiol* 2019; **4**: 854–63.
- 5 Colón-González FJ, Sewe MO, Tompkins AM, et al. Projecting the risk of mosquito-borne diseases in a warmer and more populated world: a multi-model, multi-scenario intercomparison modelling study. *Lancet Planet Health* 2021; **5**: e404–14.
- 6 Balakrishnan VS. WHO launches global initiative for arboviral diseases. *Lancet Microbe* 2022; **3**: e407.
- 7 Schreiber MJ, Ong SH, Holland RCG, et al. DengueInfo: a web portal to dengue information resources. *Infect Genet Evol* 2007; **7**: 540–41.
- 8 Atre NM, Alagarasu K, Shil P. ArVirInd—a database of arboviral antigenic proteins from the Indian subcontinent. *PeerJ* 2022; **10**: e13851.
- 9 Jagtap S, Pattabiraman C, Sankaradoss A, Krishna S, Roy R. Evolutionary dynamics of dengue virus in India. *PLoS Pathog* 2023; **19**: e1010862.
- 10 Naveca FG, Santiago GA, Maito RM, et al. Reemergence of dengue virus serotype 3, Brazil, 2023. *Emerg Infect Dis* 2023; **29**: 1482–84.

For the full list of researchers
see <https://doi.org/10.55876/p230704>

See Online for appendix