

Chikungunya virus

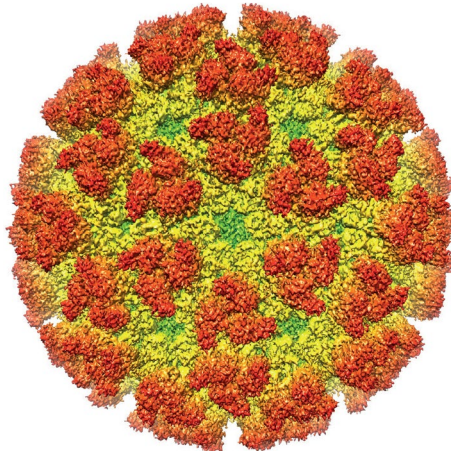
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Yajna Ramphal and Tulio de Oliveira are fascinated by the adaptive evolution of chikungunya virus.

Chikungunya virus (CHIKV) is a mosquito-borne alphavirus whose positive-sense, single-stranded RNA is neatly packed into an 11.8-kb genome. Since the CHIKV outbreak in Brazil in 2014, T.d.O. has led efforts to detect and characterize multiple outbreaks in the Americas and Africa. Y.R.'s journey with CHIKV began with her master's research to understand the transmission patterns, evolution and disease burden of the virus. What we did not expect was to uncover a virus with a remarkable capacity for adaptation and a genomic history that often left us with scientific 'cliff-hangers'.

Clinically, chikungunya (the disease caused by CHIKV) resembles dengue and other vector-borne diseases, and causes acute febrile illness, headaches, muscle pain and fatigue. It is set apart by intense and often debilitating joint pain, which earned it a name that means 'that which bends up' or 'to become contorted' (derived from the Kimakonde language of Tanzania). We have seen many patients suffer from debilitating pain, which motivates our genomic research to inform accurate diagnostics, therapeutics and vaccine development.

The virus is transmitted primarily by *Aedes* mosquitoes, and circulates through both urban outbreaks and forest transmission cycles. Nonhuman primates and other wildlife serve as reservoir hosts, with occasional spillover into nearby human populations. Genetically, CHIKV clusters into three genotypes: Asian, West African and East–Central–South



African. Although these genotypes and lineages were originally defined by their geographical range, the virus now circulates far beyond these boundaries. As T.d.O. and colleagues did for COVID-19 (S. S. A. Karim *et al. Science* **371**, 1215; 2021) and dengue (V. Hill *et al. PLoS Biol.* **22**, e3002834; 2024), we are assembling a team of international experts to fine-tune the nomenclature to be less prejudicial towards the regions where genotypes were first identified.

For decades, CHIKV remained restricted to Africa and Asia, and caused sporadic and regional outbreaks that rarely captured global attention. That changed in the early 2000s when the virus began to spread into new and more temperate regions. This expansion reflects a convergence of factors, including the influence of climate change in reshaping thermal and ecological boundaries, human mobility, and increased environmental suitability for *Aedes* vectors and viral transmission. By 2025, CHIKV had established active circulation in previously non-endemic regions, which

resulted in large outbreaks in China, France and Italy.

This small RNA virus continually redefines its ecological niche, and often adaptive evolution acts as the catalyst. Although our research has answered some questions, it has generated many more. We have seen CHIKV move silently from endemic settings and reemerge in regions thought to be epidemiologically quiet, sparking large outbreaks along the way – especially when new lineages have more transmissible mutations (such as A226V, which we recently detected in Mauritius). Each outbreak provides a real-time demonstration of how the virus adapts to environmental and ecological shifts, vector dynamics and human behaviour. As genomic data and outbreak characterization increase, our focus lies at the intersection of transmission dynamics, environmental suitability and predictive modelling approaches that can meaningfully support public health responses for chikungunya. In the context of our shifting climate realities, CHIKV offers a glimpse into the increasing likelihood and frequency of the emergence of infectious diseases that are adapted to ecological change.

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Competing interests

The authors declare no competing interests.