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Accurate Recapitulation of Chikungunya Virus Complete Coding Sequence Phylogeny Using Variable Genome Regions for Genomic Surveillance

Abstract: Chikungunya virus (CHIKV) is transmitted by mosquito bites and causes chikungunya fever (CHIKF). CHIKV has a single-stranded RNA genome and belongs to a single serotype with three genotypes distinguished by their historical geographic distributions: West African, East/Central/South African, and Asian. The Asian lineage recently emerged in the Western Hemisphere and had rapid spread throughout the Caribbean and the American mainland. This spread was accompanied with accumulation of genetic variations in the CHIKV genome creating new virus lineages. Although whole-genome sequencing offers invaluable insights, its technical complexity and associated costs can hinder its widespread application in endemic regions. To address this challenge, we identified hypervariable regions within the CHIKV genome that could serve as effective alternatives for evolutionary studies. We analyzed 1,114 CHIKV complete genome sequences to identify regions with valuable phylogenetic signals. Datasets from Africa, Asia, and America were used to perform phylogenetic analyses on highly variable regions and concatenated sequences with different levels of variability. Complete coding sequence (CDS) trees served as references to assess how accurately each region reproduced the phylogeny, focusing on branch length, topological differences, and tree confidence. Our results revealed that concatenated highly variable regions accurately reconstructed CHIKV phylogeny, exhibiting statistically indistinguishable branch lengths and tree confidence compared to CDS. In addition, these regions adequately inferred the evolutionary relationships among CHIKV isolates from the American outbreak with similar results to the CDS. This finding suggests that highly variable regions can effectively capture the evolutionary relationships among CHIKV isolates, offering a simpler approach for future studies. This approach could be useful for large-scale surveillance efforts.

Keywords: Chikungunya virus; phylogeny; genomic surveillance.

Biography: Dr. Mario H. Rodríguez holds a medical degree, specialization in Internal Medicine and master's and PhD in Medical Parasitology. He is currently emeritus investigator at the Mexican National Institute of Public Health. His areas of research include the biology of vector-borne diseases, vector and parasite interactions, epidemiology, and control strategies. His research includes immune response of and triatomines. He also works on the genetic variation of dengue and chikungunya viruses and Zika virus distribution in Mexico, as well as the evaluation of Ecohealth strategies to control dengue with the active participation of municipalities and communities.