

SARS-CoV-2 Omicron variants BA.4 and BA.5 dominated the fifth COVID-19 epidemiological wave in Mexico

Blanca Taboada¹, Selene Zarate², Rodrigo García-López¹, José Muñoz-Medina³, Bruno Gómez-Gil⁴, Alfredo Herrera-Estrella⁵, Alejandro Sanchez-Flores¹, Angel Gustavo Salas Lais³, Benjamin Roche⁶, Gabriela Martínez-Morales³, Hermilo Domínguez Zárate³, Célida Duque Molina³, Ricardo Avilés Hernández³, Susana López¹, and Carlos F. Arias¹

¹Universidad Nacional Autonoma de Mexico Instituto de Biotecnologia

²Universidad Autonoma de la Ciudad de Mexico - Plantel Del Valle

³Instituto Mexicano del Seguro Social

⁴Centro de Investigacion en Alimentacion y Desarrollo AC

⁵Laboratorio Nacional de Genomica para la Biodiversidad

⁶MiVEGEC

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Abstract

In Mexico, the BA.4 and BA.5 Omicron variants dominated the fifth epidemic wave (summer 2022), superseding BA.2, which had circulated during the inter-wave period. The present study uses genome sequencing and statistical and phylogenetic analyses to examine these variants' prevalence, distribution, and genetic diversity in Mexico from April to August 2022. Over 35% of the sequenced genomes in this period corresponded to the BA.2 variant, 8% to the BA.4, and 56% to the BA.5 variant. Multiple subvariants were identified, but only BA.2.9, BA.2.12.1, BA.5.1, BA.5.2, BA.5.2.1, and BA.4.1 circulated throughout the fifth wave across the entire country, not forming geographical clusters. Contrastingly, other subvariants exhibited a geographically restricted distribution, most notably in the Southeast region, which showed a distinct subvariant dynamic. This study supports previous results showing that this region may be a major entry point and may have contributed to the introduction and evolution of novel variants in Mexico. Furthermore, a differential distribution was observed for certain subvariants among specific States throughout time, which may have contributed to the overall increased diversity observed during this wave compared to the previous one. This study highlights the importance of sustaining genomic surveillance to identify novel variants that may impact public health.

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