

Instituto de
Biotecnología

Monitoring SARS-CoV-2 Coinfections Throughout Three Years Of The Covid-19 Pandemic In Mexico - Results From Covigen-Mex's Multi-Institutional Genomic Surveillance



Rodrigo García-López^{1*}, Blanca Taboada¹, Selene Zárate², José Esteban Muñoz-Medina³, Angel Gustavo Salas-Lais³, Alfredo Herrera-Estrella⁴, Nelly Selem Mojica⁵, Celia Boukadida⁶, Joel Armando Vazquez-Perez⁶, Bruno Gómez-Gil⁷, Alejandro Sanchez-Flores⁸, Carlos F. Arias¹

* Contact information:
Rodrigo García López, Ph.D.
rodrigo.garcia@ibt.unam.mx
 @rodrigogarlop

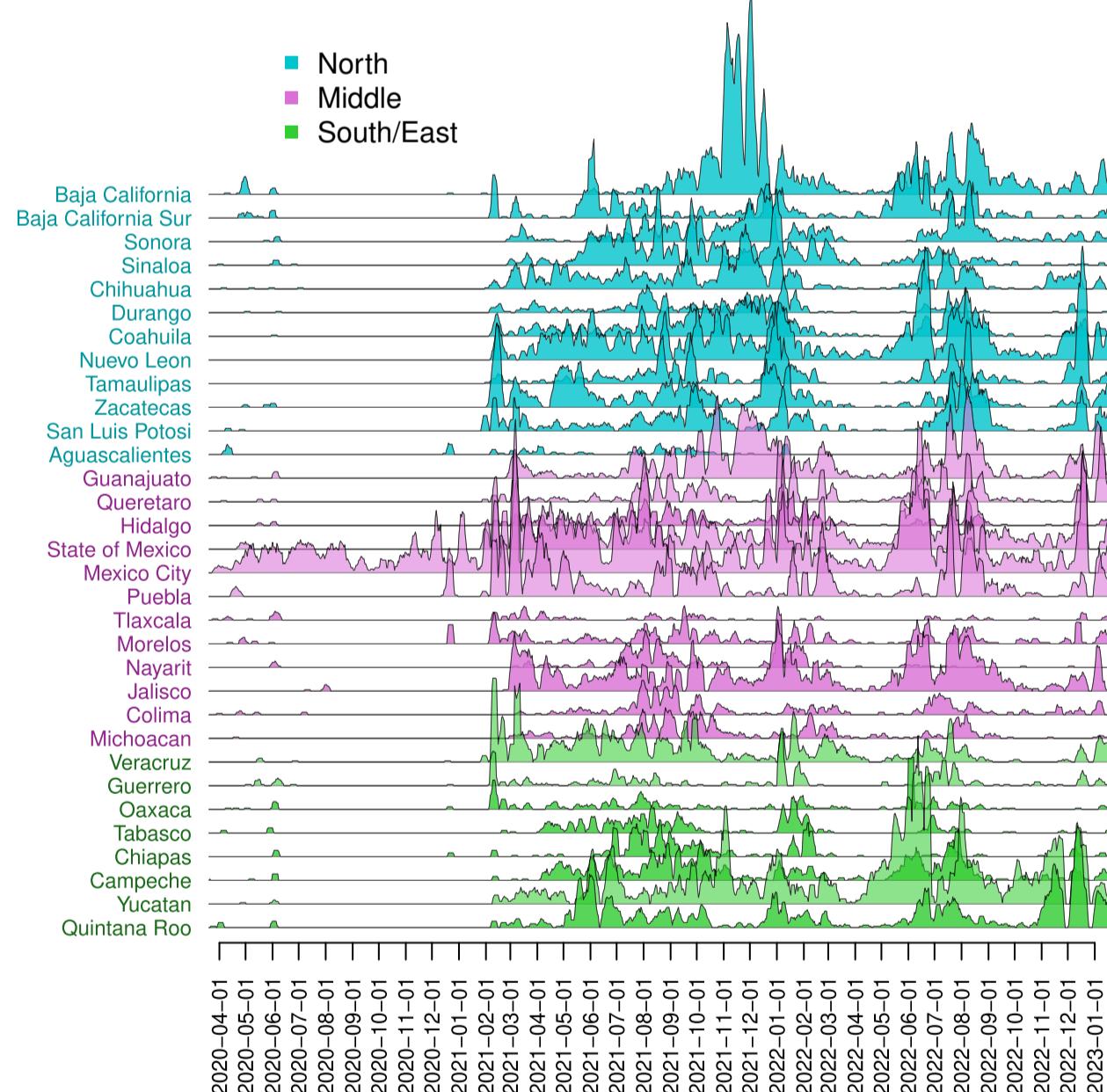
Abstract:

The COVID-19 pandemic was marked by a succession of turnover events involving different relevant variants of the SARS-CoV-2 coronavirus that drove multiple epidemiological surges (waves). In Mexico, over the span of three years and six waves, the first nationwide dominant variant, B.1.1.519, was displaced by variants Alpha and Gamma, which were then superseded by Delta subvariants and later by multiple subvariants from the Omicron clade.

Periods of high transmission where at least two of these circulated fostered the occurrence of coinfections within patients, with variable ratios. In order to detect and study them, CoViGen-Mex, Mexico's largest genomic surveillance effort, set out to analyze collections of Intra-Patient Minor Allelic Variants (IPMAVs) in 29,661 public health samples collected from March 18, 2020 to January 27, 2023.

IPMAVs were defined as low-frequency allelic variants (<0.5) found in polymorphic loci of the SARS-CoV-2 genome that finely reflect mutational variation in the RNA molecules of different virions in a sample. Detection of full sets of variant-defining mutations as IPMAVs enabled the detection of putative low-frequency variants that coexisted as coinfections, for studying their longitudinal and geographical distribution as they prove an important step for the evolutionary process of the virus that may favor recombination.

Our Dataset:
Nasopharyngeal samples from 32 States in Mexico:



~1/3 of all Mexican samples.
The largest collection of samples outside Mexico City and its suburbs.


3 years worth of SARS-CoV-2 sequencing data.

"Genomes" are consensus sequences:
Most COVID-19 studies report a single viral genome per sample, but each of those sequences is in fact a consensus constructed from multiple sequencing reads.

Fixed mutations occur in most reads of the same loci.

¹ Departamento de Genética del Desarrollo y Fisiología Molecular, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Mexico
² Departamento de Genética del Desarrollo y Fisiología Molecular, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Mexico
³ Coordinación de Calidad de Insumos y Laboratorios Especializados, Instituto Mexicano del Seguro Social, Mexico City, Mexico
⁴ Laboratorio Nacional de Genómica para la Biodiversidad-Unidad de Genómica Avanzada, Centro de Investigación y de Estudios Avanzados del IPN, Irapuato, Mexico
⁵ Centro de Ciencias Matemáticas, Universidad Nacional Autónoma de México, Morelia, Mexico
⁶ Centro de Investigación en Enfermedades Infecciosas, Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas, Mexico City, Mexico
⁷ Centro de Investigación en Alimentación y Desarrollo AC, Unidad Mazatlán, Mazatlán, Mexico
⁸ Unidad Universitaria de Secuenciación Masiva y Bioinformática, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Mexico

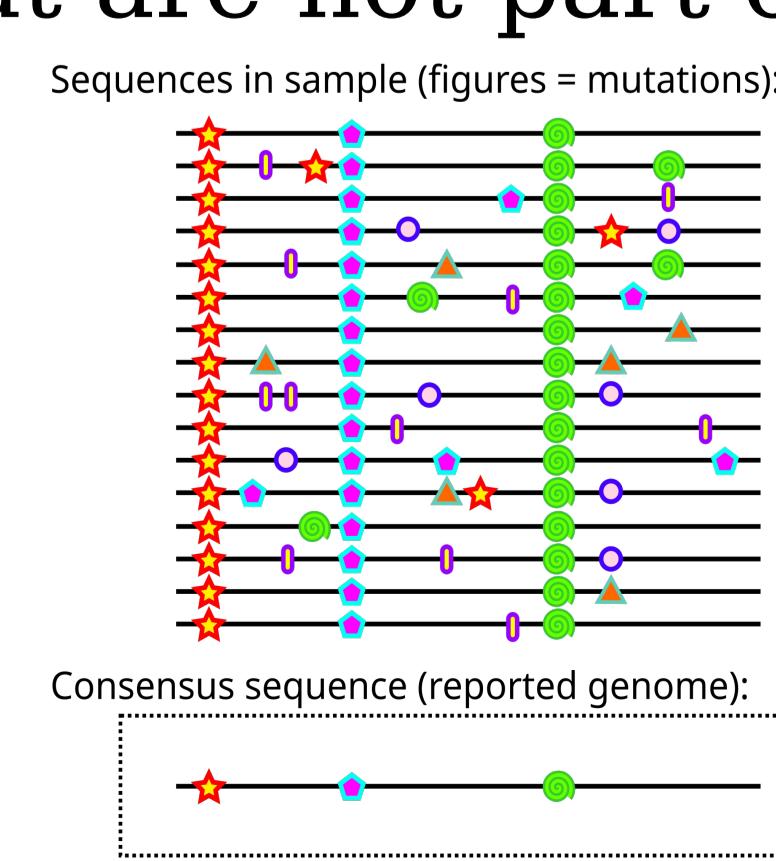
Virus art by Sirir Changhuana and Nur Muhammad at Vecteezy



! Main Focus of the Study:
Intra-Patient Minor Allelic Variants (IPMAVs), mutations that are not part of the consensus sequence

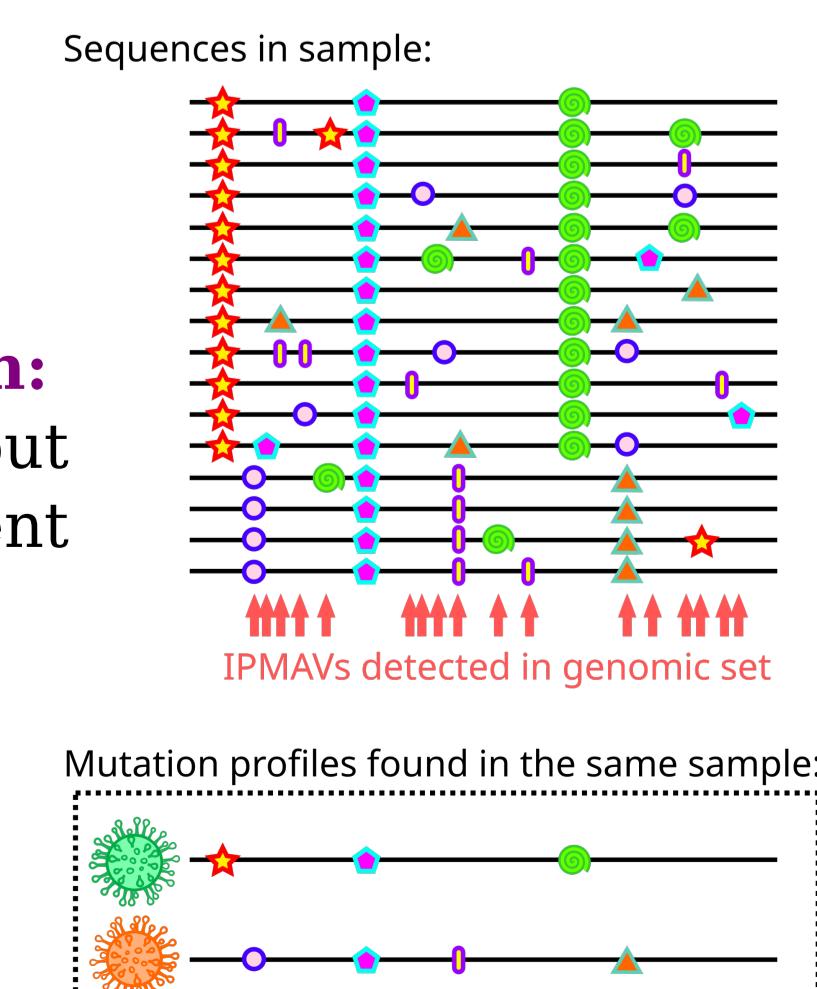
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IPMAVs provide valuable information:
Not just inner patient variation, but coinfections occurring within a patient are commonly ignored.

IPMAVs occur with allelic frequency <0.5%



An example of one of 379 coinfections:

Two profiles were found in a female patient from Baja California. The consensus sequence was determined as a Gamma variant. The secondary variant was determined as Alpha. Both had complete mutation profiles.

