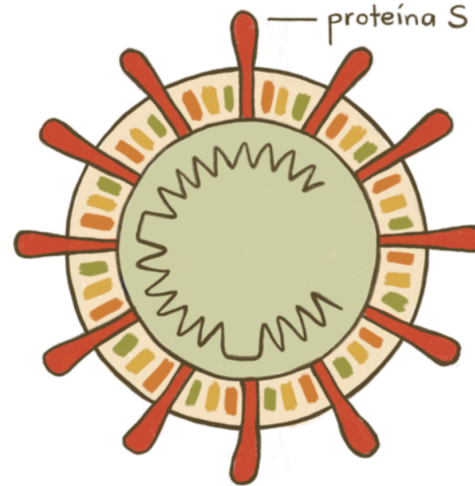


# Evolución molecular del SARS-CoV-2 en México



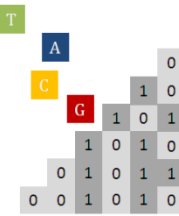
**Grupo de Genómica Evolutiva**

Dr. Luis José Delaye Arredondo  
luis.delaye@cinvestav.mx

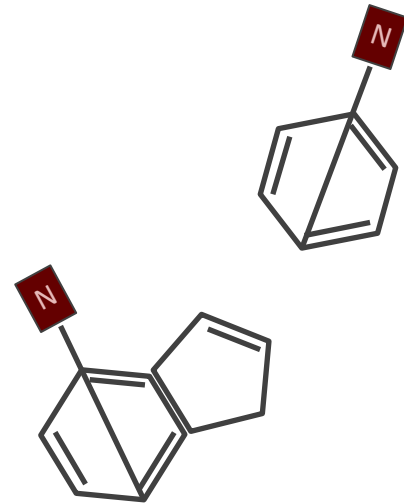
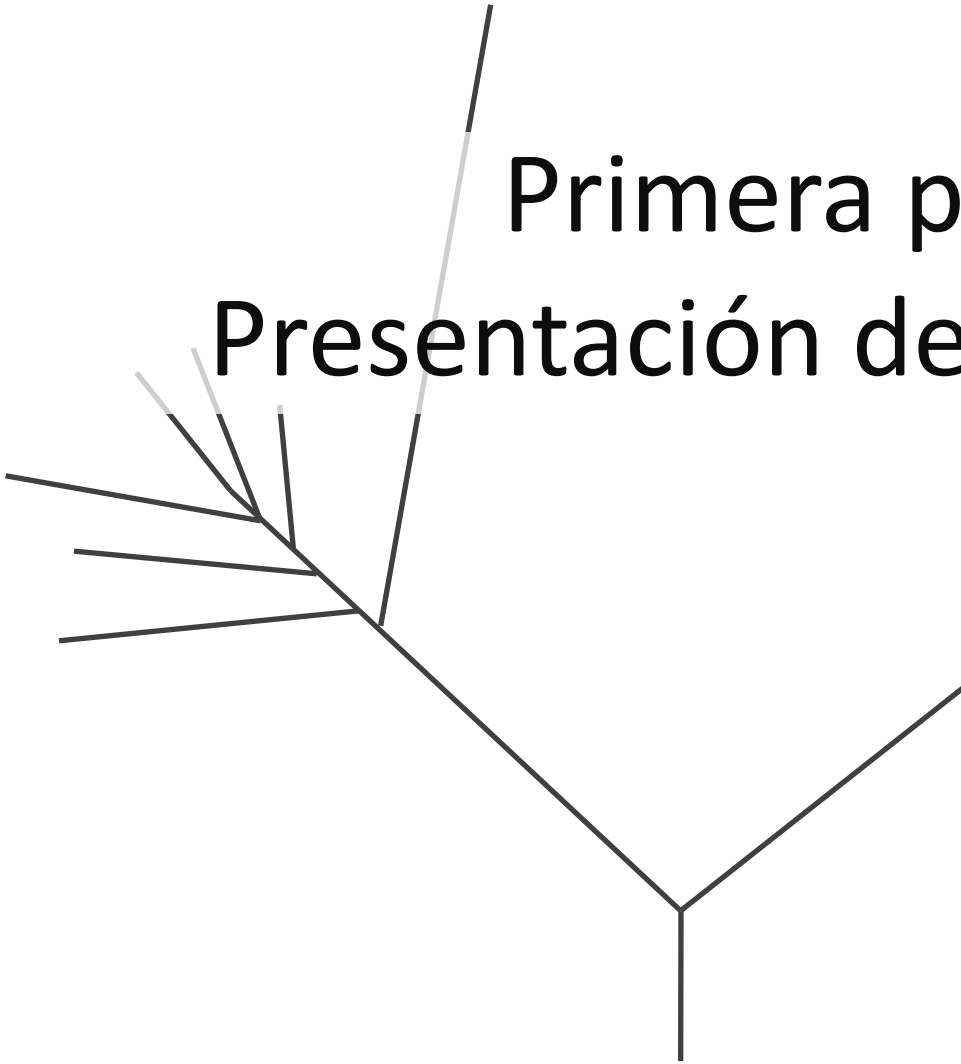
Departamento de Ingeniería Genética

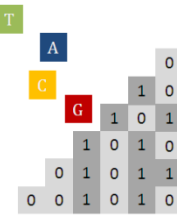
**Cinvestav**  
Unidad Irapuato





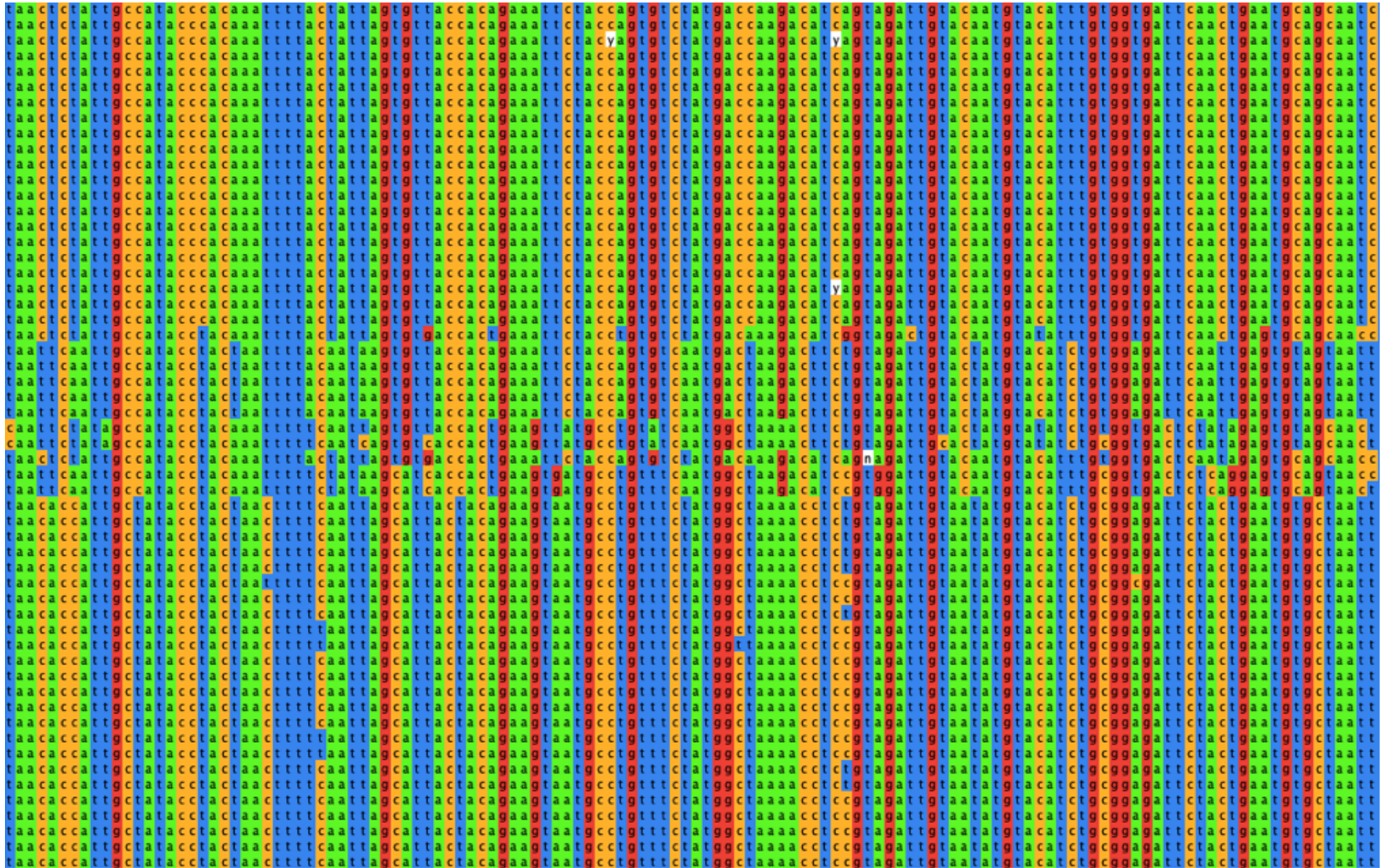
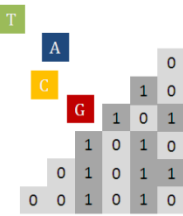
# Primera parte: Presentación del problema

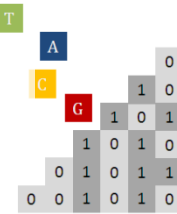




Veremos un problema real de investigación en el cual estoy trabajando y para el cual aún no tengo una solución

# ¿Cómo estudiar la diversidad genética del SARS-CoV-2 en México?





# Preguntas

¿Qué variantes genéticas hay en nuestro país?

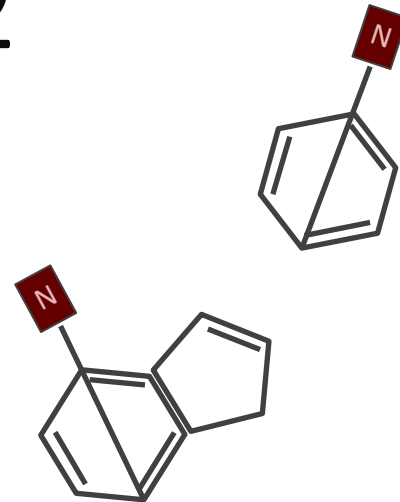
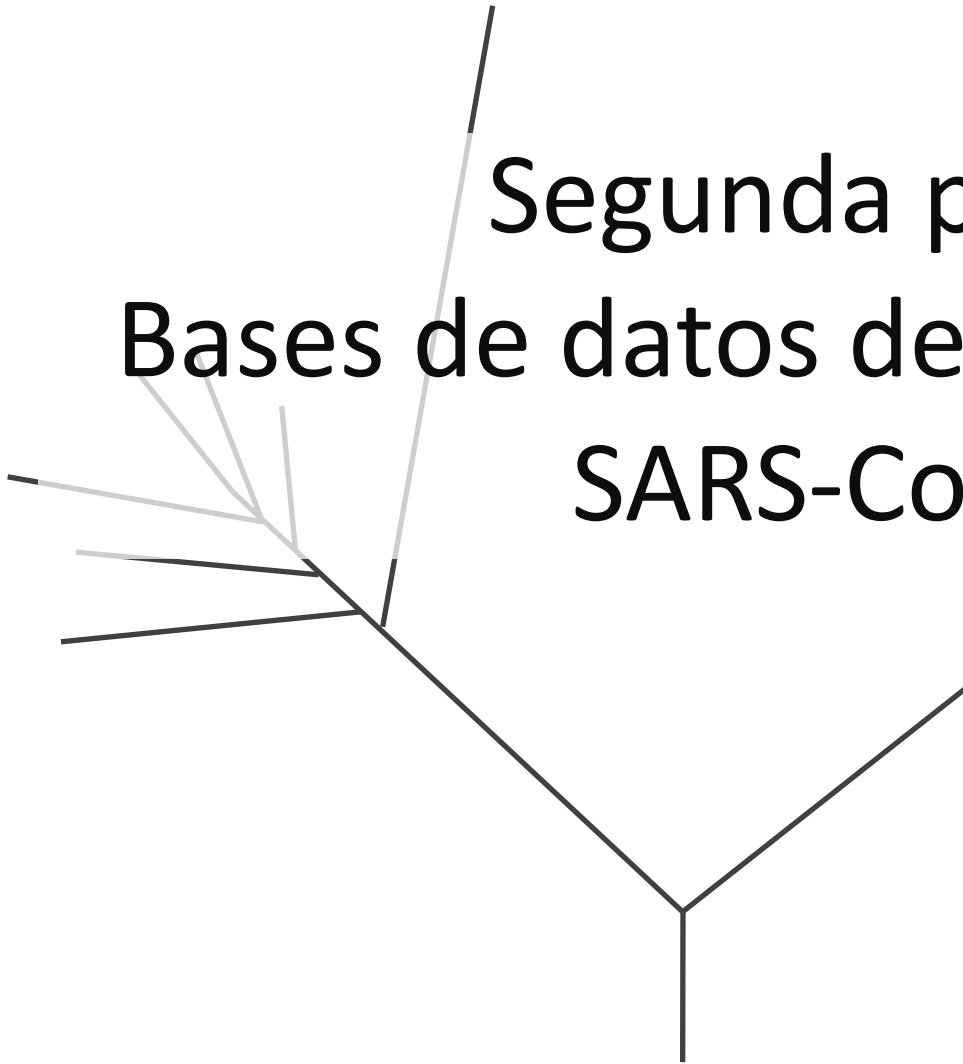
¿Cómo y cuándo llegaron estas variantes genéticas?

¿Hay variantes genéticas nuevas?

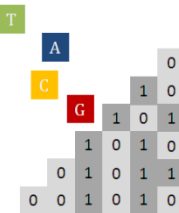





# Segunda parte: Bases de datos del genoma del SARS-CoV-2



# Genómica del SARS-CoV-2



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### In Focus


#### Novel variant 501Y.V2 with triple spike receptor binding site substitutions

By 21 December, 301 new virus genomes collected in South Africa since November 1 were submitted to GISAID, bringing the total number of virus genome submissions from South Africa to 2,730. The 301 recent virus genomes include 182 from clade GH; 71 from clade GR; 45 from clade G; one from clade GV; and two from other clades. Of the 182 genomes from clade GH, 89% have three mutations in the spike receptor binding site (K417N, E484K, and N501Y). 27% of the 182 have a nine-nucleotide deletion in NSP6 in addition to the three mutations. Spike mutation N501Y is also found in the novel UK variant under investigation, which is from a different clade.


It has been reported, based on high-throughput experiments, that all three spike receptor binding site mutations (K417N, E484K and N501Y) were shown to mildly increase receptor binding. Because receptor binding interfaces are also common epitopes, receptor binding interface mutations could also affect binding of some antibodies to the virus and, in rare cases, have the potential to affect vaccine response. A triple mutant at the interface has not been observed yet in larger outbreaks and should be investigated in detail. Experimental data would be welcome to clarify the impact of the mutations. [> read more](#)

●●●●●●●●●●

### Genomic epidemiology of hCoV-19



### hCoV-19 Tracking of Variants



### Enabled by hCoV-19 data from GISAID

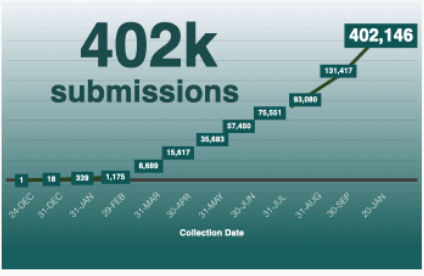
#### VirusSurf Search

*Politecnico di Milano (Italy)*  
Integrated search server for virus sequences of COVID-19 and their variants

#### Geographic Mutation Tracker

*KAUST (Saudi Arabia)*  
COVID-19 virus geographic mutation tracker and visualization tool

### hCoV-19 Data Sharing via GISAID



| Collection Date | Submissions |
|-----------------|-------------|
| 1 DEC 2019      | 1           |
| 1 DEC 2019      | 18          |
| 31 DEC 2019     | 339         |
| 31 JAN 2020     | 1,175       |
| 29 FEB 2020     | 8,559       |
| 31 MAR 2020     | 15,617      |
| 30 APR 2020     | 30,685      |
| 31 MAY 2020     | 57,450      |
| 30 JUN 2020     | 75,551      |
| 31 JUL 2020     | 93,080      |
| 30 AUG 2020     | 131,417     |
| 30 SEP 2020     | 182,146     |
| 20 JAN 2021     | 402,146     |

### Recent hCoV-19 Data Submissions

[hCoV-19/Hebei/IVDC-10-01/2021](#)  
[hCoV-19/Australia/NSW3878/2021](#)  
[hCoV-19/Romania/GR-93715/2021](#)

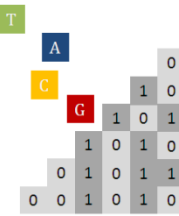
### Recent Influenza Data Submissions

[A/turkey/Poland/464/2020\(H5N8\)](#)

<https://www.gisaid.org>



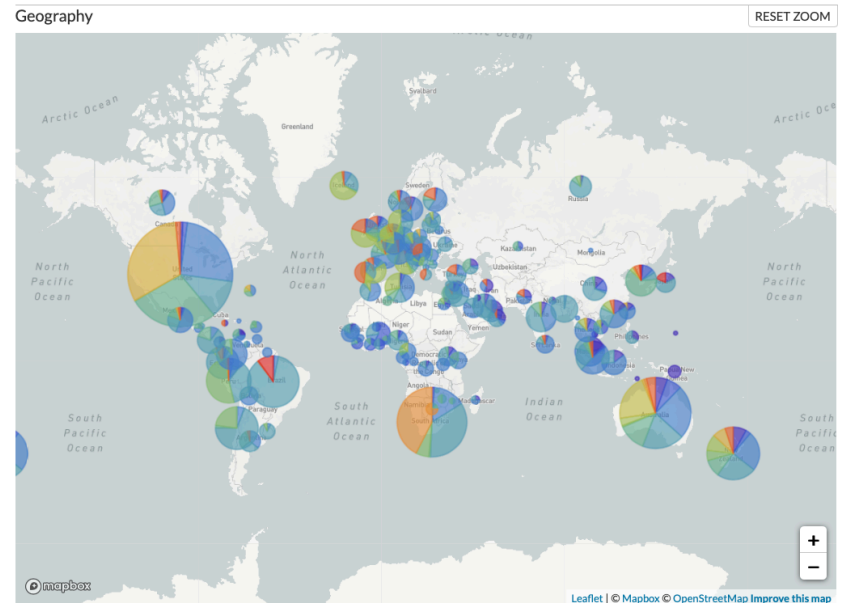
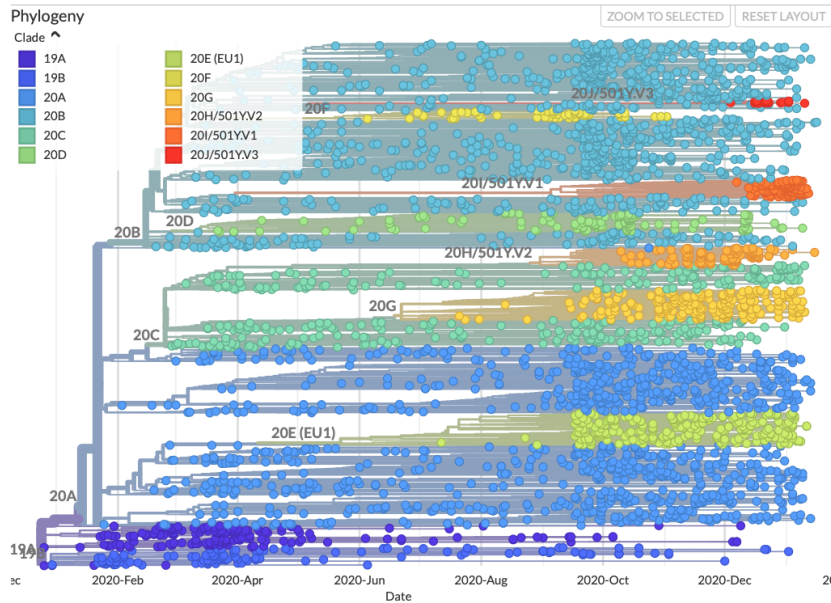
# Filodinámica del SARS-CoV-2



## Genomic epidemiology of novel coronavirus - Global subsampling

Maintained by the [Nextstrain team](#). Enabled by data from [GISAID](#)

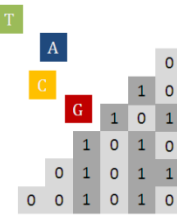
Showing 3894 of 3894 genomes sampled between Dec 2019 and Jan 2021.



<https://nextstrain.org/ncov/global>



# Filodinámica del SARS-CoV-2



**National Library of Medicine**  
National Center for Biotechnology Information

Search



**COVID-19 is an emerging, rapidly evolving situation.**



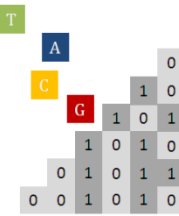
Get the latest public health information from CDC: <https://www.coronavirus.gov>

Get the latest research information from NIH: <https://www.nih.gov/coronavirus>

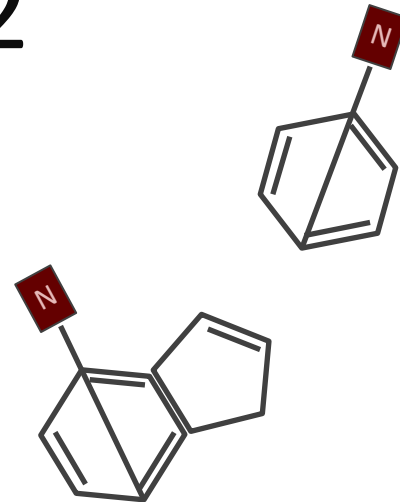
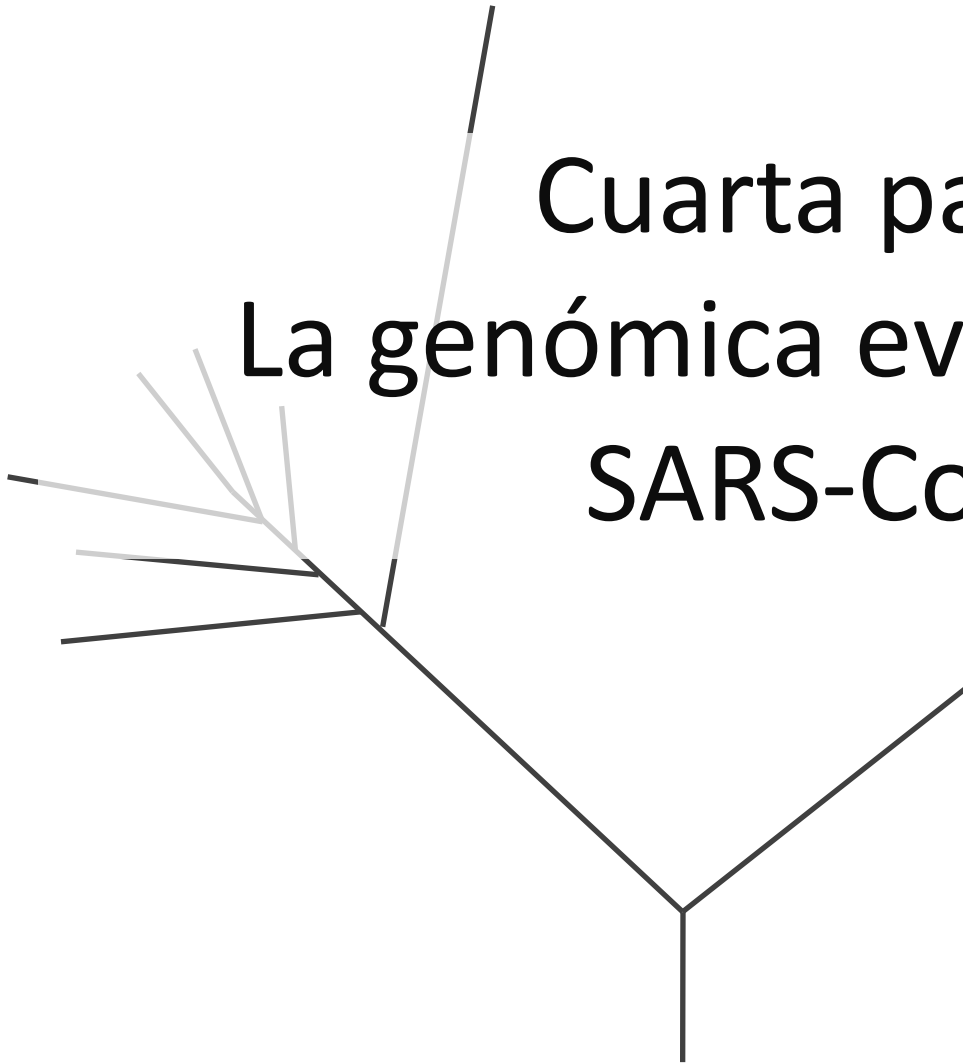
A detailed 3D rendering of a SARS-CoV-2 virus particle, showing its characteristic spherical shape with a textured surface and numerous red, crown-like spikes (glycoprotein spikes) protruding from it. The background is a dark teal color with some faint, lighter particles.

## NCBI SARS-CoV-2 Resources

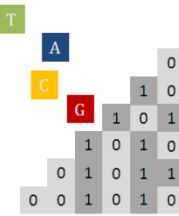
<https://www.ncbi.nlm.nih.gov/sars-cov-2/>



# Cuarta parte: La genómica evolutiva del SARS-CoV-2



# Evolución del SARS-CoV-2

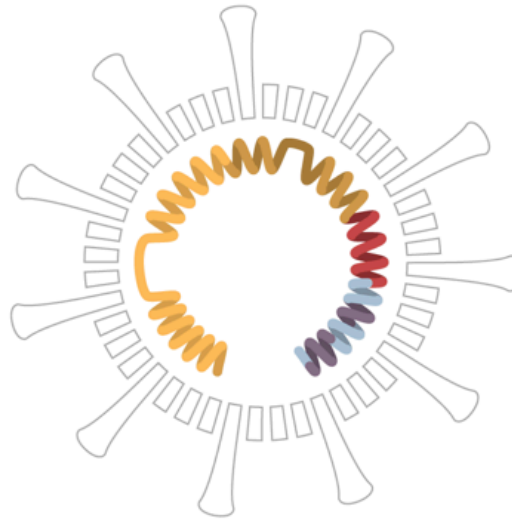


The New York Times

## Así muta y se propaga el coronavirus

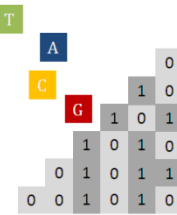
Por Jonathan Corum y Carl Zimmer April 30, 2020

[Read in English](#)



<https://www.nytimes.com/es/interactive/2020/04/30/science/coronavirus-mutacion.html>

# Evolución del SARS-CoV-2 en México



## Mexstrain

Evolución molecular del SARS-CoV-2 en México

### Introducción

Gracias al trabajo de diversos grupos de investigación a nivel internacional, la comunidad científica cuenta con varios miles de secuencias genómicas del SARS-CoV-2. Estas secuencias genómicas se encuentran depositadas en la base de datos GISAID (<https://www.gisaid.org>). A partir de ellas, es posible comenzar a inferir la evolución del SARS-CoV-2.

La plataforma Nextstrain (<https://nextstrain.org>) ofrece una serie de funciones que facilitan la visualización y análisis de los genomas secuenciados del SARS-CoV-2 (Hadfield et al. 2018). Entre otras cosas, la plataforma Nextstrain permite la visualización de: i) la evolución del coronavirus mediante el uso de filogenias calibradas en el tiempo; ii) mapas geográficos de transmisión del coronavirus; y iii) posiciones variables a lo largo del genoma. La visualización puede mostrar la evolución del coronavirus a nivel mundial o acotarse a una región determinada (por ejemplo, a un país).

El objetivo de esta página es ofrecer a la comunidad científica del país, un sitio en donde sea posible visualizar la evolución del SARS-CoV-2 en México a través de una versión local de Nextstrain: Mexstrain. Pretendemos también contextualizar la información derivada de Nextstrain con artículos de investigación y otras bases de datos especializadas en SARS-CoV-2 tales como <http://covid19.datamonkey.org/#>.

<http://www.ira.cinvestav.mx/ncov.evol.mex.aspx>

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|   |   | C |   |  |  |  |  |  | 1 | 0 |
|   |   |   | G |  |  |  |  |  | 1 | 0 |
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|   |   |   |   |  |  |  |  |  | 0 | 0 |
|   |   |   |   |  |  |  |  |  | 1 | 0 |
|   |   |   |   |  |  |  |  |  | 1 | 0 |

¡Gracias!

