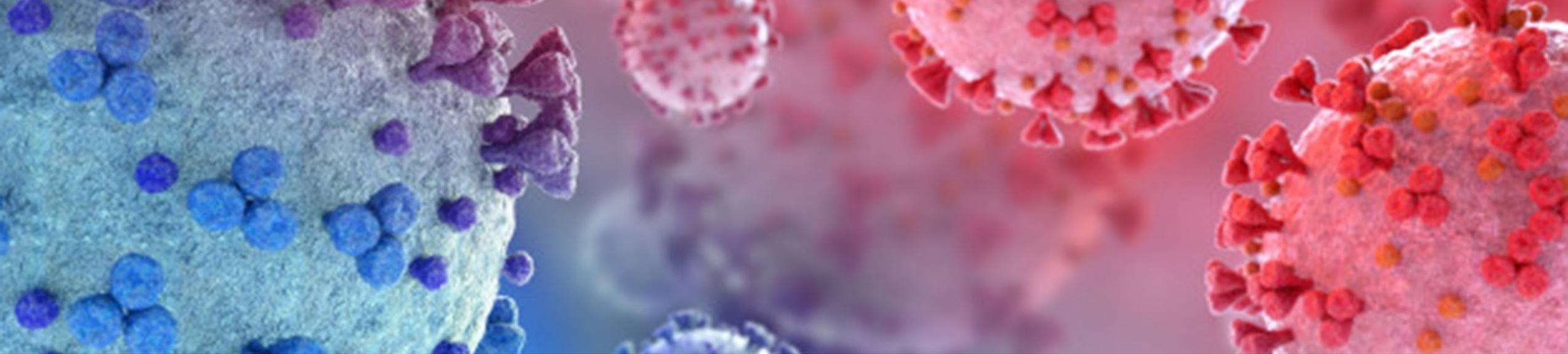


GENOMIC SURVEILLANCE

COVID-19 WEBINAR SERIES
30th JUNE 2021





1

How can national public health institutes further develop SARS-CoV-2 genomic sequencing as part of their surveillance systems through regional and international networks?



Alarming COVID variants show the vital role of genomic surveillance



Detect **phylogenetic relationships**
(follow viral spread - surveillance and evolution)



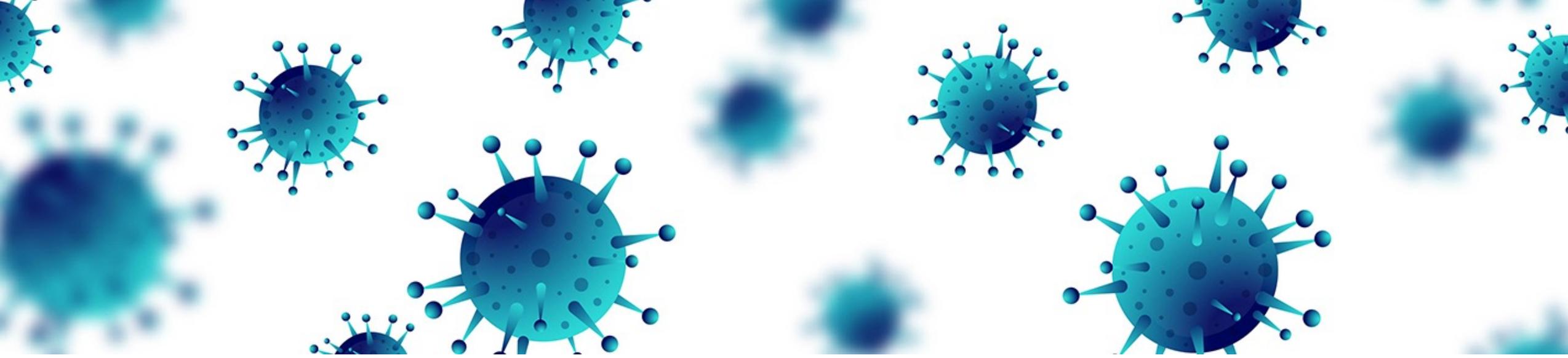
Detect **nucleotide changes** in patient isolates
(e.g. D614G, B.1.1.7, B.1.351)



Identify **potential new strains**



Detect **emerging resistant mutations**
to antiviral drugs and vaccines



2

Strategies to Develop Genomic Surveillance in Argentina



Strategies to Develop Genomic Surveillance in Argentina

- **Inter-institutional Argentine Project on SARS-CoV-2 Genomics (PAIS)**

A project dependent on the National Ministry of Science and Technology.

This Consortium is currently dedicated to the surveillance of community circulation of SARS-CoV-2 variants in the 24 jurisdictions of the country. This evaluation has to be representative of the different characteristics of age groups, sex, territorial units, and clinical severity criteria, by defined time unit.

- **Genomics and Bioinformatics Platform of the National Administration of Laboratories and Institutes of Health, ANLIS “Dr. Carlos G. Malbrán”**

An institution dependent on the National Ministry of Health.

This platform is currently dedicated to the evaluation of the variants entering the country through the allowed airports of entry, of suspected re-infections, and of infection cases in vaccinated patients.

PAIS Project



[INICIO](#) [PROYECTO](#) [NOSOTROS](#) [REPORTES](#) [DESARROLLO](#) [CONTACTO](#) 

Vigilancia activa de SARS-CoV-2 - 07/06/2021

Proyecto Argentino Interinstitucional de genómica de SARS-CoV-2

Desarrollado por el Consorcio Argentino de Genómica de SARS-CoV-2.

Financiado, a través del subsidio FONARSEC IP COVID-19 N° 247, por la Agencia Nacional de la Promoción de la Investigación, el Desarrollo Tecnológico y la Innovación del Ministerio de Ciencia, Tecnología e Innovación, Argentina.

Reportes

Proyecto

Genómica

PAIS Project

PROJECT OBJECTIVE

- As a general objective, we propose to analyze the evolution of SARS-CoV-2 strains circulating in Argentina in order to study their origin and spread around the country, within the context of worldwide strains, as well as analyze the mutations that may affect the diagnosis, transmission, and virulence of the virus.

PAIS Project

CONSORTIUM COMPOSITION

Central Node

Nodes to collect and process samples, and contribute to clinical-epidemiological data – 49

Nodes for sample genomic NGS sequencing – 8

Nodes for bioinformatic processing – 11

Group for molecular evolution analysis – 9

Group of epidemiologist physicians – 7

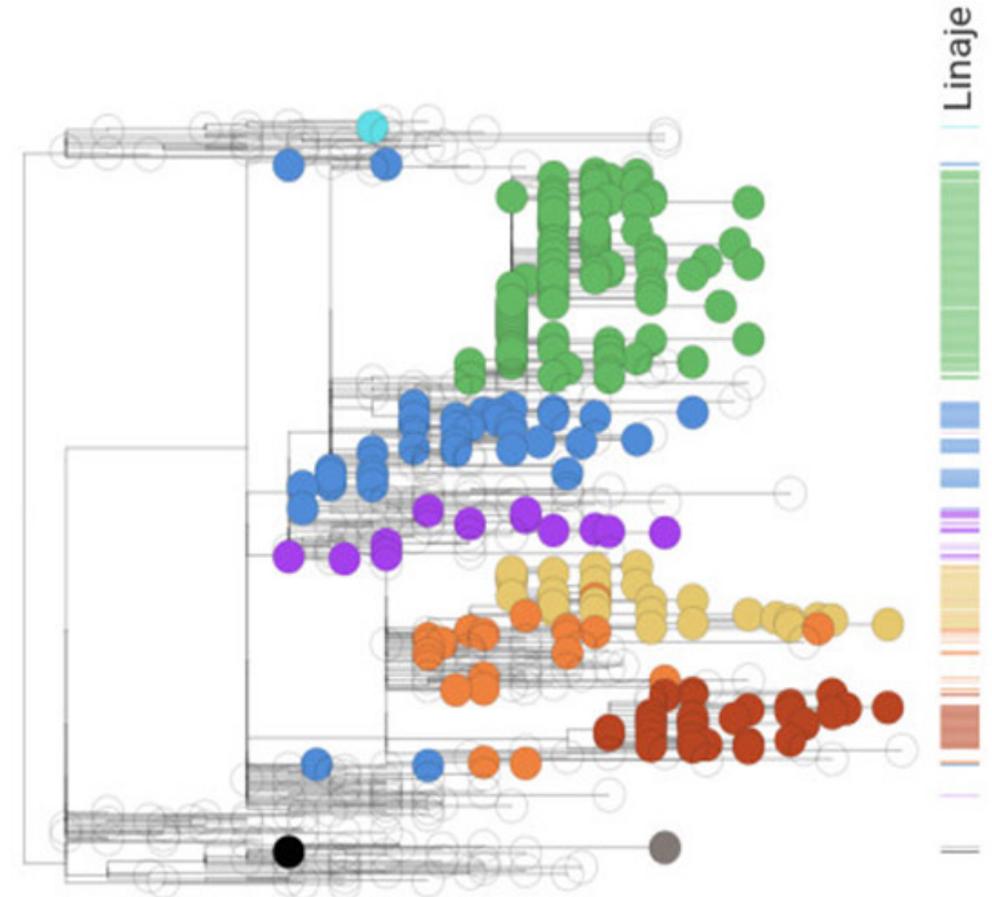
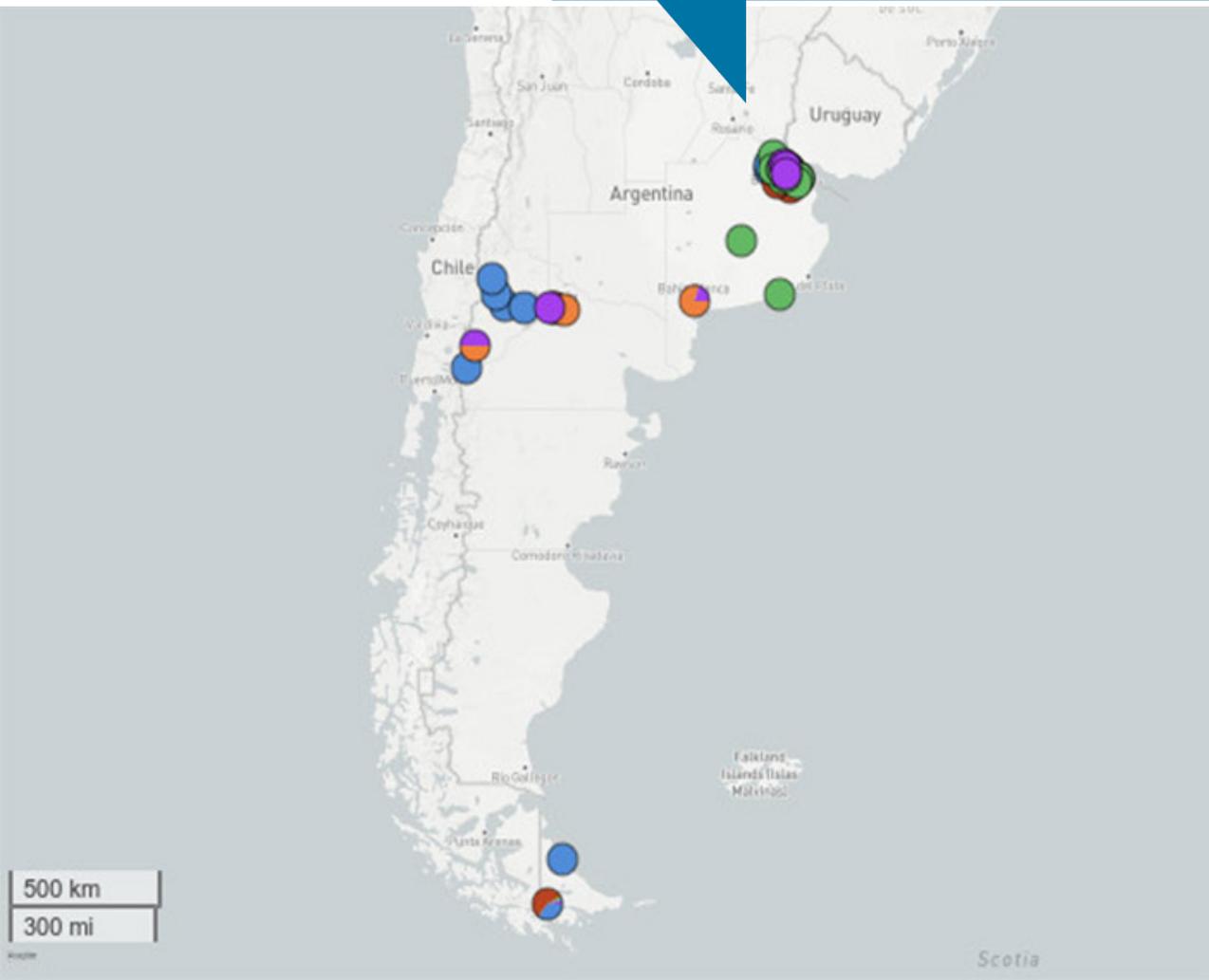
PAIS Project



PAIS Project

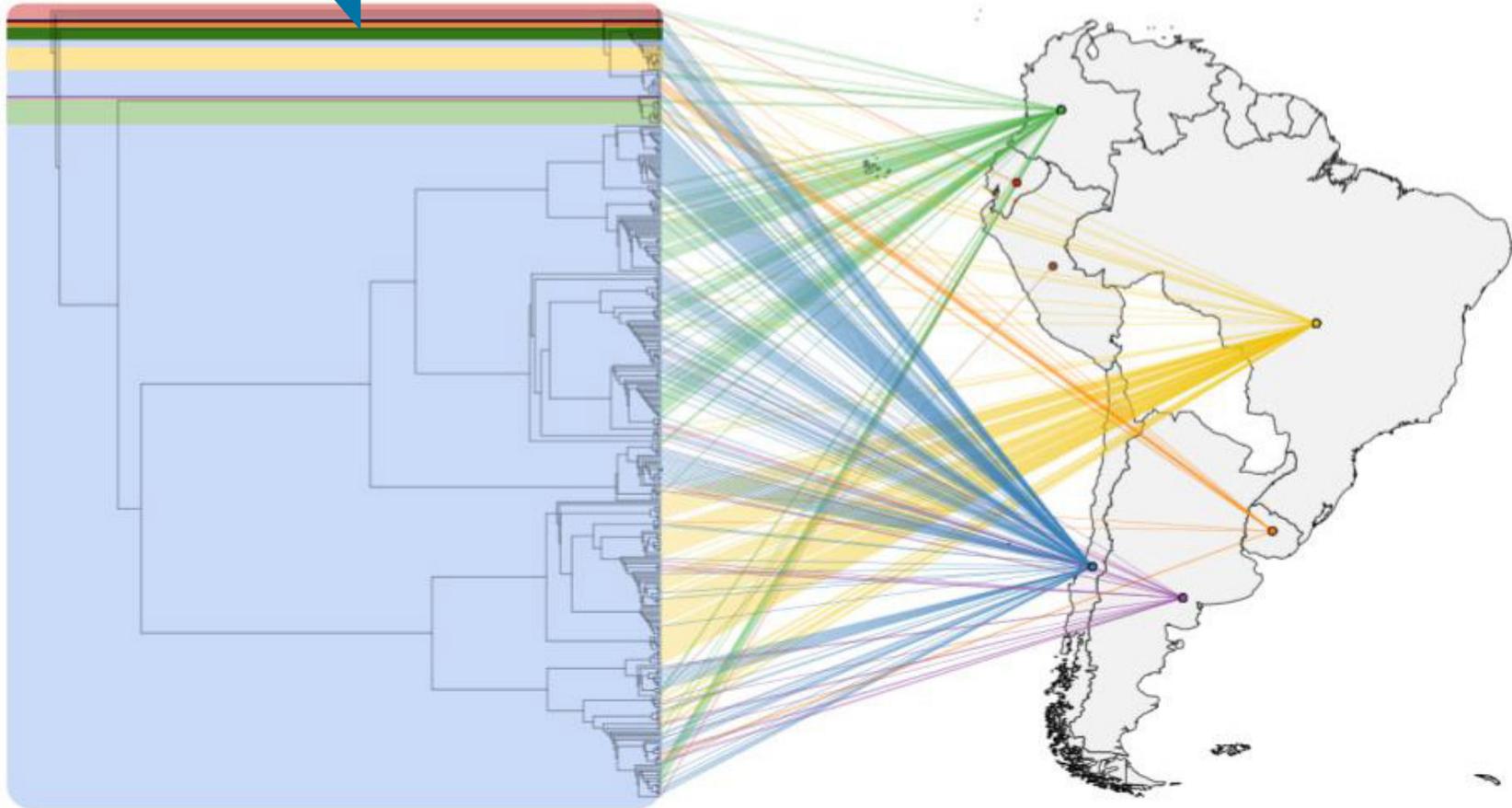


PAIS Project

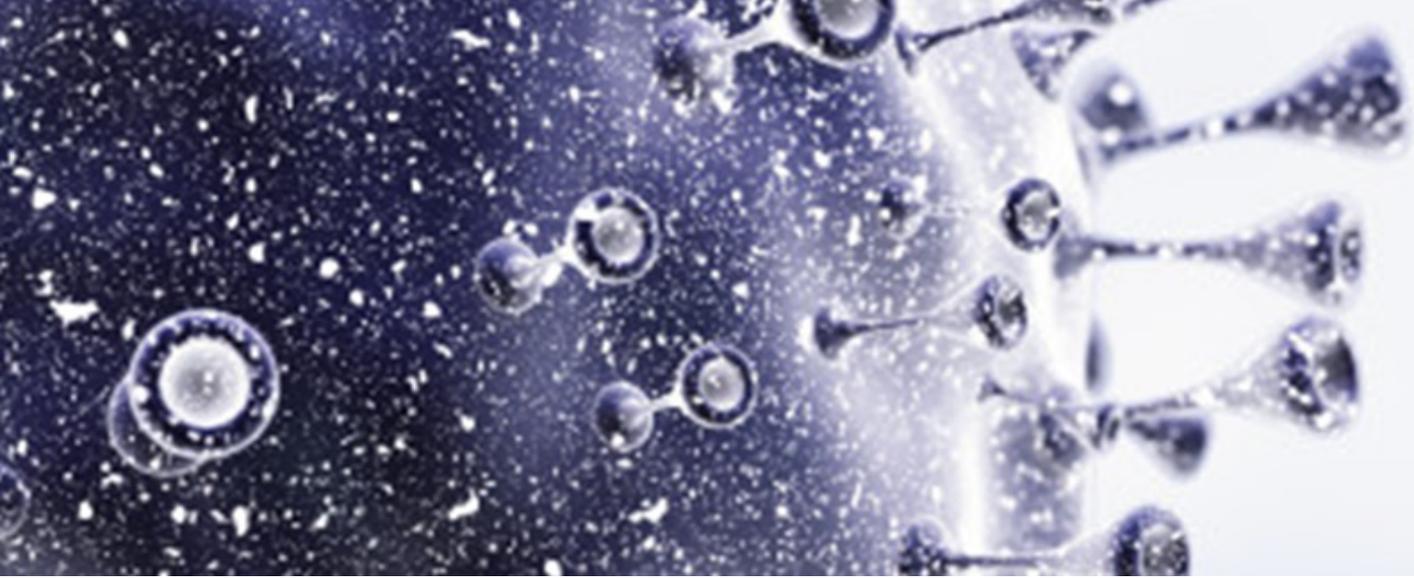


PAIS Project

- Linajes**
- B
 - B.1
 - B.2
 - B.3
 - B.6
 - A
 - A.1
 - A.2
 - A.5



- Mapa**
- Argentina
 - Brazil
 - Chile
 - Colombia
 - Ecuador
 - Perú
 - Uruguay



3

Results obtained by the PAIS Project



PAIS Project



1235

samples from all
over the country
already sequenced



100

investigators and
health professionals
involved



10

research protocols
developed



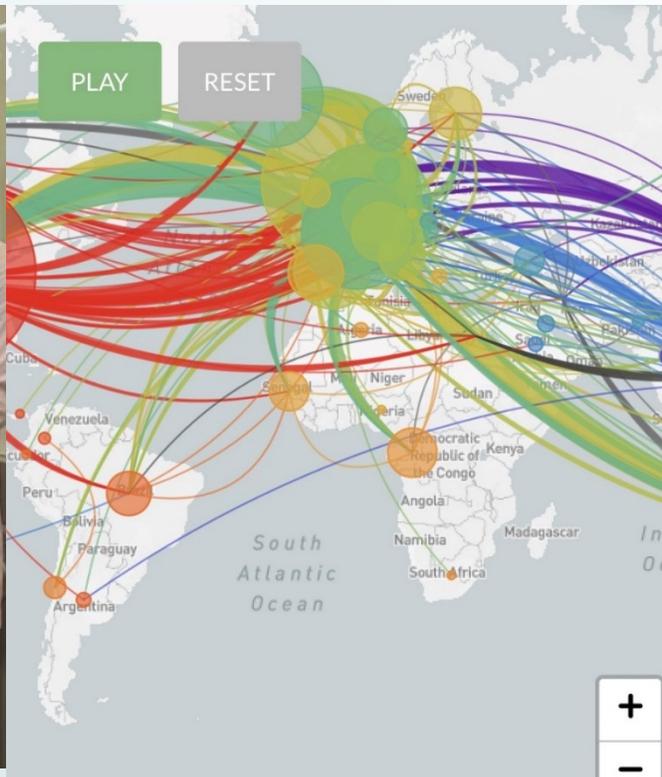
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participating
public and private
institutions



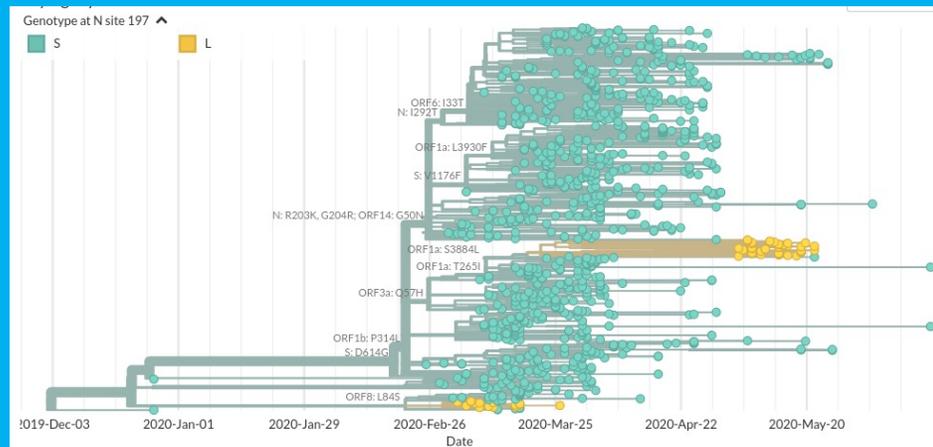
**Genomics and Bioinformatics Platform
ANLIS “Dr. Carlos G. Malbrán”**

Genomic Sequencing

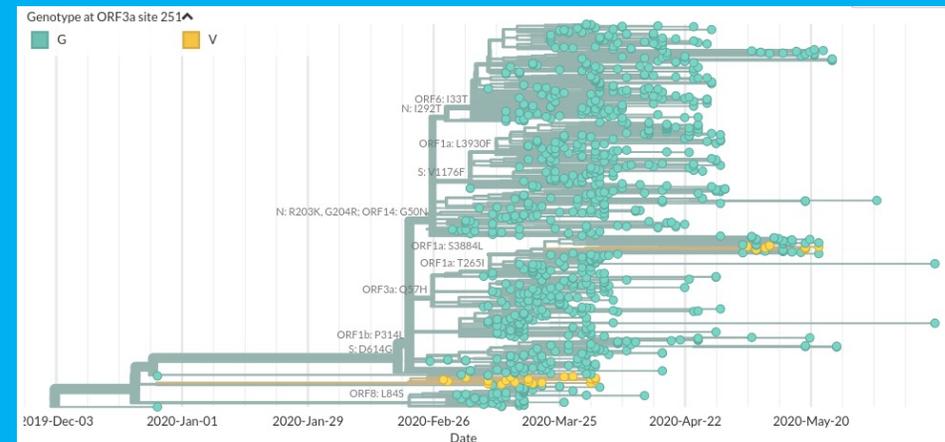


- On April 6, 2020, ANLIS-Malbrán managed to sequence the whole genome of the 3 strains circulating at that time in Argentina, coming from different regions around the world – Asia, Europe, and the United States.

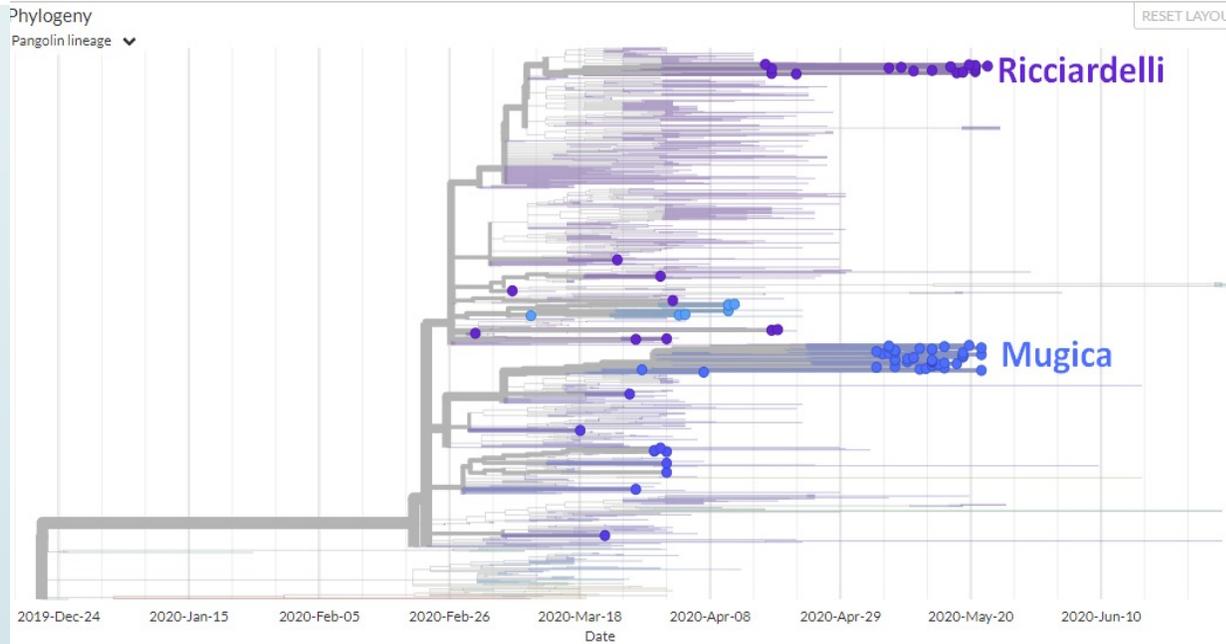
The lineages introduced in the country and the relevant mutations were studied



Phylogenetic tree of whole genomes viewed with Nextstrain's Augur of lineage B 1.3 from Argentina and other countries, showing the sequences from Barrio Mugica that presented variant (SNP) C28863T which translates into an amino acid change in protein N: S197L



Phylogenetic tree of whole genomes viewed with Nextstrain's Augur of lineage B 1.3 from Argentina, showing the sequences from Barrio Mugica that share SNP G26144T, which produces mutation G251V in protein ORF3a.



In the recent samples collected within the framework of the *Detectar* Plan, the presence of only two sub-lineages with a significant geographic signature was observed in the popular neighborhoods, which corresponds with the epidemiological situation of ASPO (preventive mandatory social isolation). This coincides with community transmission, different from what was observed in the first introductions.

Phylogenetic tree of genomes from Argentina in context with Latin American genomes published in GISAID, showing the geographic signature of the neighborhoods in the city of Buenos Aires.

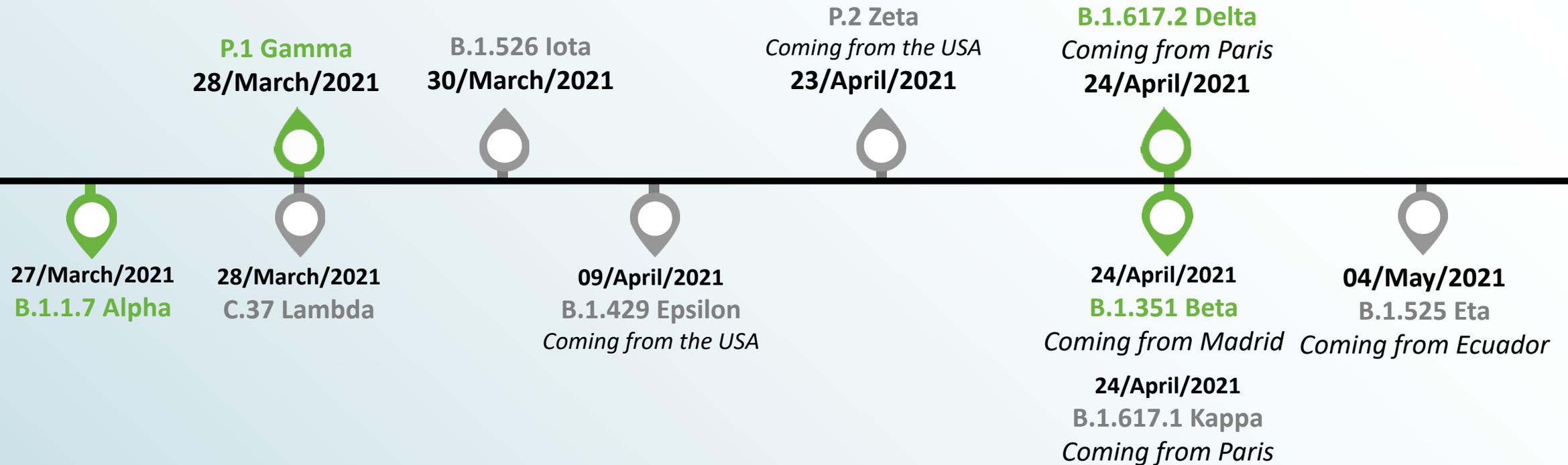


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Results obtained by the Genomics and Bioinformatics Platform of ANLIS “Dr. Carlos G. Malbrán”



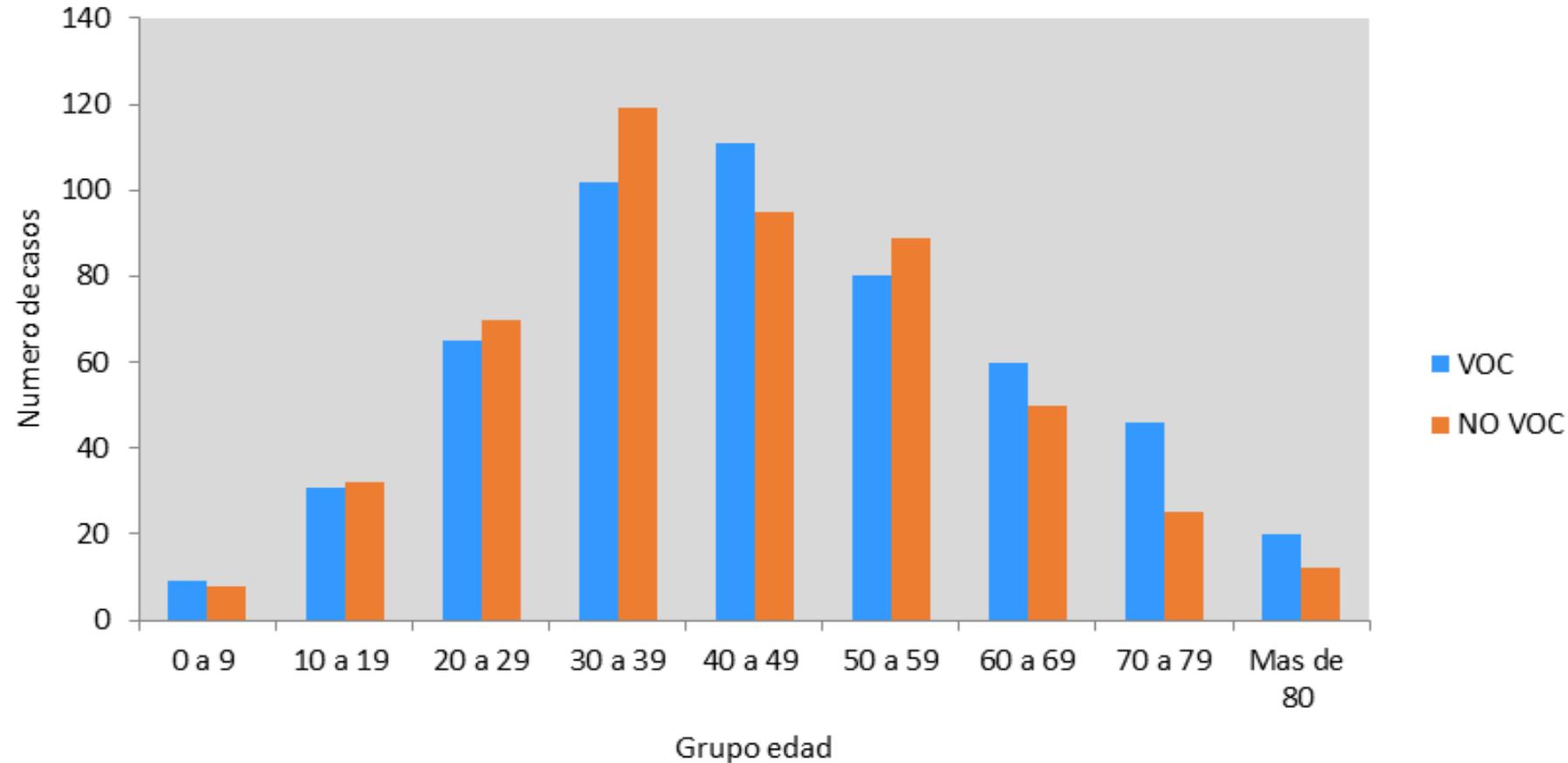
Incoming Variants of Interest and Variants of Concern (VOI and VOC)
of SARS-CoV-2 in Argentina



Total sequenced samples

- From January 2021 to June 7, 1261 samples were sequenced, including the surveillance of travelers, in unusual serious presentations, vaccinated individuals, and regular surveillance of circulating variants.

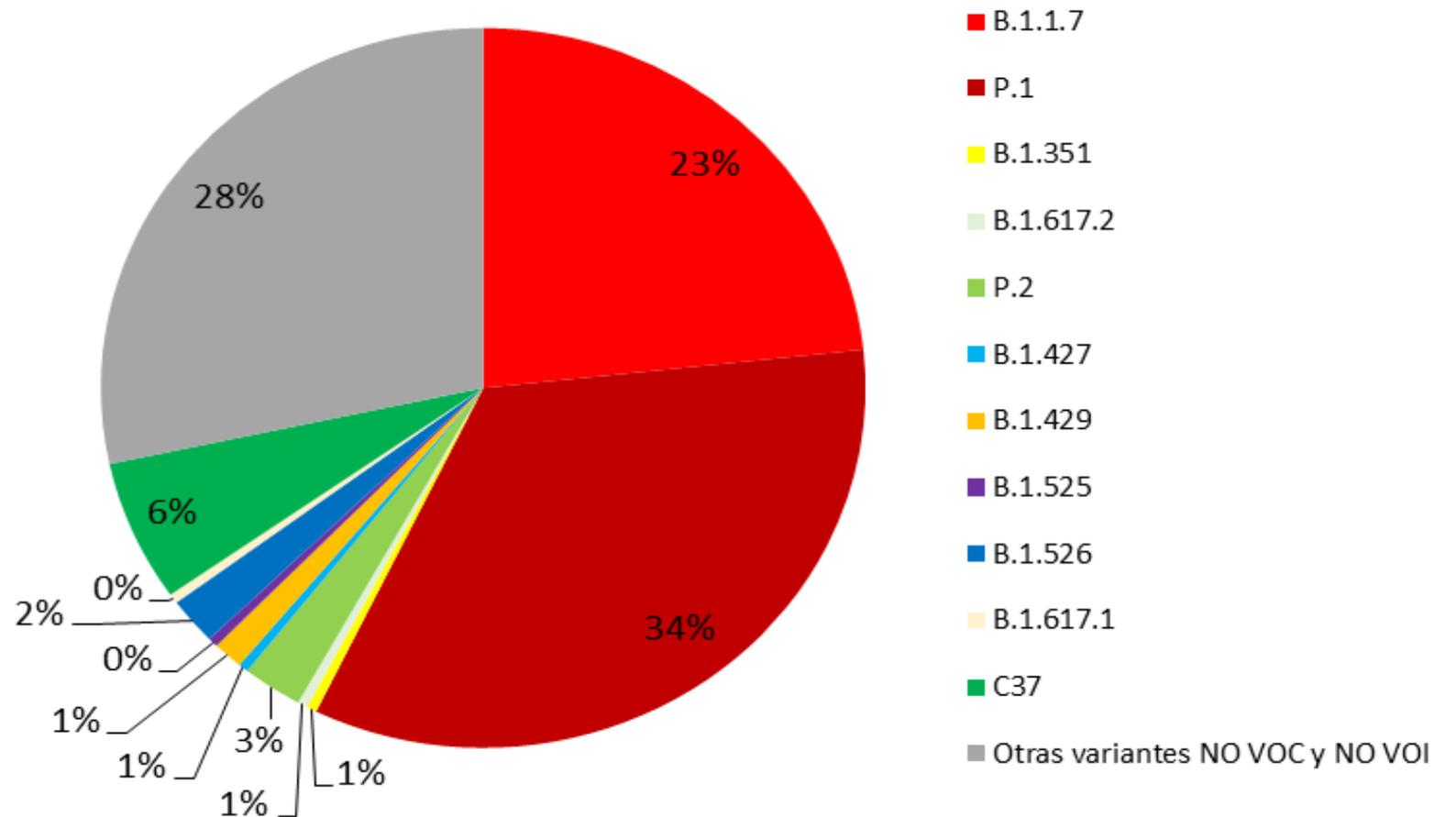
Distribution by age group of sequenced cases with VOC and non-VOC detection for the whole country.



Genomic surveillance of SARS-CoV-2 in international travelers

- Genomic sequencing conducted on 237 samples from travelers who entered the country and had a positive result, from January to June 03.

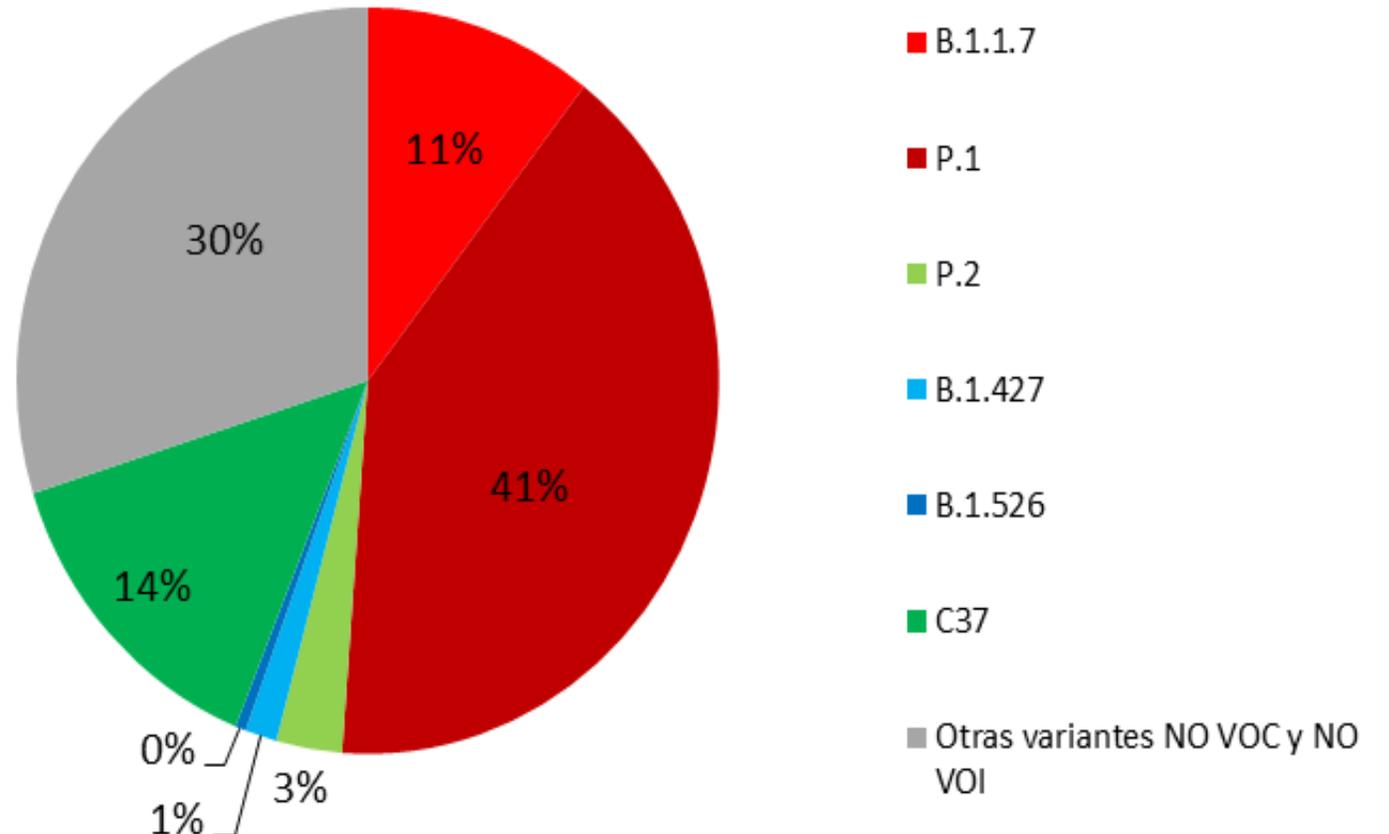
Percent distribution of samples from priority and non-priority variants in travelers.
n = 237



Genomic surveillance of SARS-CoV-2 in individuals with no travel history

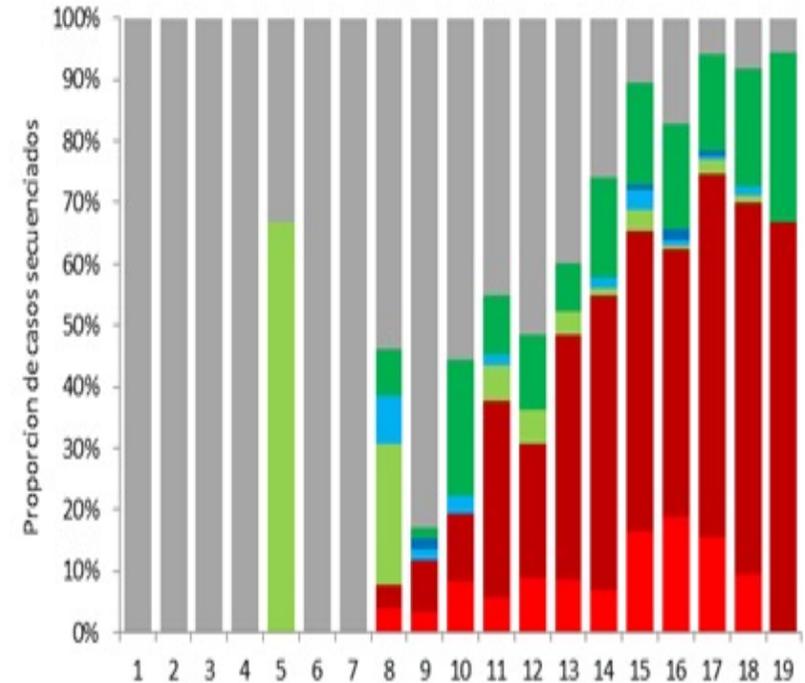
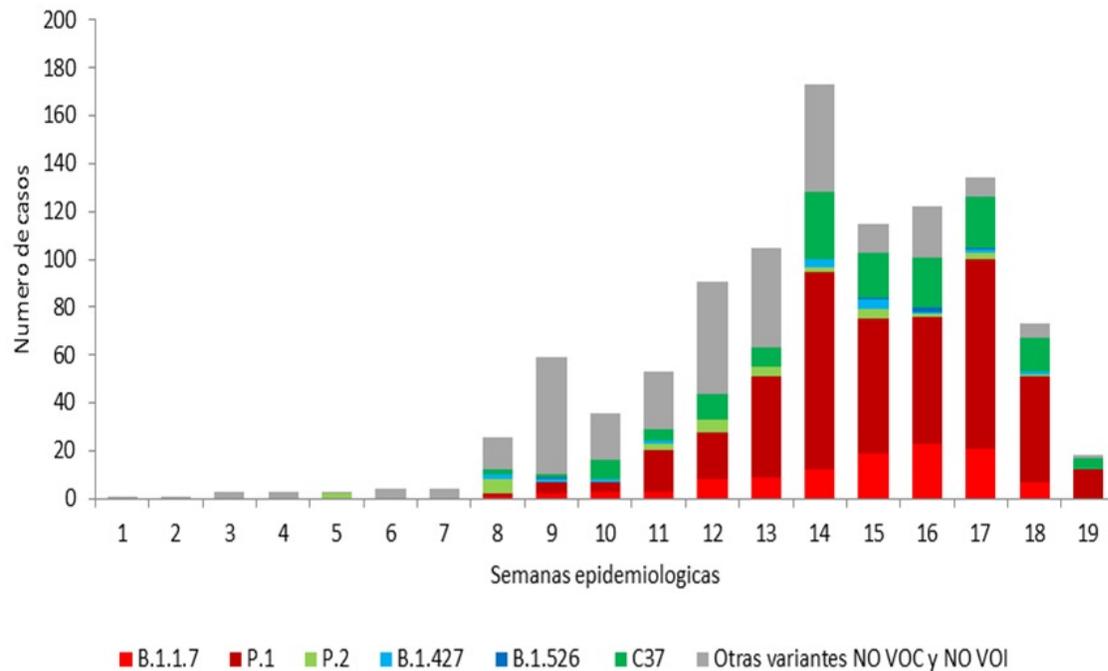
- Genomic sequencing conducted on 1024 samples from individuals with a positive result, with no history of traveling to an international destination, from January to June 03.

Percent distribution of samples from priority and non-priority variants in non-travelers. Country-wide total. Accumulated as of EW23. n = 1024.



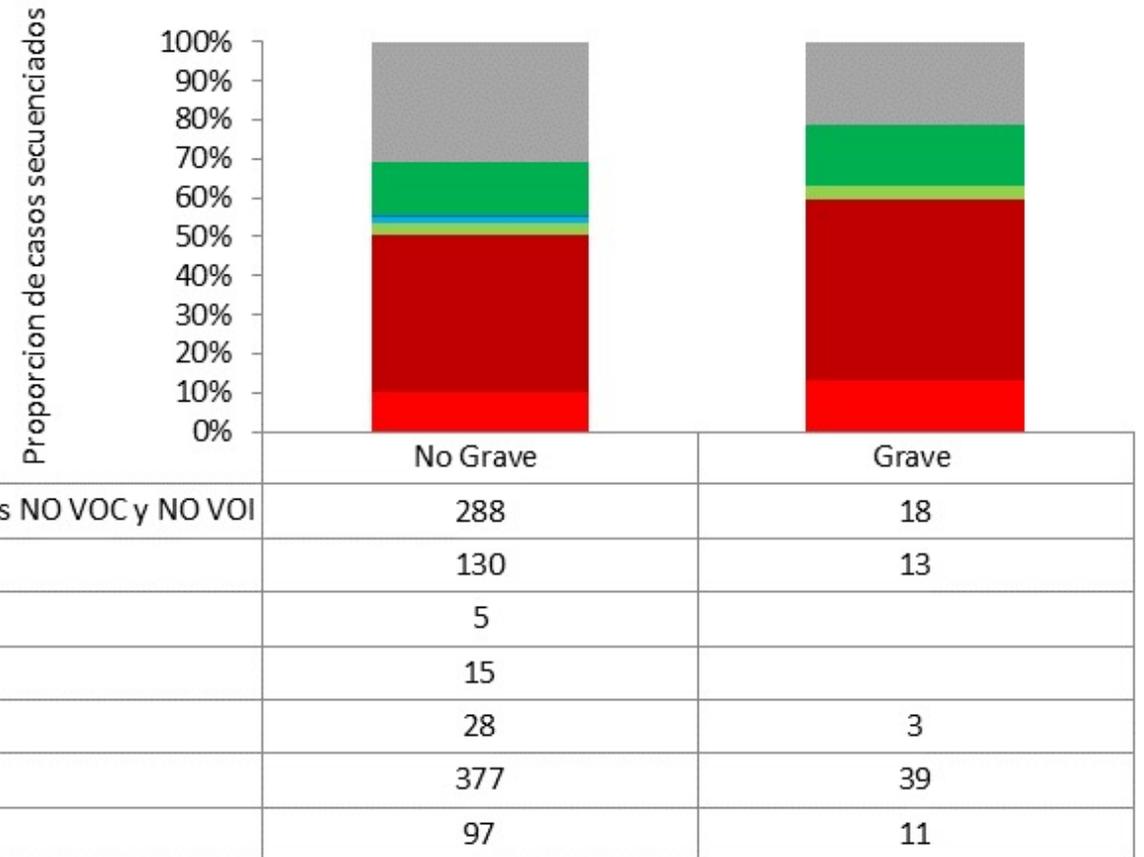
Genomic surveillance of SARS-CoV-2 in individuals with no travel history

- Percent distribution of samples from priority and non-priority variants in non-travelers, per EW of sample collection date. Accumulated as of EW23. Country-wide total: 1024.



Genomic surveillance of SARS-CoV-2 in individuals with no travel history

- Percent distribution of variants in sequenced cases per severity criteria, country-wide total (n=1024).



Genomic surveillance of SARS-CoV-2 in cases with a vaccination history

- A total of 408 cases with a history of vaccination against SARS-CoV-2 were studied by genomic sequencing, 167 cases after the application of the first vaccine dose, and 241 cases after the application of the second dose. Results distribution is described according to number of doses received and immunization status.

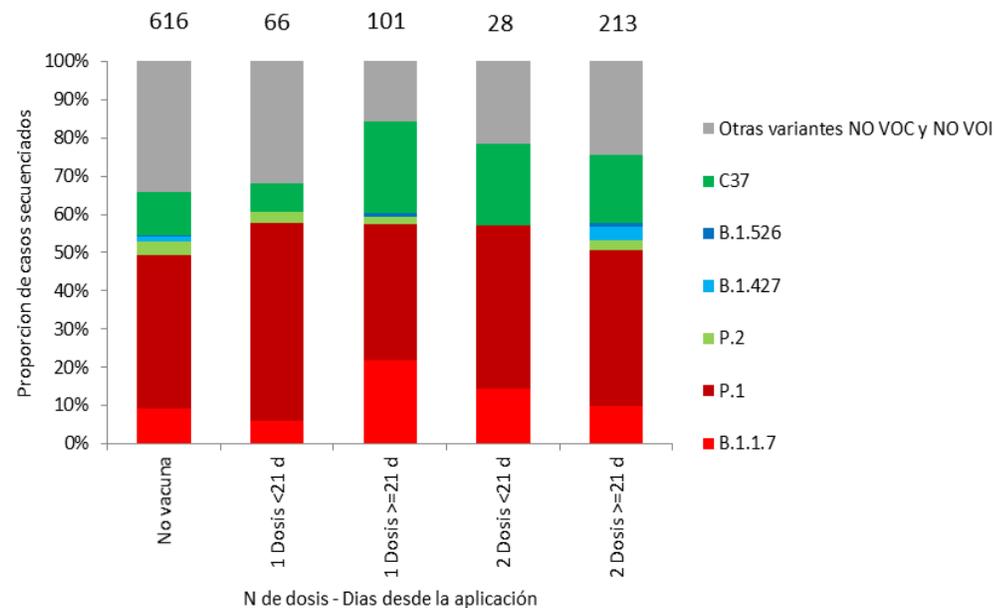
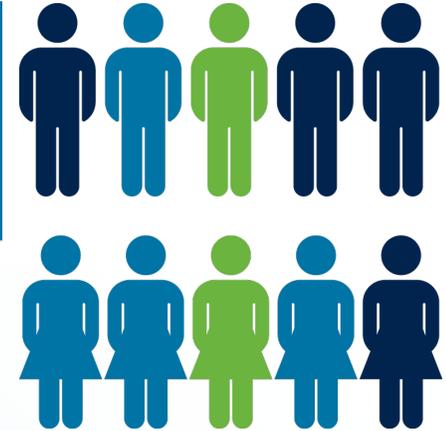


Tabla 1: Distribución absoluta de variantes prioritarias y no prioritarias en casos fallecidos según condición de inmunización.

Lineage	Not immunized	Immunized	Completed schedule
Alpha (B.1.1.7)		4	
Gamma (P.1)	6	5	
Zeta (P.2)	1	1	
C37	2	3	1
Other variants, Non-VOC and Non-VOI	1	3	
Overall total	10	16	1

Achievements and strengths of SARS-CoV-2 genomic surveillance in Argentina



STEP 1

- Strategies have been established which have guaranteed active genomic surveillance.

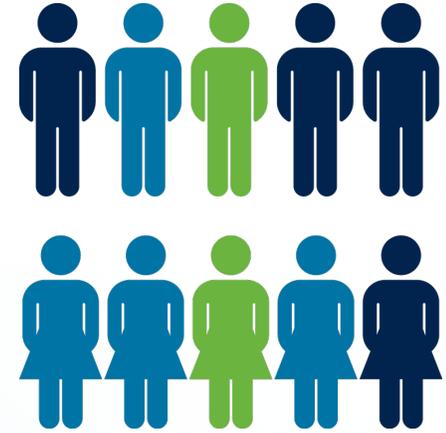
STEP 2

- The development of genomic sequencing has been strengthened by equipment acquisition and human resources training.

STEP 3

- The results have been key inputs for Public Health decision making.

Weaknesses of SARS-CoV-2 genomic surveillance in Argentina



STEP
1

- Difficulties to unify criteria to communicate results.

STEP
2

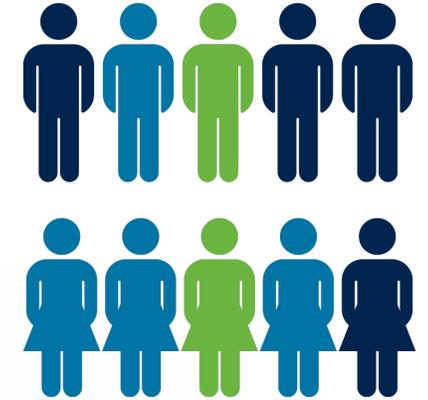
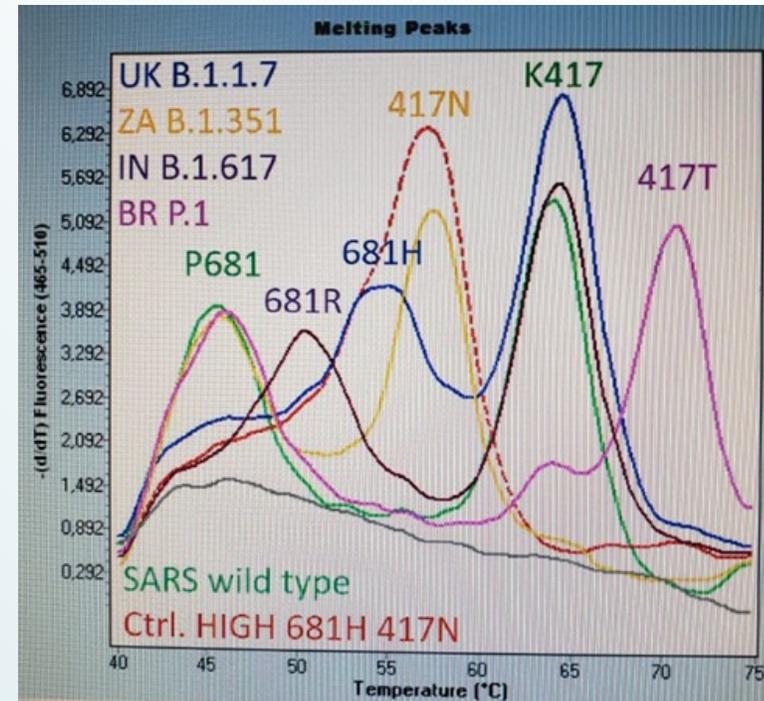
- Excessive representation of some geographic areas at the expense of others.

STEP
3

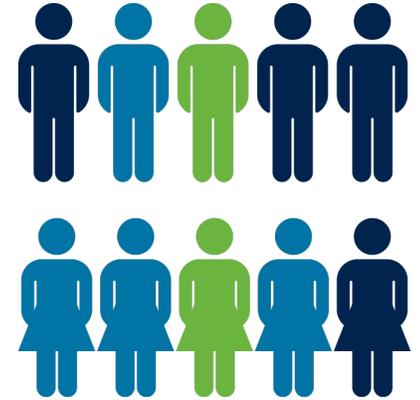
- Lack of harmonization in the techniques used for genomic sequencing.

Lack of harmonization in the techniques used for genomic sequencing

- There are diverse strategies available to identify the different SARS-CoV-2 variants: whole genome sequencing, partial viral spike (S Spike) sequencing, and assessment of spike mutations by PCR (HRM-PCR). They have different scopes and limitations, which are essential to take into account when reports are drafted.



Lack of validation in the techniques used for genomic sequencing

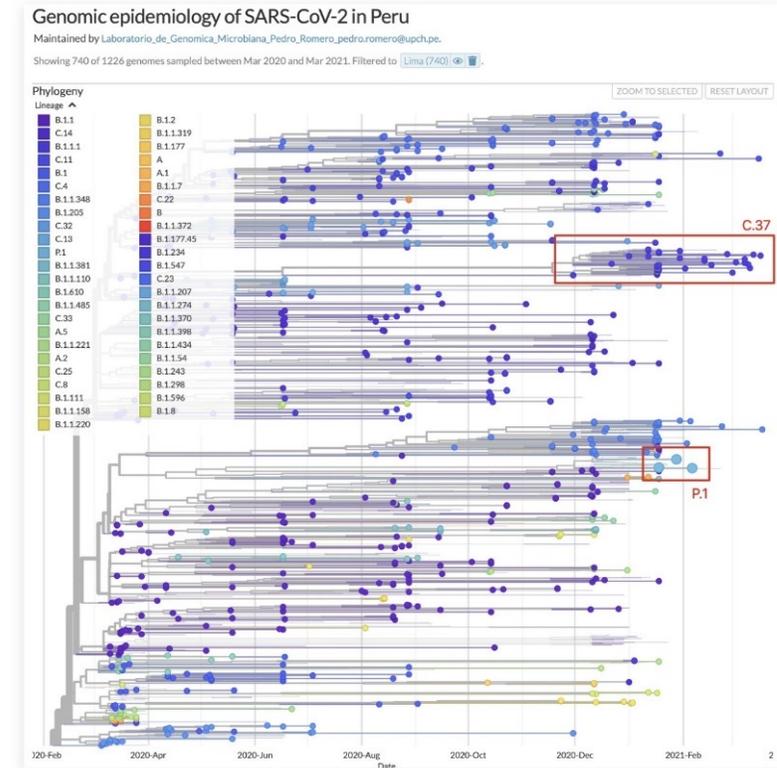


- **Background: the Peru experience, mentioned by Dr. Pablo Tsukayama.**

 **Pablo Tsukayama**
@pablotsukayama

Esta semana reportamos la identificación de un nuevo linaje (variante) de SARS-CoV-2 que parece expandirse rápidamente en Perú y Chile. Le llamamos C.37. Les cuento lo que sabemos y no sabemos al respecto. 🧵

1/25



Relevant topics to analyze

1

Significant delays in uploading sequences

- The median/mean CSTlag values vary between countries, from one day to one year (or even more).

2

Sequencing rates

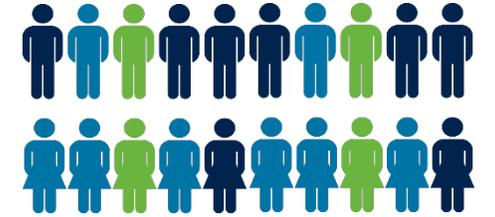
- The pattern seen over Asia, Africa and South America, where sequencing covers less than 0.1% to 0.4% of cases. Europe has sequenced ~2%, and North America 1.4%, but Oceania 37% of cases.

3

Population-based sequencing rates

- First World countries in the west (Europe and the USA) lead the pack, along with Israel and Reunion, at over 1,000 per million population. North American average is 600, vs. 1,000 for Europe, but 600 for Oceania.

Future perspectives for genomic sequencing



- The identification of the different SARS-CoV-2 variants by genomic sequencing is an essential tool to:

**Purchase and
distribute vaccines**

**Promote national
vaccine production**

**Develop different
therapeutic
strategies for
SARS-CoV-2**



THANK YOU



ANLIS
MALBRÁN
INSTITUTO NACIONAL DE LABORATORIOS
E INVESTIGACIONES DE SALUD "DR. CARLOS MALBRÁN"

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