Sistema Descentralizado de Vigilancia Genómica

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SHARING MINDS, CHANGING LIVES

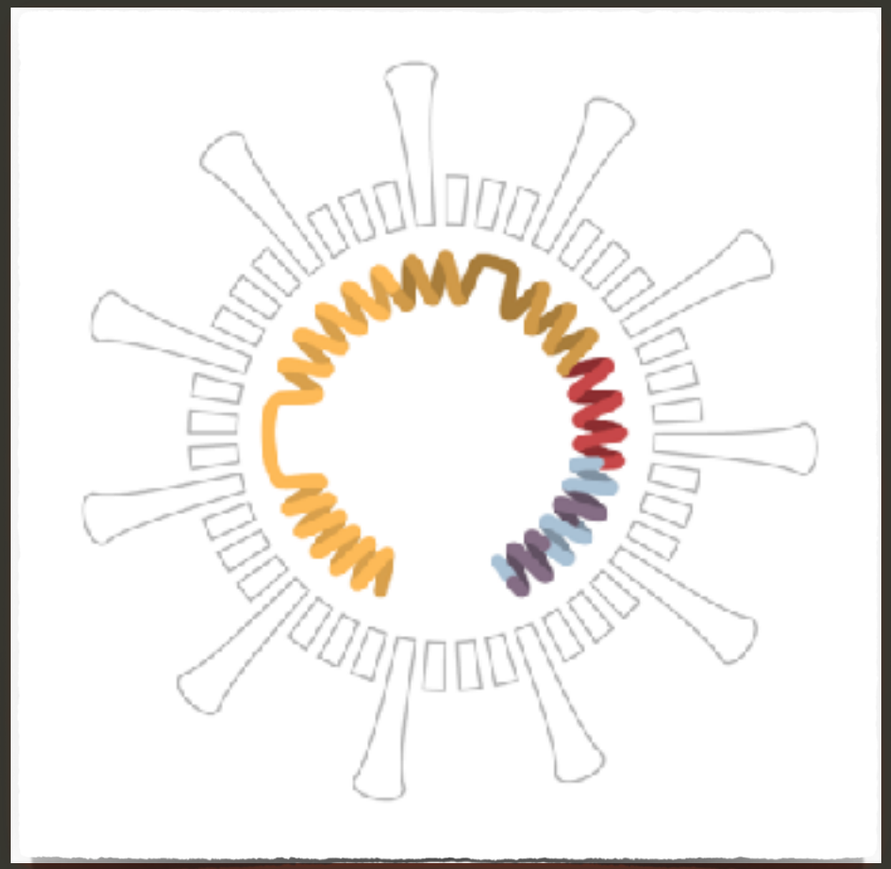
TUMI Genomics

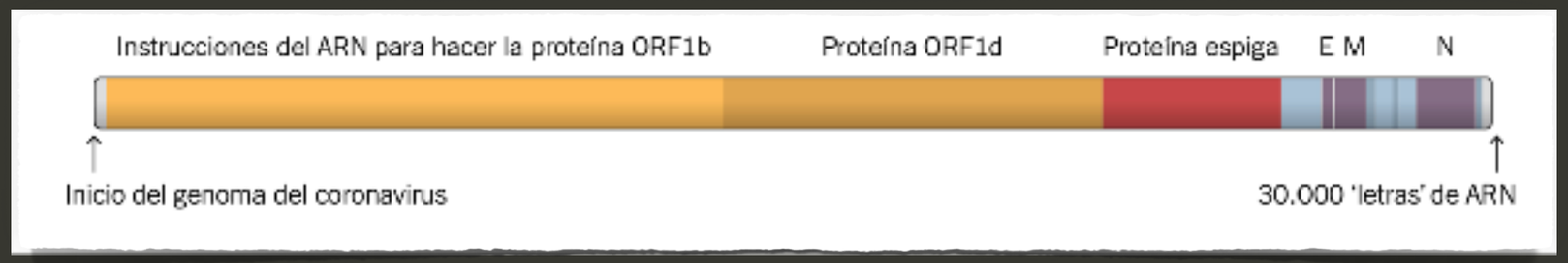
BID LAB

OBJETIVO

Establecer un sistema de procesamiento, secuenciamiento y análisis de genomas de SARS-CoV-2 para generar información epidemiológica que sea interpretable y accionable por autoridades de salud pública.

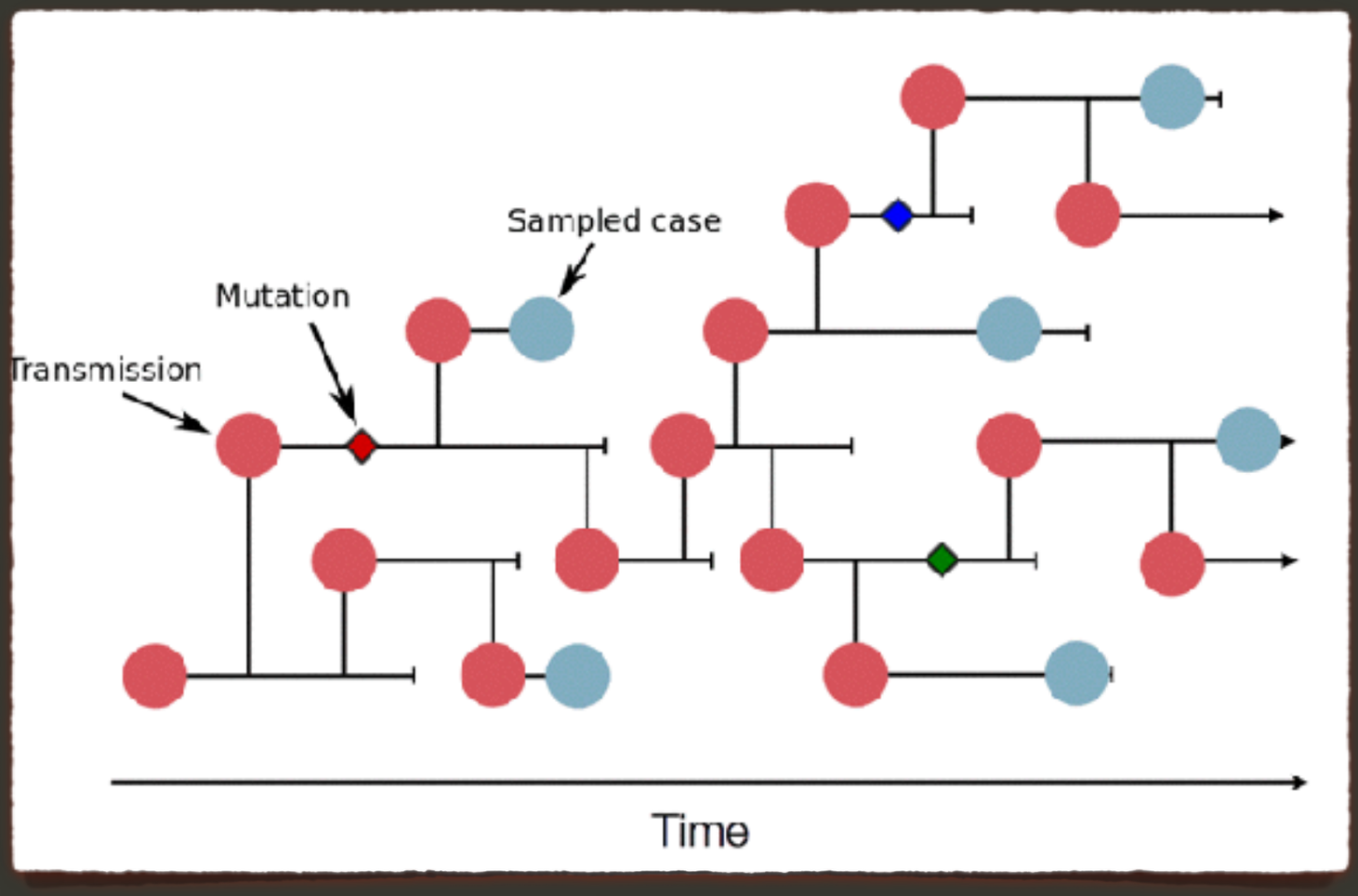
El genoma de SARS-CoV-2





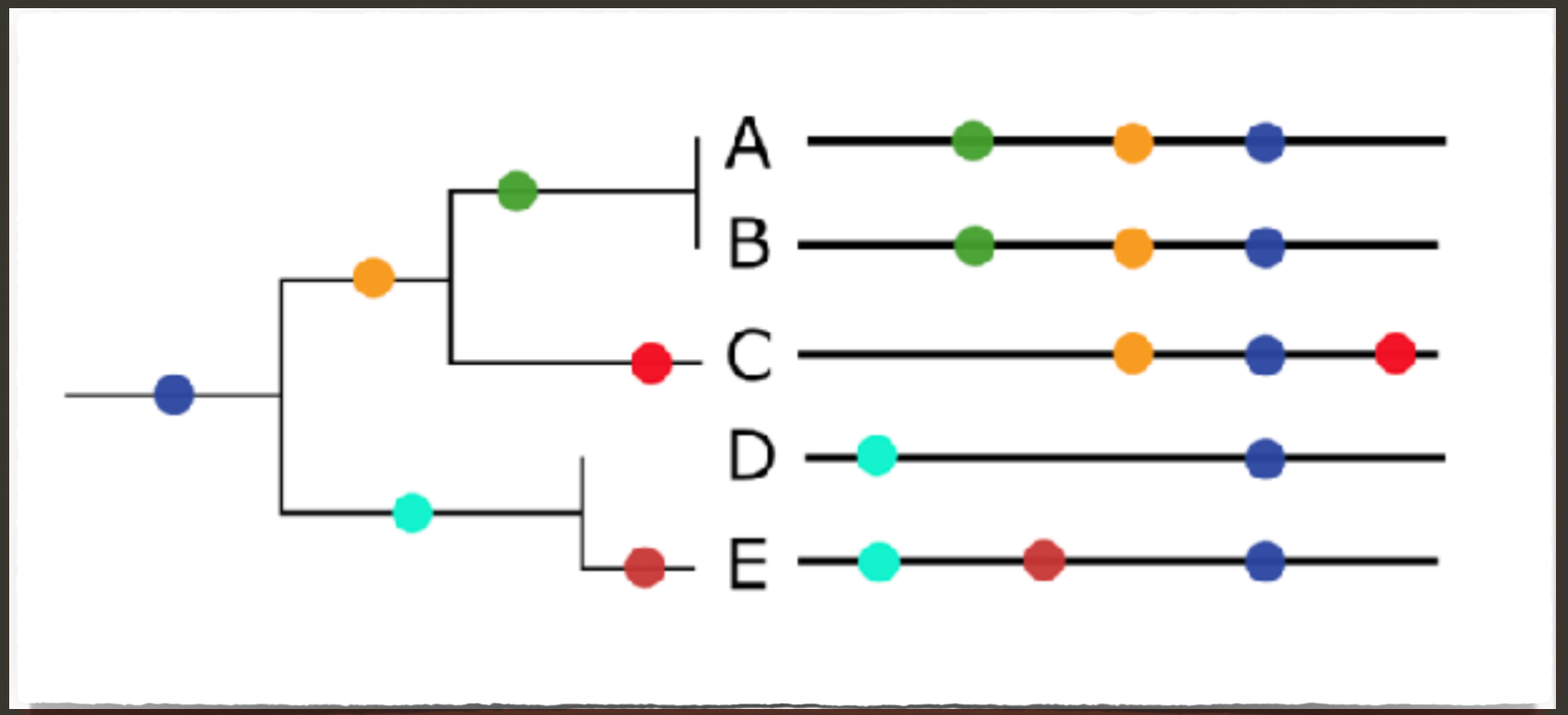
www.nytimes.com/es/interactive/2020/04/30/science/coronavirus-mutacion.html

Utilizamos mutaciones para inferir cadenas de transmisión



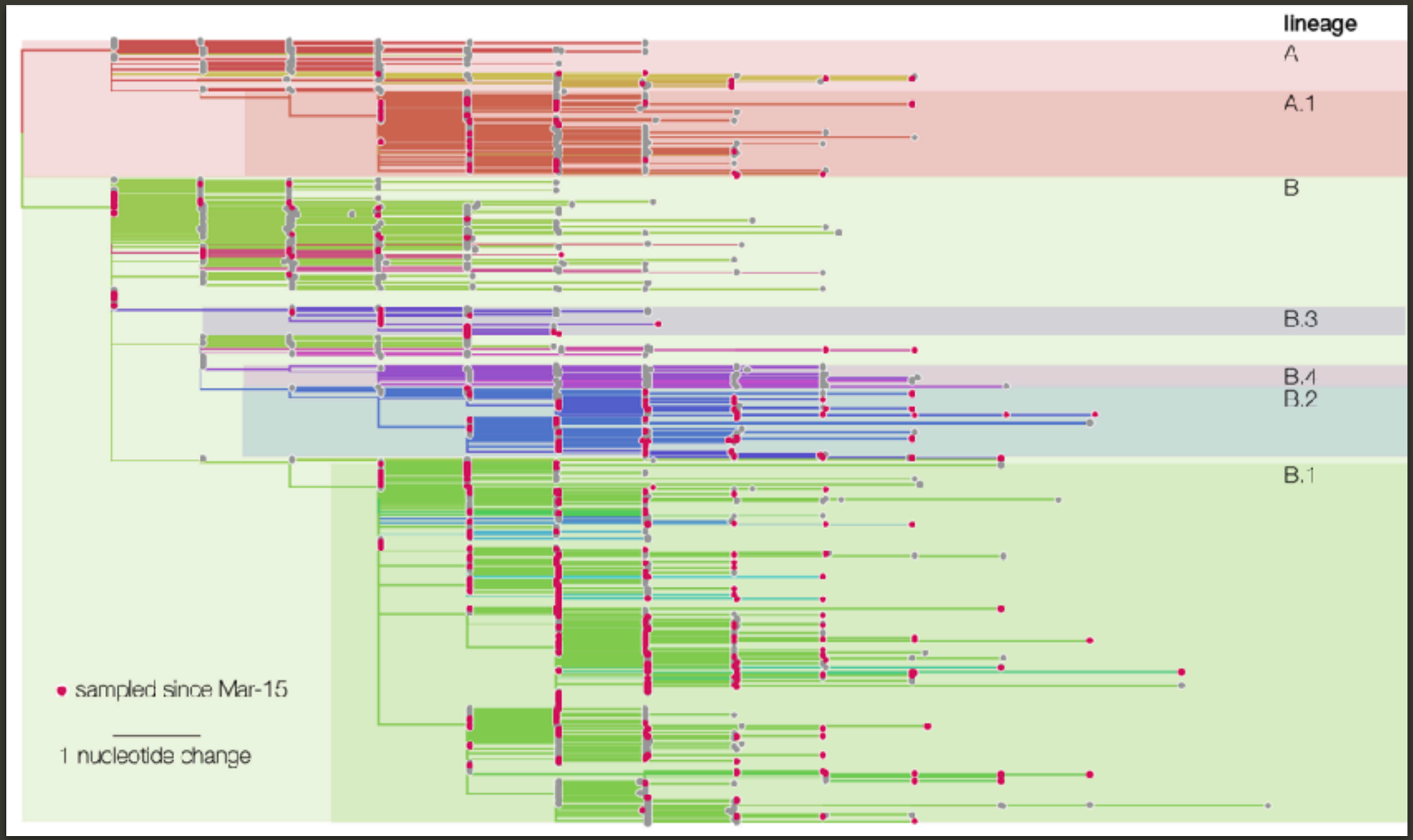
nextstrain.org/help/general/how-to-read-a-tree

Y reconstruir relaciones filogenéticas



nextstrain.org/help/general/how-to-read-a-tree

Octubre 2020: Varios linajes de SARS-CoV-2 circulando en el mundo



virological.org/t/a-dynamic-nomenclature-proposal-for-sars-cov-2-to-assist-genomic-epidemiology/458

135,000 genomas de SARS-CoV-2 en GISAID al 2-Octubre

www.gisaid.org

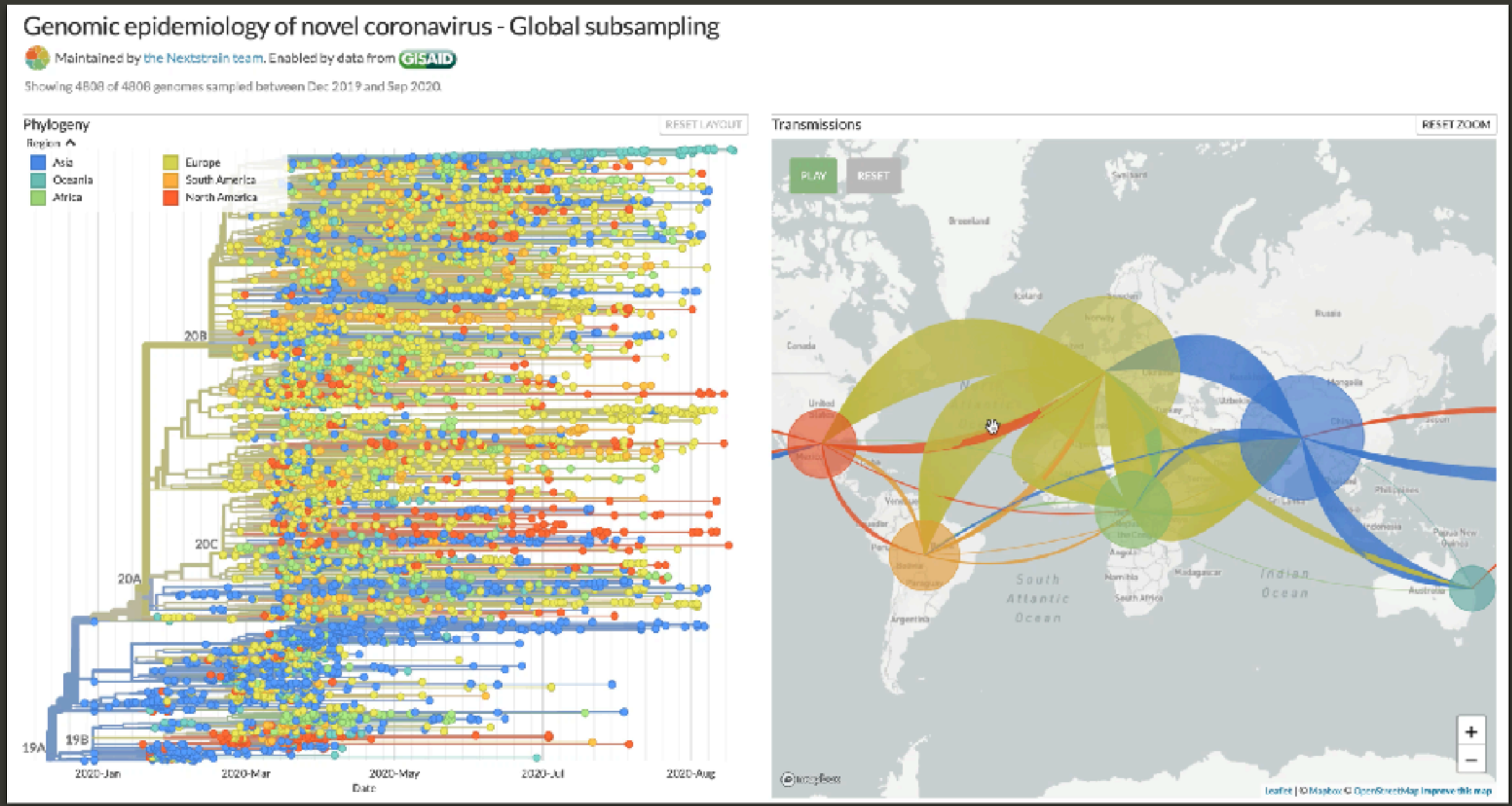
Solo hemos secuenciado el 0.4% de los 35 millones de casos reportados (cuidado con inferencias basadas en sesgos de muestreo)

Los investigadores solo han secuenciado una pequeña fracción de los coronavirus que hoy infectan a más de tres millones de personas en todo el mundo.

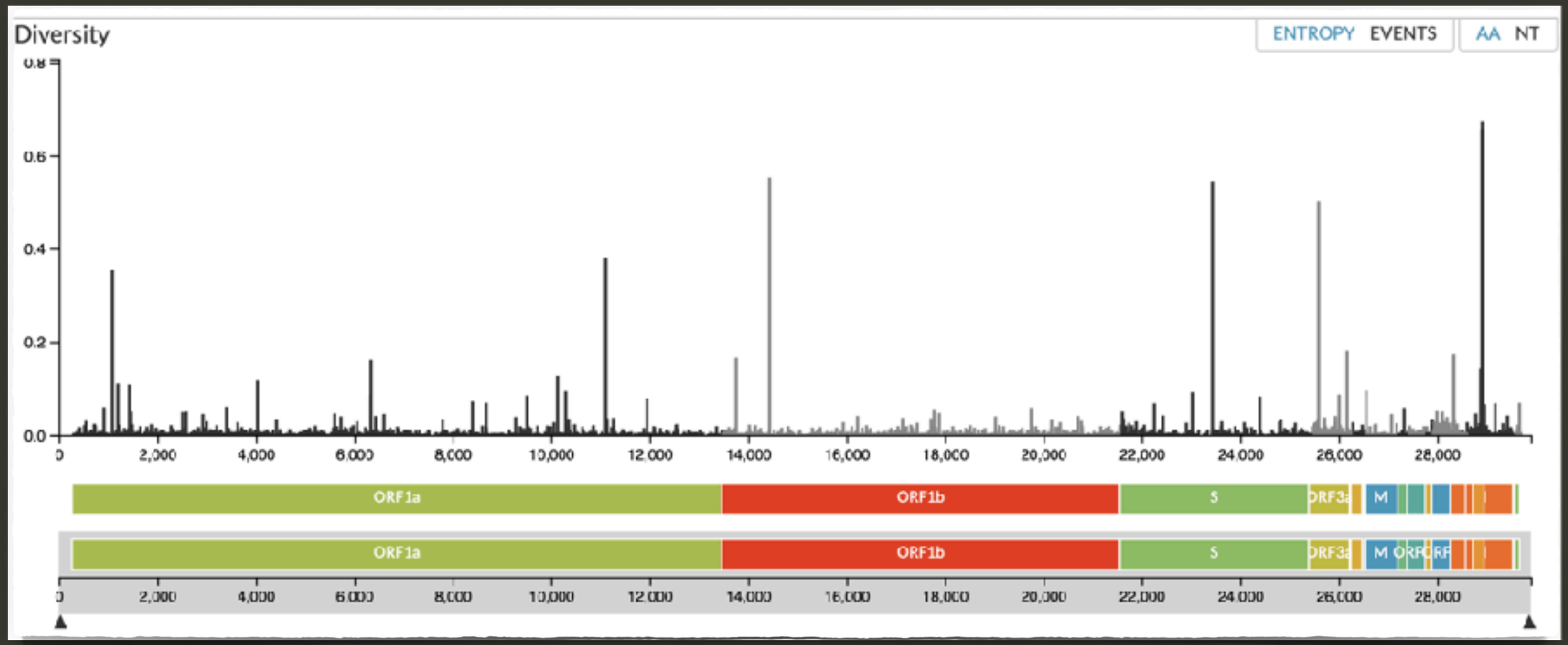
La secuenciación de más genomas descubrirá más capítulos en la historia del virus, y los científicos están particularmente expectantes por estudiar las mutaciones de regiones donde se han secuenciado pocos genomas, como África y América del Sur.

www.nytimes.com/es/interactive/2020/04/30/science/coronavirus-mutacion.html

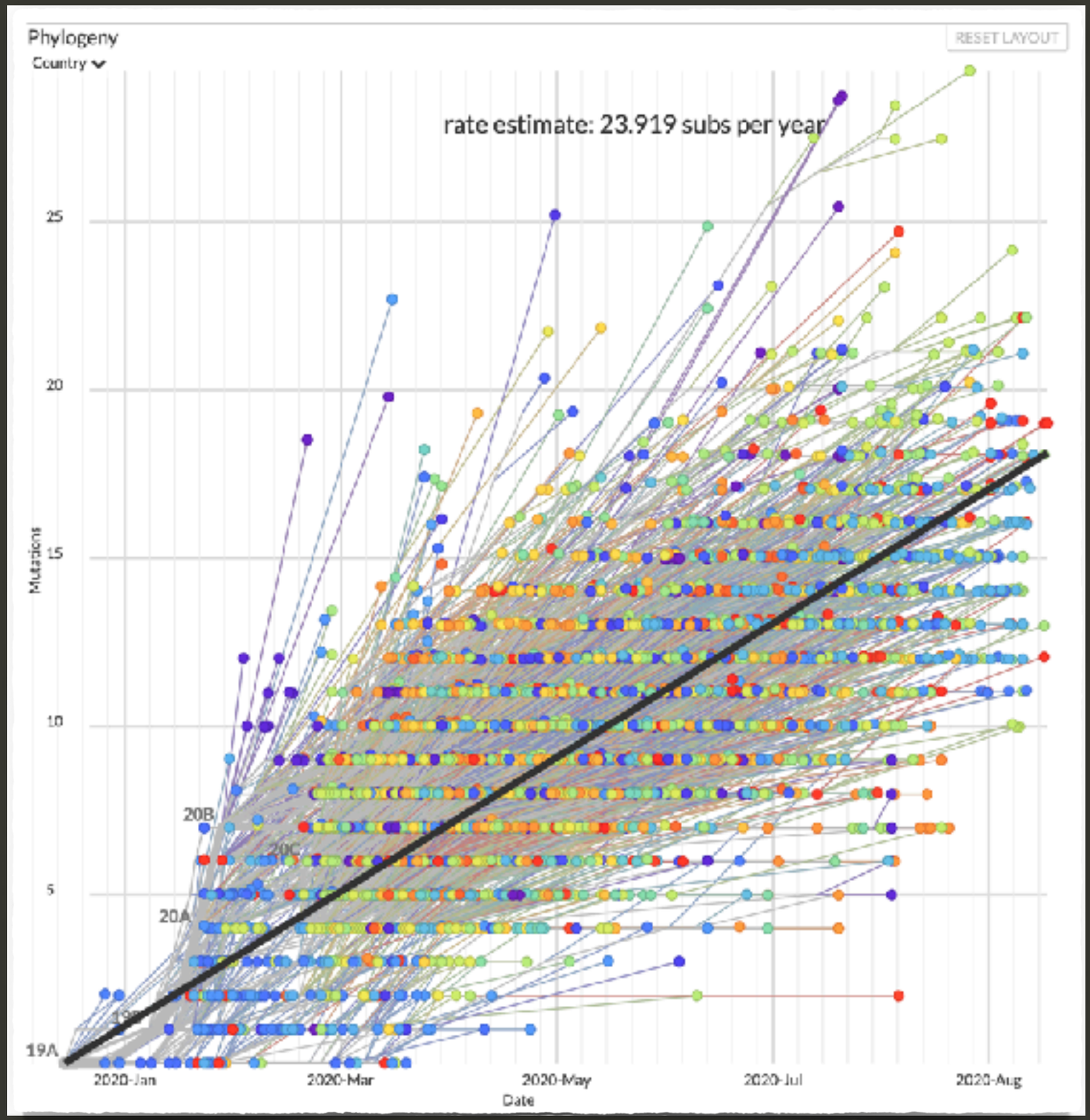
Datos genómicos permiten estudio de transmisión y evolución a nivel global



Miles de mutaciones descritas desde enero 2020



Genoma SARS-CoV-2 varía ~2 mutaciones por mes



Genomas revelan la transmisión temprana de SARS-2 en Australia

nature medicine

LETTERS

https://doi.org/10.1038/s41591-020-1000-7

Check for updates

Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling

Rebecca J. Rockett[1,2,10], Alicia Arnott[1,2,3,10], Connie Lam[1,2], Rosemarie Sadsad[1,2,4], Verlaine Timms[1,2], Karen-Ann Gray[1,2], John-Sebastian Eden[1,5], Sheryl Chang[6], Mailie Gall[3], Jenny Draper[3], Eby M. Sim[2,3], Nathan L. Bachmann[2,3], Ian Carter[3], Kerri Basile[3], Roy Byun[7], Matthew V. O'Sullivan[1,2,3], Sharon C-A Chen[1,2,3], Susan Maddocks[3], Tania C. Sorrell[1,2,8], Dominic E. Dwyer[1,2,3], Edward C. Holmes[1,9], Jen Kok[1,2,3], Mikhail Prokopenko[1,6] and Vitali Sintchenko[1,2,3,8] ✉

In January 2020, a novel betacoronavirus (family *Coronaviridae*), named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was identified as the etiological agent of a cluster of pneumonia cases occurring in Wuhan City, Hubei Province, China[1,2]. The disease arising from SARS-CoV-2 infection, coronavirus disease 2019 (COVID-19), subsequently spread rapidly causing a worldwide pandemic. Here we examine the added value of near real-time genome sequencing of SARS-CoV-2 in a subpopulation of infected patients during the first 10 weeks of COVID-19 containment in Australia and compare findings from genomic surveillance with predictions of a computational agent-based model (ABM). Using the Australian census data, the ABM generates over 24 million software agents representing the population of Australia, each with demographic attributes of an anonymous individual. It then simulates transmission of the disease over

The World Health Organization (WHO) declared COVID-19 a pandemic on 11 March 2020, when 118,000 cases had been reported from 110 countries. At the time of writing (18 April 2020), the number of global cases had surpassed 2,000,000 after multiple independent importations of infection from visitors and returned travelers, making the control of this disease of prime global public health importance[3,4]. Major outbreaks have been documented in South Korea, Iran, the United States and Europe[2,5] and person-to-person transmission has been documented primarily through household contacts[5], with up to 85% of human-to-human transmission occurring in family or household clusters[6,7]. To date, our understanding of the mechanisms of disease spread is limited.

These events, combined with estimations from epidemic models, have led to unprecedented measures of disease control being implemented by national governments with profound costs to citizens and economies. Epidemic models of COVID-19 have sug-

Información genómica informa intervenciones en Países Bajos

nature medicine

LETTERS

https://doi.org/10.1038/s41591-020-0997-y

Check for updates

Rapid SARS-CoV-2 whole-genome sequencing and analysis for informed public health decision-making in the Netherlands

Bas B. Oude Munnink[1], David F. Nieuwenhuijse[1], Mart Stein[2], Áine O'Toole[3], Manon Haverkate[2], Madelief Mollers[2], Sandra K. Kamga[2], Claudia Schapendonk[1], Mark Pronk[1], Pascal Lexmond[1], Anne van der Linden[1], Theo Bestebroer[1], Irina Chestakova[1], Ronald J. Overmars[1], Stefan van Nieuwkoop[1], Richard Molenkamp[1], Annemiek A. van der Eijk[1], Corine GeurtsvanKessel[1], Harry Vennema[2], Adam Meijer[2], Andrew Rambaut[3], Jaap van Dissel[2], Reina S. Sikkema[1], Aura Timen[2,33], Marion Koopmans[1,33] ✉ and The Dutch-Covid-19 response team*

In late December 2019, a cluster of cases of pneumonia of unknown etiology were reported linked to a market in Wuhan, China[1]. The causative agent was identified as the species *Severe acute respiratory syndrome-related coronavirus* and was named SARS-CoV-2 (ref. [2]). By 16 April the virus had spread to 185 different countries, infected over 2,000,000 people and resulted in over 130,000 deaths[3]. In the Netherlands, the first case of SARS-CoV-2 was notified on 27 February. The outbreak started with several different introductory events from Italy, Austria, Germany and France followed by local amplification in, and later also outside, the south of the Netherlands. The combination of near to real-time whole-genome sequence analysis and epidemiology resulted in reliable assessments of the extent of SARS-CoV-2 transmission in the community, facilitating early decision-making to control local transmission of SARS-CoV-2 in the Netherlands. We demonstrate how these data were generated and analyzed, and how SARS-CoV-2 whole-genome sequencing, in combination with epidemiologi-

27 February and WGS was performed in near to real-time using an amplicon-based sequencing approach.

From 22 January, symptomatic travelers from countries where SARS-CoV-2 was known to circulate were routinely tested. The first case of SARS-CoV-2 infection in the Netherlands was identified on 27 February in a person with recent travel history to Italy and an additional case was identified one day later, also in a person with recent travel history to Italy. The genomes of these first two positive samples were generated and analyzed by 29 February. These two viruses clustered differently in the phylogenetic tree, confirming separate introductions (Fig. 1a).

The advice to test hospitalized patients with serious respiratory infections was issued on 24 February and subsequent attempts to identify possible local transmission chains triggered testing for SARS-CoV-2 on a large scale in hospitals. By 9 March local clusters of epidemiologically related cases of SARS-CoV-2 started to appear in the province of Noord-Brabant. The increase in cases was caused by several co-circulating viruses, and is likely to have been triggered

Introducciones múltiples e independientes en Nueva York

CORONAVIRUS

Introductions and early spread of SARS-CoV-2 in the New York City area

Ana S. Gonzalez-Reiche[1*], Matthew M. Hernandez[2,3*], Mitchell J. Sullivan[1], Brianne Ciferri[1], Hala Alshammary[2], Ajay Obla[1], Shelcie Fabre[4], Giulio Kleiner[2], Jose Polanco[1,2], Zenab Khan[1], Bremy Alburquerque[1,3], Adriana van de Guchte[1], Jayeeta Dutta[1], Nancy Francoeur[1], Betsaida Salom Melo[1,5], Irina Oussenko[1,5], Gintaras Deikus[1,5], Juan Soto[1,5], Shwetha Hara Sridhar[1,5], Ying-Chih Wang[1,5], Kathryn Twyman[6], Andrew Kasarskis[1,5,6], Deena R. Altman[1,7], Melissa Smith[1,5], Robert Sebra[1,5,8,9], Judith Aberg[7], Florian Krammer[2,10], Adolfo García-Sastre[2,7,10,11], Marta Luksza[1,12], Gopi Patel[5], Alberto Paniz-Mondolfi[3], Melissa Gitman[3], Emilia Mia Sordillo[3]††, Viviana Simon[2,5,6]†‡, Harm van Bakel[1,8]†‡

New York City (NYC) has emerged as one of the epicenters of the current severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic. To identify the early transmission events underlying the rapid spread of the virus in the NYC metropolitan area, we sequenced the virus that causes coronavirus disease 2019 (COVID-19) in patients seeking care at the Mount Sinai Health System. Phylogenetic analysis of 84 distinct SARS-CoV-2 genomes indicates multiple, independent, but isolated introductions mainly from Europe and other parts of the United States. Moreover, we found evidence for community transmission of SARS-CoV-2 as suggested by clusters of related viruses found in patients living in different neighborhoods of the city.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; previously known as 2019-nCoV) is an emerging viral pathogen that was first reported to cause severe respiratory infections in Wuhan, China, in late December 2019. Over the past months, it rapidly spread across the globe, and the World Health Organization (WHO) declared a pandemic on 11 March 2020. Targeted screening of suspected coronavirus disease 2019 (COVID-19) cases, as well as a series of successive nationwide travel restrictions, were put in place to curtail SARS-CoV-2 introductions into the continental United States from outbreak hotspots in China (2 February 2020), Iran (2 March 2020), mainland European countries

COVID-19 cases in New York state, including 172,354 (55%) in NYC [New York State Department of Health (NYS DOH); https://coronavirus.health.ny.gov]. With more than 13,300 fatalities in the metropolitan area, NYC has been one of the major epicenters of SARS-CoV-2 infections in the United States.

The Pathogen Surveillance Program (PSP) at the Icahn School of Medicine at Mount Sinai is a multidisciplinary, institutional infrastructure that seeks to generate high-resolution, near real-time genetic information on pathogens found to cause disease in the large and diverse patient population seeking care at the Mount Sinai Health System in NYC. After biospecimen coding, nucleic acid extraction, and polymerase chain reaction quantification, next-generation sequencing approaches based on Illumina and Pacific Biosciences technology provide information on the pathogen's genome. The process has been optimized for quick turnaround, optimized data assembly, and integration with deidentified demographic information.

We took advantage of the existing PSP infrastructure to investigate the origins of SARS-CoV-2 strains circulating in NYC and to dissect the spread of the virus in this metropolitan area with a high-density population. Here, we present the genomic diversity of 90 SARS-CoV-2 isolates obtained from 84 patients seeking care at the Mount Sinai Health System between 29 February 2020 and 18 March 2020. These genomes provide clear evidence for multiple, independent SARS-CoV-2 introductions into NYC during the first weeks of March 2020.

Más de 100 introducciones en Brasil entre Feb-22 y Mar-11

CORONAVIRUS

Evolution and epidemic spread of SARS-CoV-2 in Brazil

Darlan S. Candido[1,2†], Ingra M. Claro[2,3†], Jaqueline G. de Jesus[2,3*], William M. Souza[4*], Filipe R. R. Moreira[5*], Simon Dellicour[6,7*], Thomas A. Mellan[8*], Louis du Plessis[1], Rafael H. M. Pereira[9], Flavia C. S. Sales[2,3], Erika R. Manuli[2,3], Julien Thézé[10], Luiz Almeida[11], Mariane T. Menezes[5], Carolina M. Voloch[5], Marcilio J. Fumagalli[4], Thaís M. Coletti[2,3], Camila A. M. da Silva[2,3], Mariana S. Ramundo[2,3], Mariene R. Amorim[12], Henrique H. Hoeltgebaum[13], Swapnil Mishra[8], Mandev S. Gill[7], Luiz M. Carvalho[14], Lewis F. Buss[2], Carlos A. Prete Jr.[15], Jordan Ashworth[16], Helder I. Nakaya[17], Pedro S. Peixoto[18], Oliver J. Brady[19,20], Samuel M. Nicholls[21], Amilcar Tanuri[5], Átila D. Rossi[5], Carlos K. V. Braga[9], Alexandra L. Gerber[11], Ana Paula de C. Guimarães[11], Nelson Gaburo Jr.[22], Cecila Salete Alencar[23], Alessandro C. S. Ferreira[24], Cristiano X. Lima[25,26], José Eduardo Levi[27], Celso Granato[28], Giulia M. Ferreira[29], Ronaldo S. Francisco Jr.[11], Fabiana Granja[12,30], Marcia T. Garcia[31], Maria Luiza Moretti[31], Mauricio W. Perroud Jr.[32], Terezinha M. P. P. Castiñeiras[33], Carolina S. Lazari[34], Sarah C. Hill[1,35], Andreza Aruska de Souza Santos[36], Camila L. Simeoni[12], Julia Forato[12], Andrei C. Sposito[37], Angelica Z. Schreiber[38], Magnun N. N. Santos[38], Camila Zolini de Sá[39], Renan P. Souza[39], Luciana C. Resende-Moreira[40], Mauro M. Teixeira[41], Josy Hubner[42], Patricia A. F. Leme[43], Renman G. Moreira[44], Maurício L. Nogueira[45], Brazil-UK Centre for Arbovirus Discovery, Diagnosis, Genomics and Epidemiology (CADDE) Genomic Network, Neil M. Ferguson[8], Silvia F. Costa[2,3], José Luiz Proenca-Modena[12], Ana Tereza R. Vasconcelos[11], Samir Bhatt[8], Philippe Lemey[7], Chieh-Hsi Wu[46], Andrew Rambaut[47], Nick J. Loman[21], Renato S. Aguiar[39], Oliver G. Pybus[1], Ester C. Sabino[2,3]†, Nuno Rodrigues Faria[1,2,8]†

Brazil currently has one of the fastest-growing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemics in the world. Because of limited available data, assessments of the impact of nonpharmaceutical interventions (NPIs) on this virus spread remain challenging. Using a mobility-driven transmission model, we show that NPIs reduced the reproduction number from >3 to 1 to 1.6 in São Paulo and Rio de Janeiro. Sequencing of 427 new genomes and analysis of a geographically representative genomic dataset identified >100 international virus introductions in Brazil. We estimate that most (76%) of the Brazilian strains fell in three clades that were introduced from Europe between 22 February and 11 March 2020. During the early epidemic phase, we found that SARS-CoV-2 spread mostly locally and within state borders. After this period, despite sharp decreases in air travel, we estimated multiple exportations from large urban centers that coincided with a 25% increase in average traveled distances in national flights. This study sheds new light on the epidemic transmission and evolutionary trajectories of SARS-CoV-2 lineages in Brazil and provides evidence that current interventions remain insufficient to keep virus transmission under control in this country.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a novel beta-

Challenges of real-time assessment of transmission

obfuscate the real-time assessment of virus transmission using SARS-CoV-2 case counts (*15*). Consequently, a more accurate measure of SARS-CoV-2 transmission in Brazil is the number of reported deaths caused by severe acute respiratory infections (SARIs), which is provided by the Sistema Único de Saúde (SUS) (*18*). Changes in the opportunity for SARS-CoV-2 transmission are strongly associated with changes in average mobility (*18*–*20*) and can typically be measured by calculating the effective reproduction number, R, defined as the average number of secondary infections caused by an infected person. $R > 1$ indicates a growing epidemic, whereas $R < 1$ is needed to achieve a decrease in transmission.

We used a Bayesian semimechanistic model (*21*, *22*) to analyze SARI mortality statistics and human mobility data to estimate daily changes in R in São Paulo city (12.2 million inhabitants) and Rio de Janeiro city (6.7 million inhabitants), the largest urban metropoles in Brazil (Fig. 1, C and D). NPIs in Brazil consisted of school closures implemented between 12 and 23 March 2020 across the country's 27 federal units/states and store closures implemented between 13 and 23 March 2020. In São Paulo city, schools started closing on 16 March 2020 and stores closed 4 days later. At the start of the epidemics, we found $R > 3$ in São Paulo and Rio de Janeiro and, concurrent with the timing of state-mandated NPIs, R values fell close to 1.

Mobility-driven changes in *R*

Analysis of R values after NPI implementation highlights several notable mobility-driven features. There was a period immediately after NPIs, between 21 and 31 March 2020, when R was consistently <1 in São Paulo city (Fig. 1C). However, after this initial decrease, the R value for São Paulo rose to >1 and increased

Más de 100 introducciones en Brasil entre Feb-22 y Mar-11

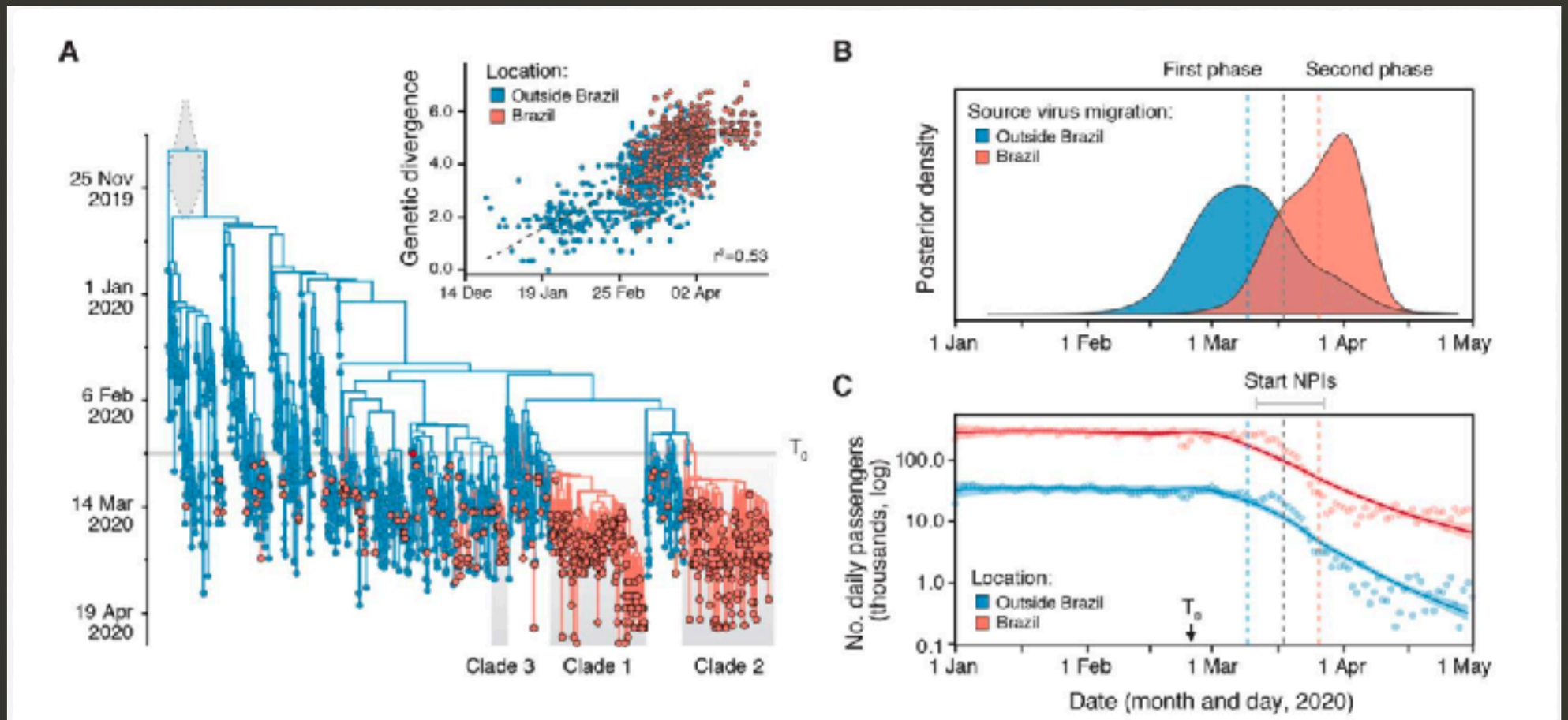


Fig. 3. Evolution and spread of SARS-CoV-2 in Brazil. (A) Time-resolved maximum clade credibility phylogeny of 1182 SARS-CoV-2 sequences, 490 from Brazil (red) and 692 from outside Brazil (blue). The largest Brazilian clades are highlighted by grey boxes (*Clade 1*, *Clade 2* and *Clade 3*). The panel A inset shows a root-to-tip regression of genetic divergence against dates of sample collection. (B) Dynamics of SARS-CoV-2 import events in Brazil. Dates of international and national (between federal states) migration events were estimated from virus genomes using a phylogeographic approach. The first phase was dominated by virus migrations from outside Brazil while the second phase is marked by virus spread within Brazil. Dashed vertical lines correspond to the mean posterior estimate for migration events from outside Brazil (blue) and within Brazil (red). (C) Locally estimated scatterplot smoothing of the daily number of international (blue) and national (red) air passengers in Brazil in 2020. T_0 = date of first reported case in Brazil (25 February 2020).

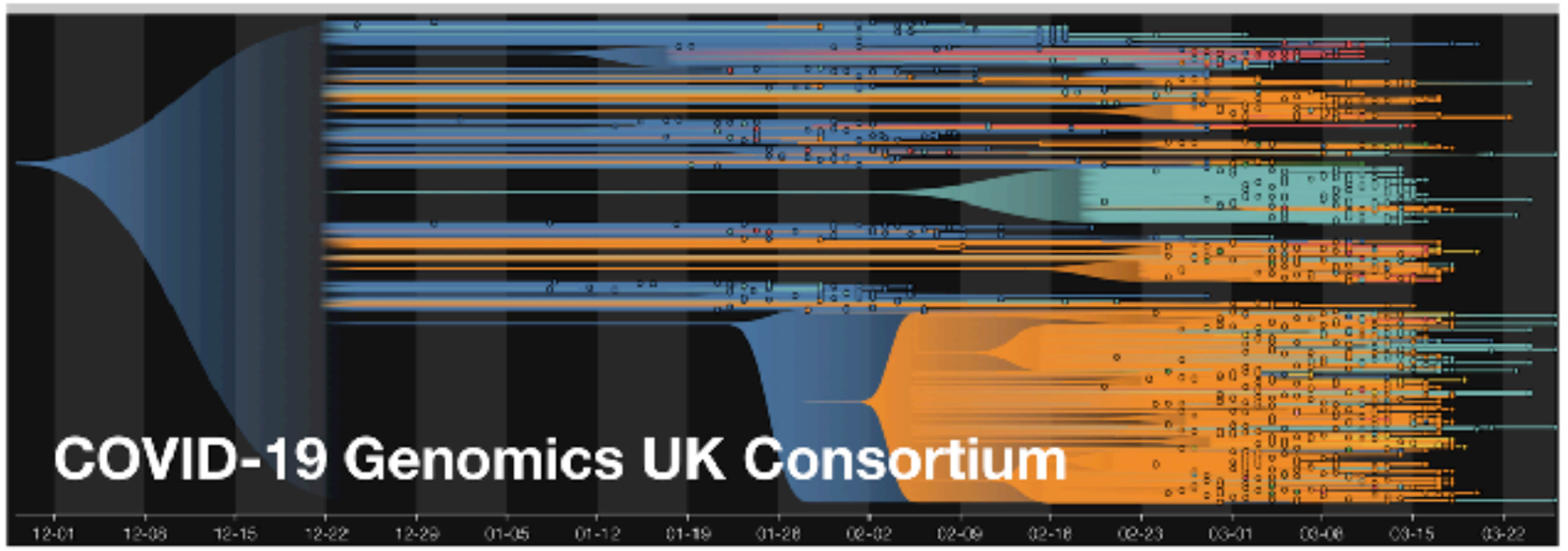
Candido et al - Science 2020

Reino Unido ha secuenciado 63,000 genomas

COG-UK Consortium – COVID-19 Genomics UK Consortium

COG UK
COVID-19 GENOMICS UK CONSORTIUM

WHO WE ARE HOW WE WORK UPDATES DATA PROTOCOLS STUDIES CONTACT



The current COVID-19 pandemic, caused by the SARS-CoV-2 virus, represents a major threat to health. The COVID-19 Genomics UK (COG-UK) consortium has been created to deliver large-scale and rapid whole-genome virus sequencing to local NHS centres and the UK government.

COG-UK is made up of an innovative partnership of NHS organisations, the four Public Health Agencies of the UK, the Wellcome Sanger Institute and over twelve academic partners providing sequencing and analysis capacity.

COG-UK is supported by £20 million funding from the UK Department of Health and Social Care (DHSC), UK Research and Innovation (UKRI) and the Wellcome Sanger Institute, administered by UK Research and Innovation.

NHS University Hospitals Birmingham NHS Foundation Trust

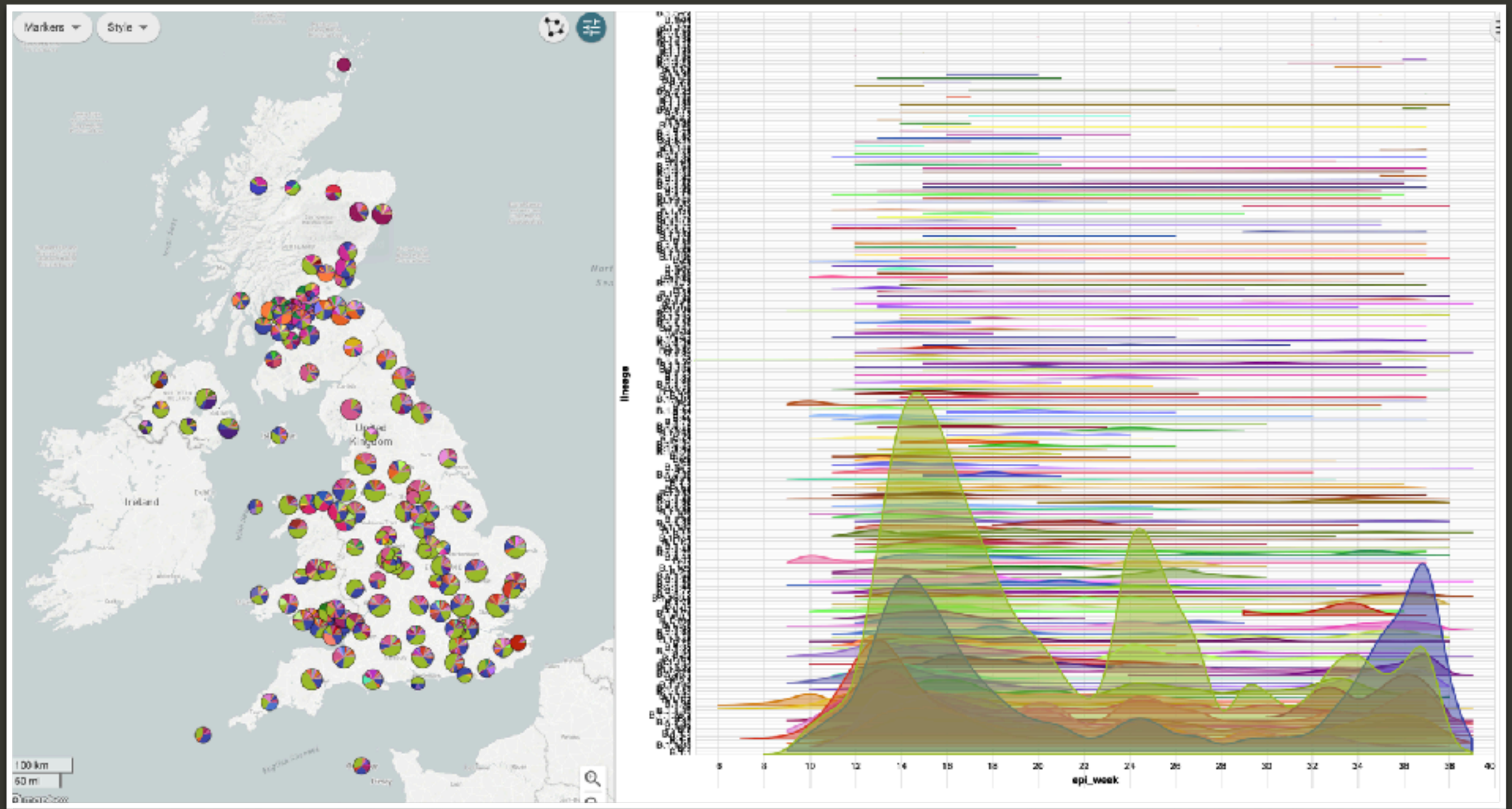
UNIVERSITY OF CAMBRIDGE

NHS Cambridge University Hospitals NHS Foundation Trust

CARDIFF UNIVERSITY
PRIFYSGOL CAERDYDD

The virus genome data is combined with clinical and epidemiological datasets in order to help to guide UK public health interventions and policies. The subsequent analysis will permit evaluation of the effectiveness of novel treatments and non-pharmacological interventions on SARS-CoV-2 populations and spread. It will provide information on whether or not outbreaks are due to introductions from outside or ongoing transmission within the community. The data will also enable researchers to identify and understand genetic changes that affect how easily the virus is passed on and the severity of the symptoms it causes. Finally, the information help us target the development of treatments and vaccines and monitor their impact as they are introduced.

Reino Unido ha secuenciado 63,000 genomas



El consorcio prepara reportes periódicos para gobiernos y agencias de salud pública

www.cogconsortium.uk

COVID-19 Genomics UK (COG-UK) Consortium

Report #11 - 8th September 2020

This report is provided at the request of SAGE and includes information on the ongoing state of the research being carried out. It should not be considered formal or informal advice. The conclusions of the ongoing scientific studies may be subject to change as further evidence becomes available and as such any firm conclusions would be premature.

Executive Summary

- COG-UK researchers have collaborated with PHAs to use rapid genome sequencing to understand the dynamics underpinning a growing number of local SARS-CoV-2 outbreaks across the UK during the summer.

- Rapid genome sequencing coupled with integration of epidemiological data has enabled the identification of transmission points and informed intervention measures during outbreaks among highly vulnerable patients in renal dialysis units (RDUs) in Scotland and the East of England.

- In addition to existing COG-UK tools and pipelines, a newly developed sequence reporting tool that has been applied to the RDU outbreaks will provide simple statistical support to public health workers and clinicians seeking to understand whether infections seen at a local level represent transmissions within a given healthcare setting or transmission from the surrounding community.

COG-UK genomic surveillance in action

The sequencing pipelines, genomic data and tools that have been created during the six months since the establishment of COG-UK provide the foundations necessary for the consortium to transition into a new

El consorcio español lleva 3,800 secuencias

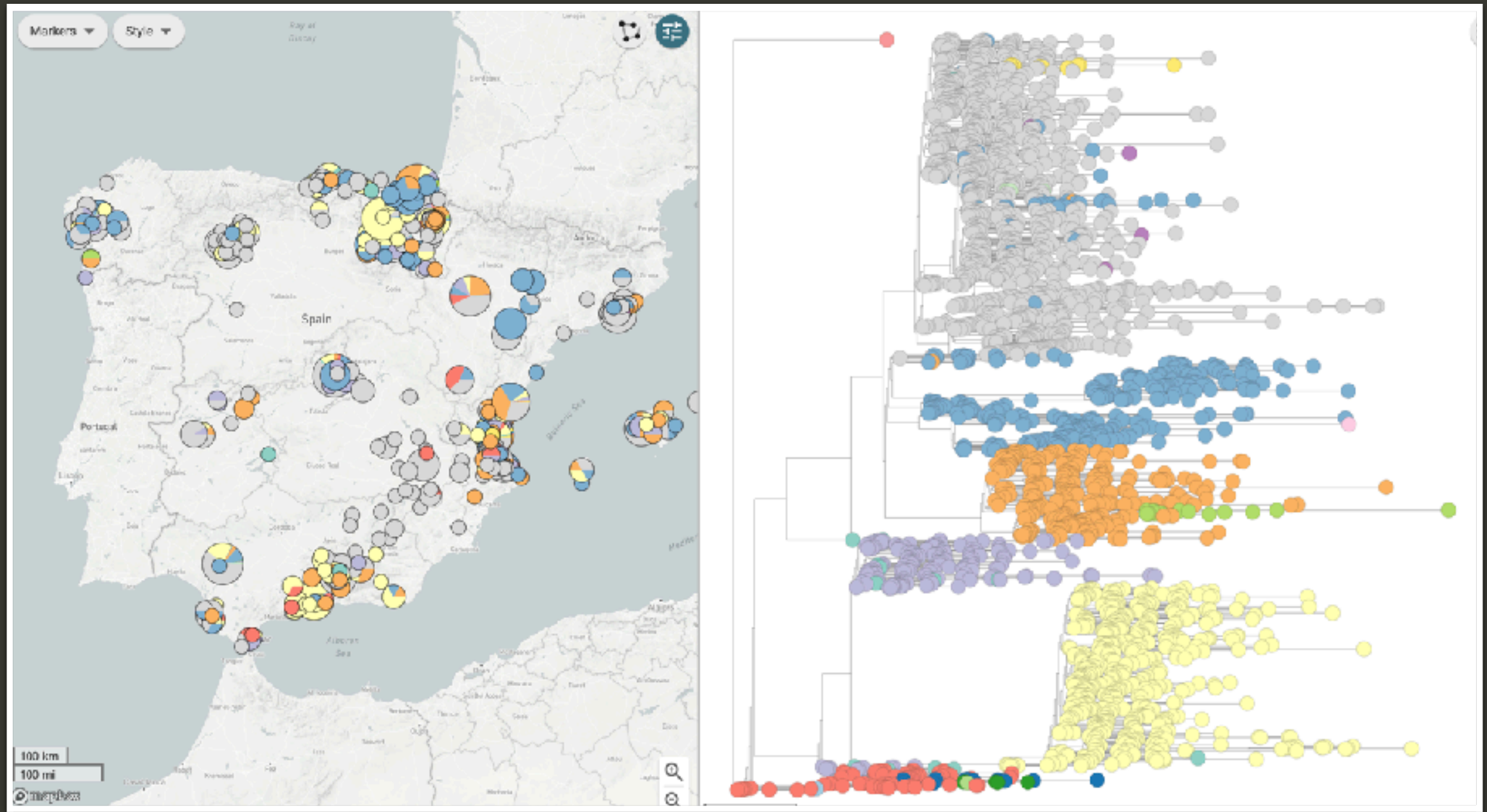
El proyecto

INFORMACIÓN GENERAL

CONTACT

[Aaki Comas Espadas

El consorcio español lleva 3,800 secuencias



seqcovid.csic.es/microreact/

OBJETIVO

Establecer un sistema de procesamiento, secuenciamiento y análisis de genomas de SARS-CoV-2 para generar información epidemiológica que sea interpretable y accionable por autoridades de salud pública.

Desde Julio, INS nos transfiere 200 muestras por mes

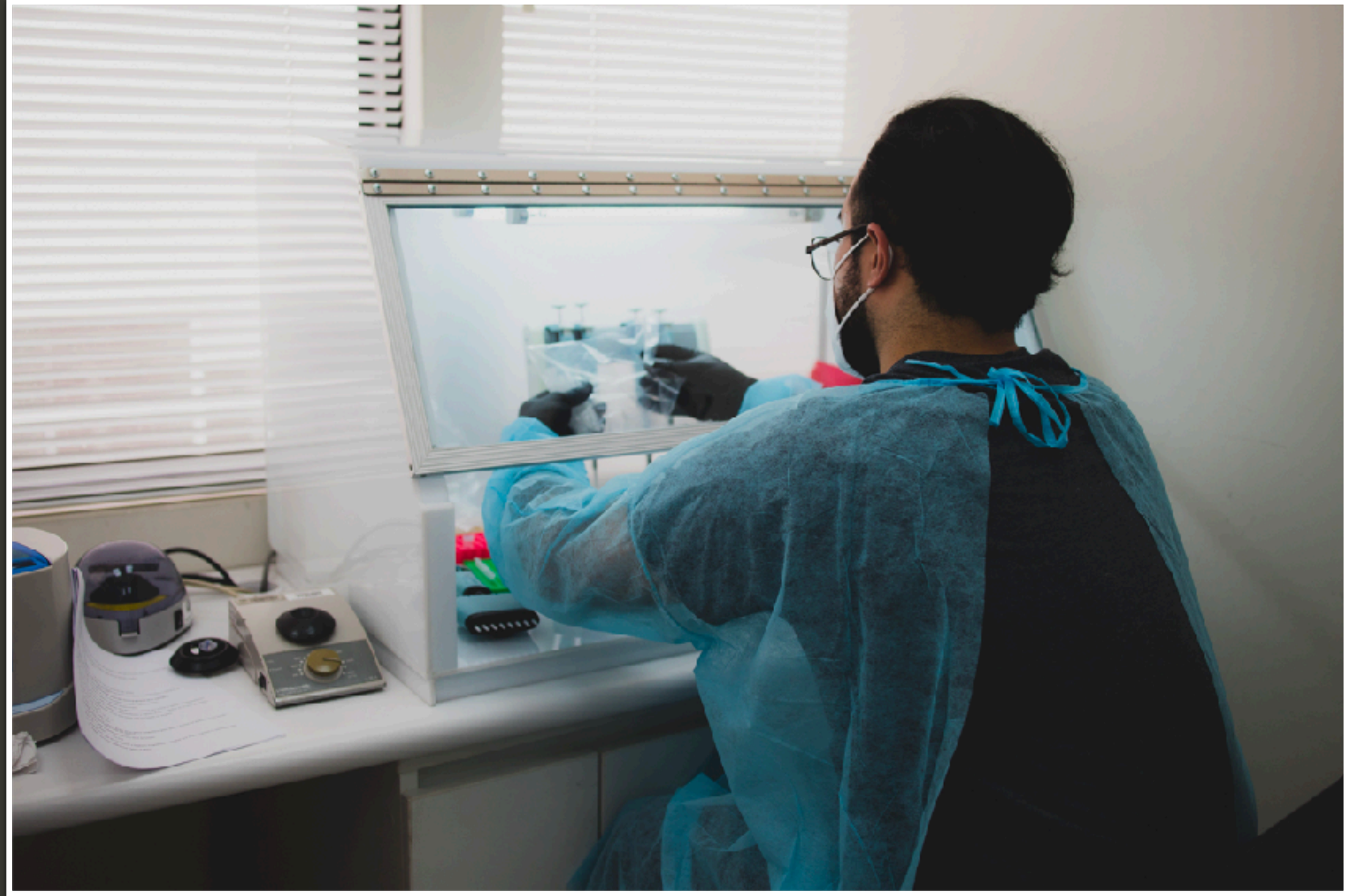
Muestras almacenadas a -80° en UPCH

Extracción de ARN en laboratorio BSL-2+ de Emerge UPCH

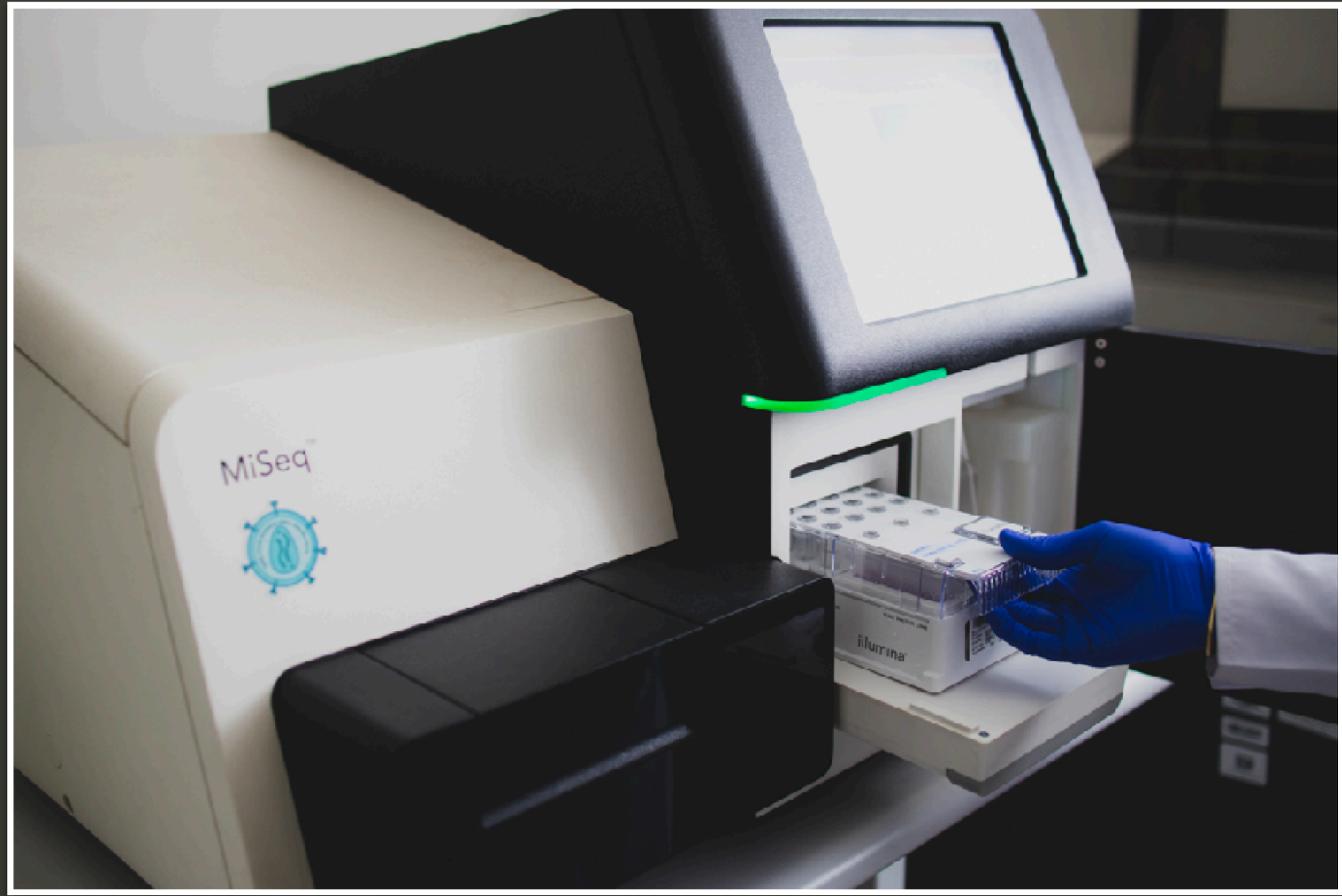
Transcripción reversa y manipulación de ARN en LGM-UPCH

Transcripción reversa y manipulación de ARN en LGM-UPCH

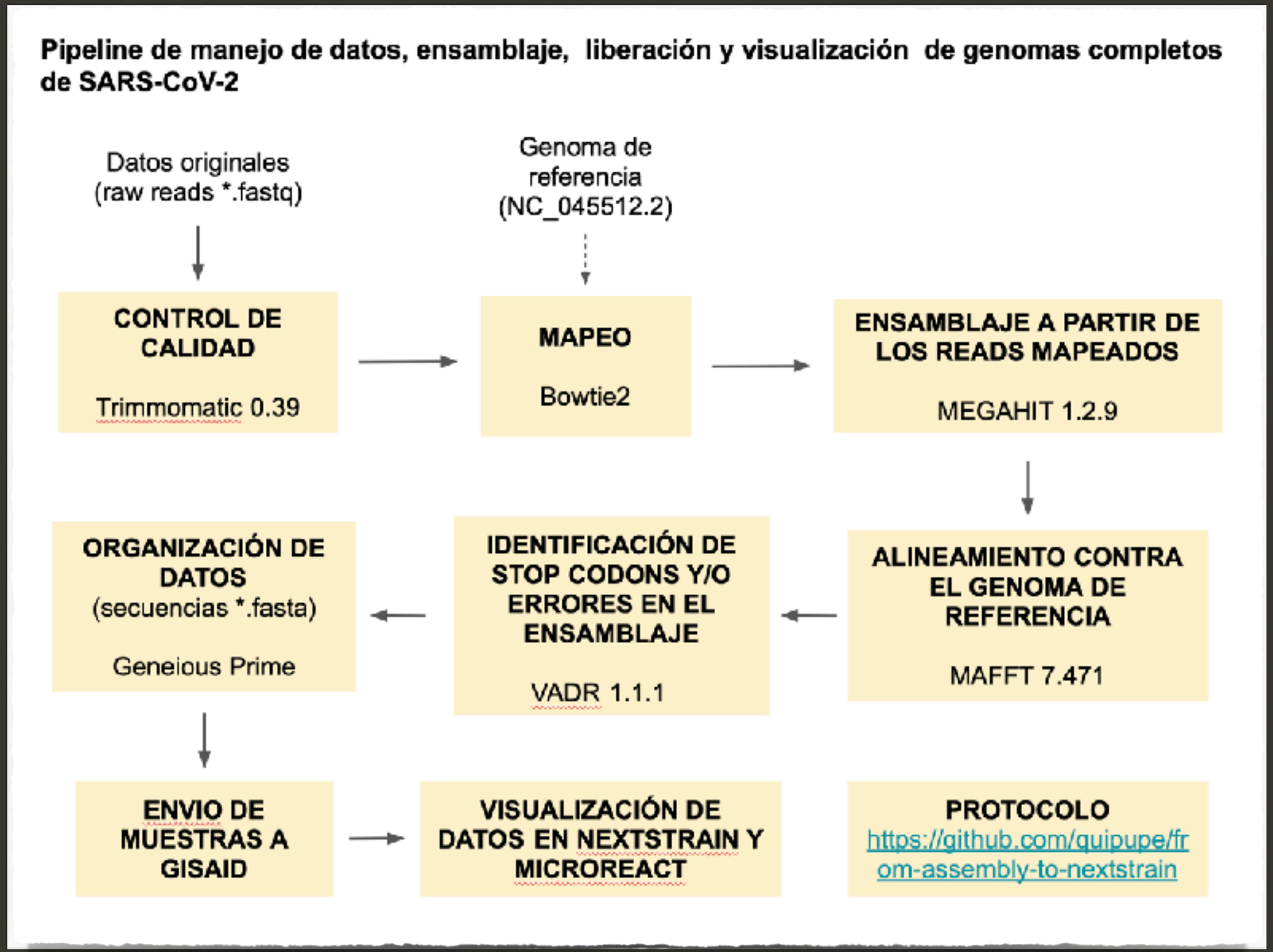
Preparación de librerías NGS en UEM-UPCH



Secuenciamiento en Illumina MiSeq, cartuchos v2



Los datos crudos pasan al equipo de análisis

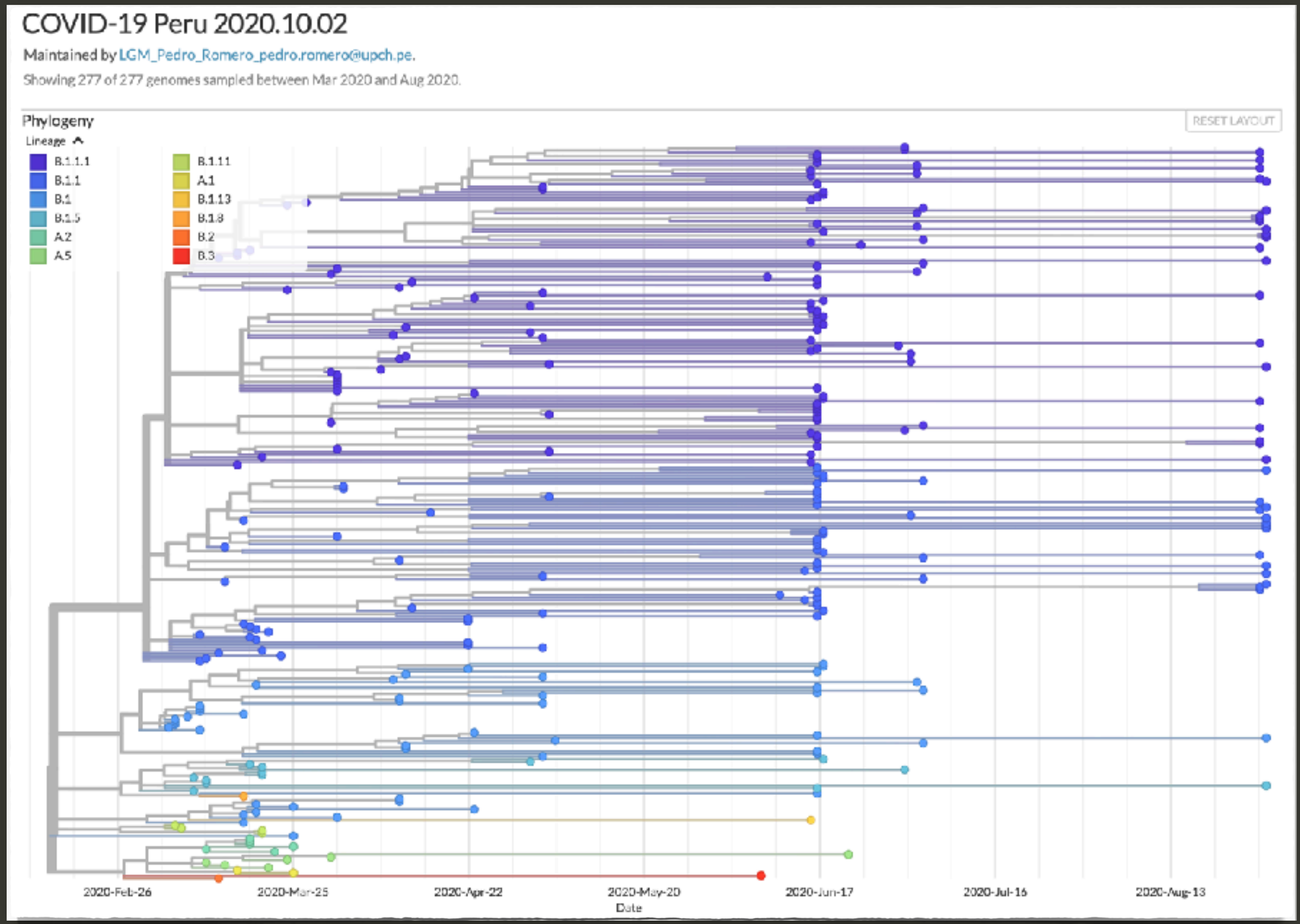


1-5 millones de secuencias cortas para reconstruir el genoma SARS-2

Análisis de 277 secuencias peruanas al 2-octubre-2020

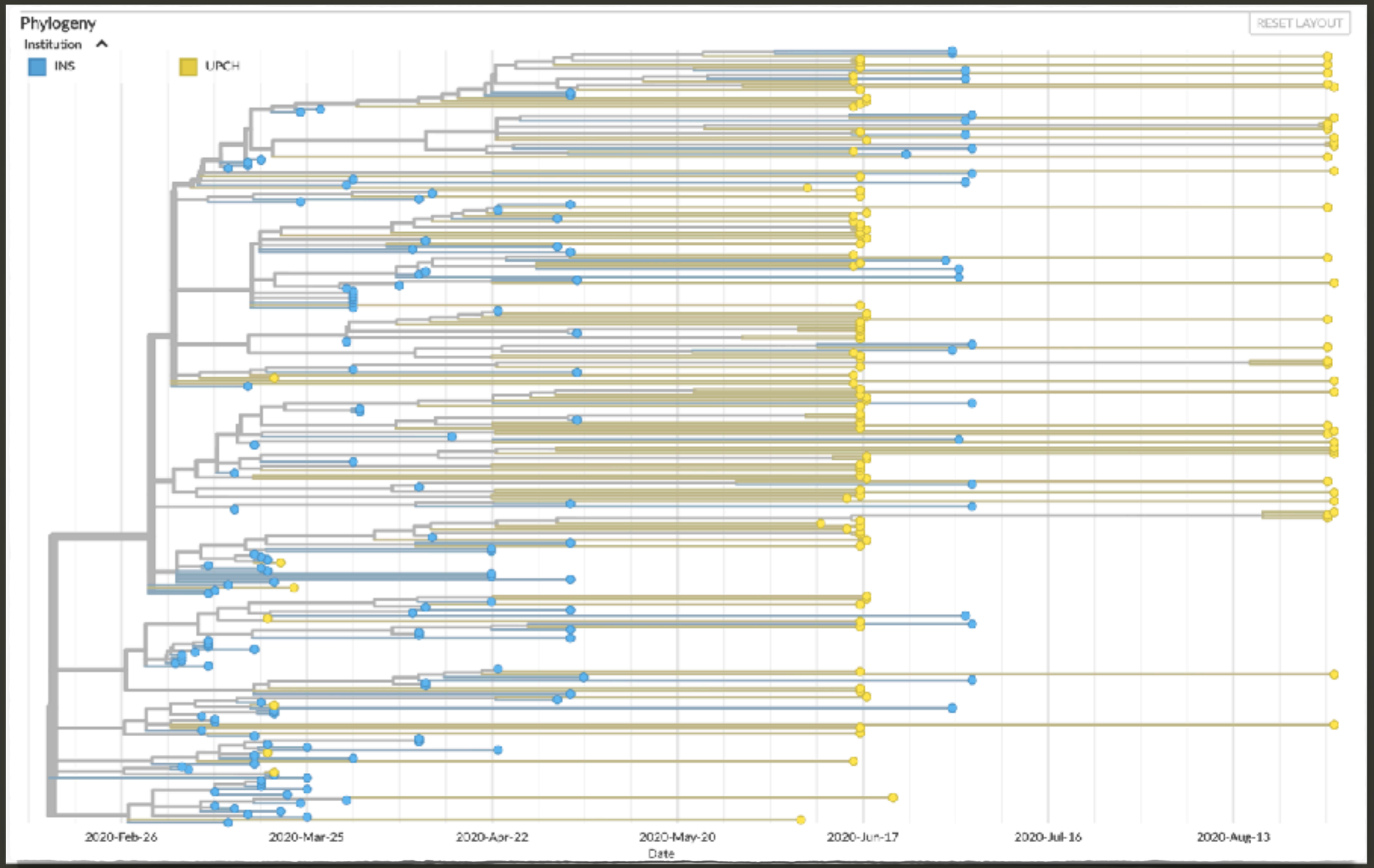
- 379 genomas peruanos en GISAID
- Descartamos 19 genomas incompletos (<29,000 bp) y con gaps (>1% Ns)
- 83 secuencias de INS no incluyen datos de región ni información de paciente. Duplicados?
- = 277 genomas (146 INS + 131 UPCH)

277 genomas peruanos al 2-octubre-2020



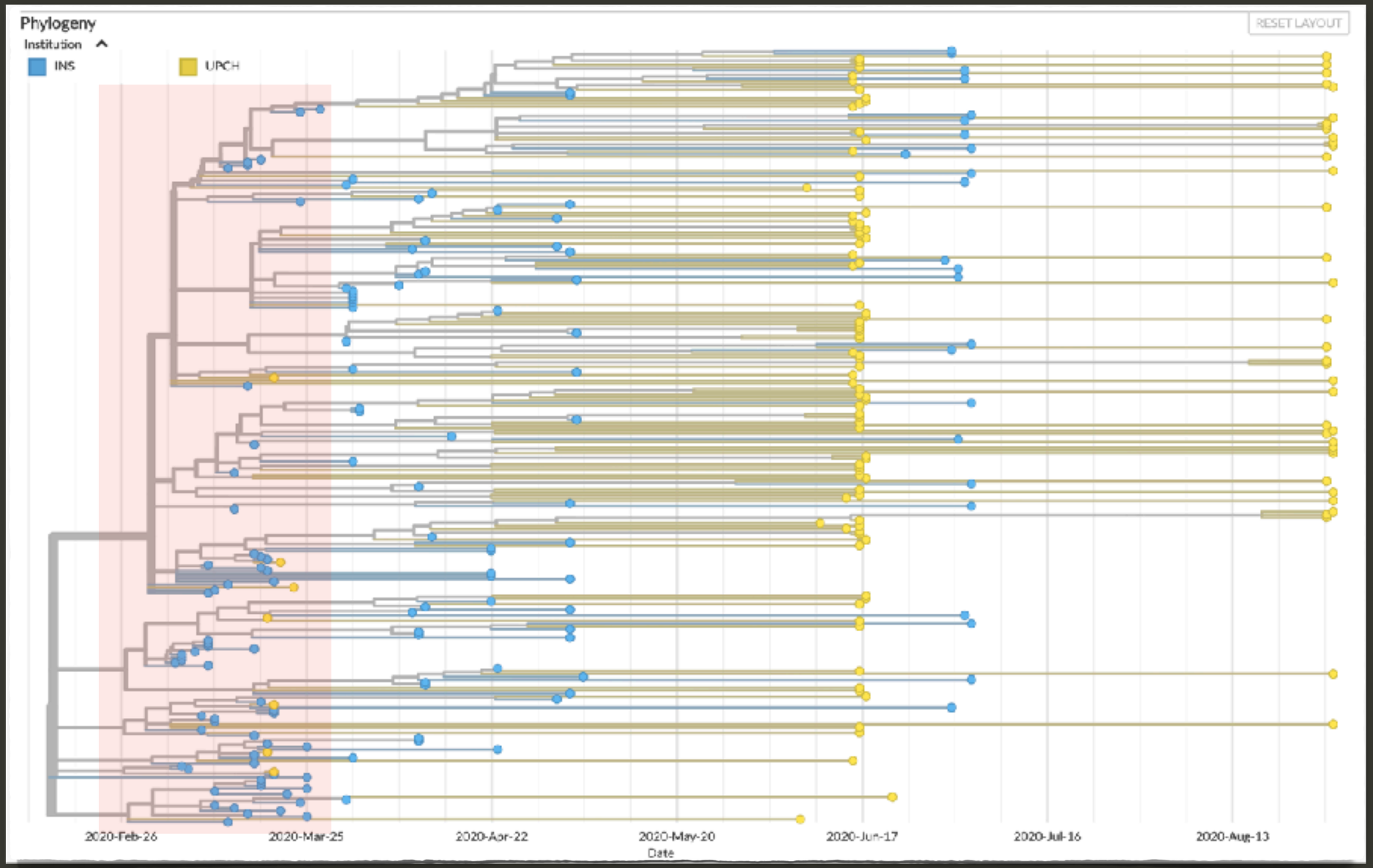
Elaboración: Pedro Romero

Muestreos complementarios entre INS y UPCH



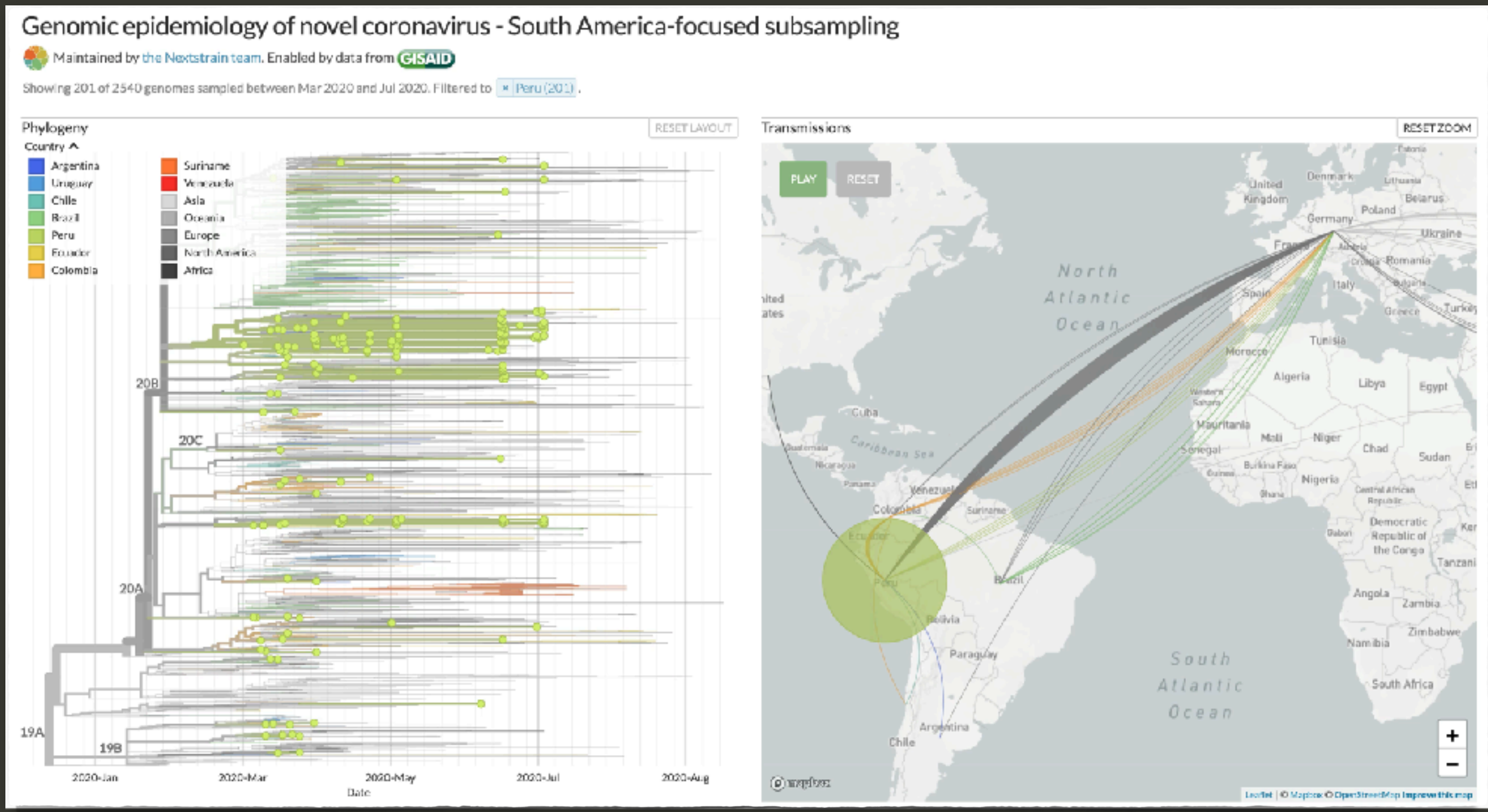
Elaboración: Pedro Romero

Que permiten estudiar eventos tempranos de la pandemia en Perú

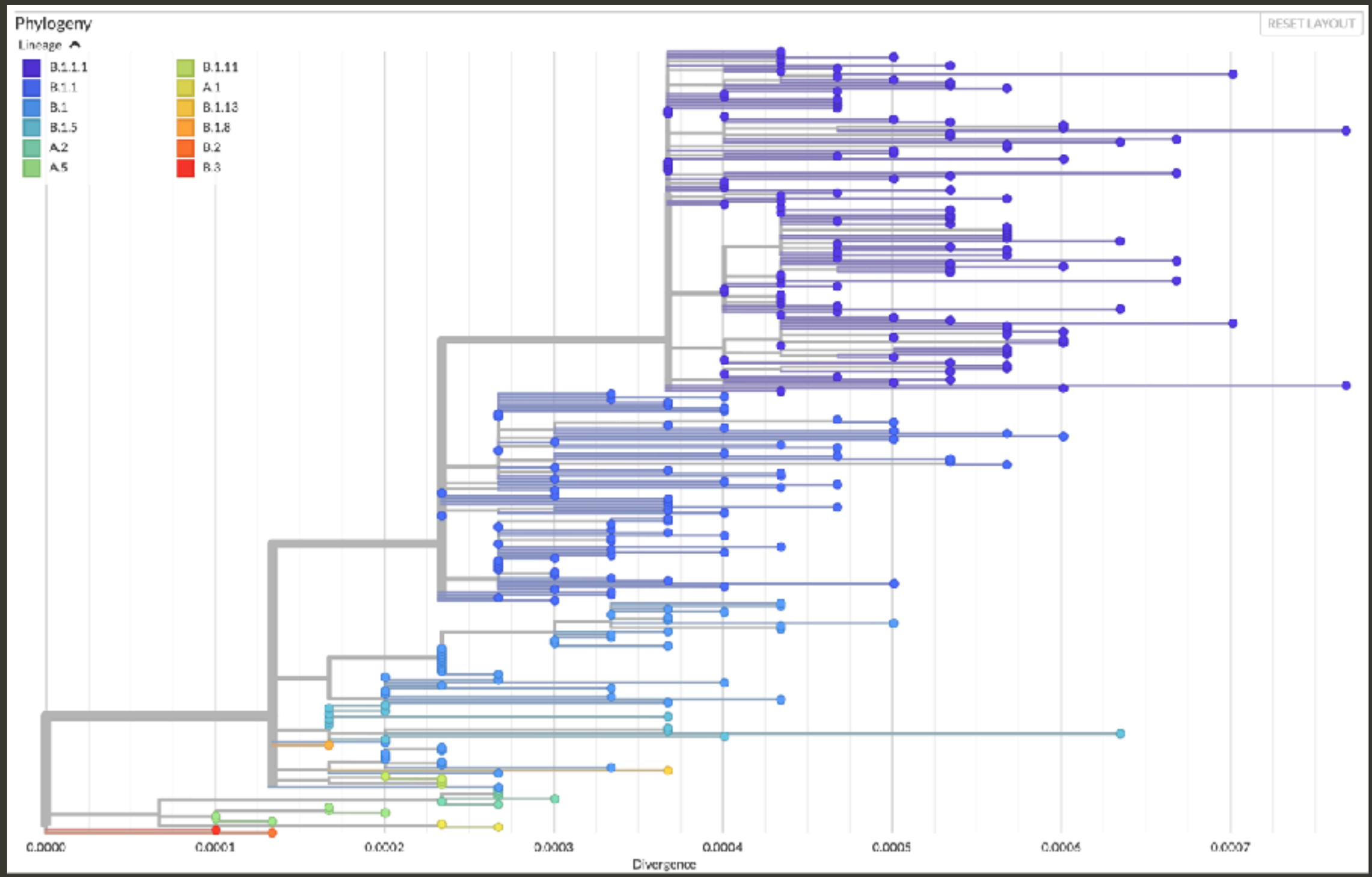


Elaboración: Pedro Romero

Múltiples introducciones en marzo 2020



Que generan múltiples cadenas de transmisión local



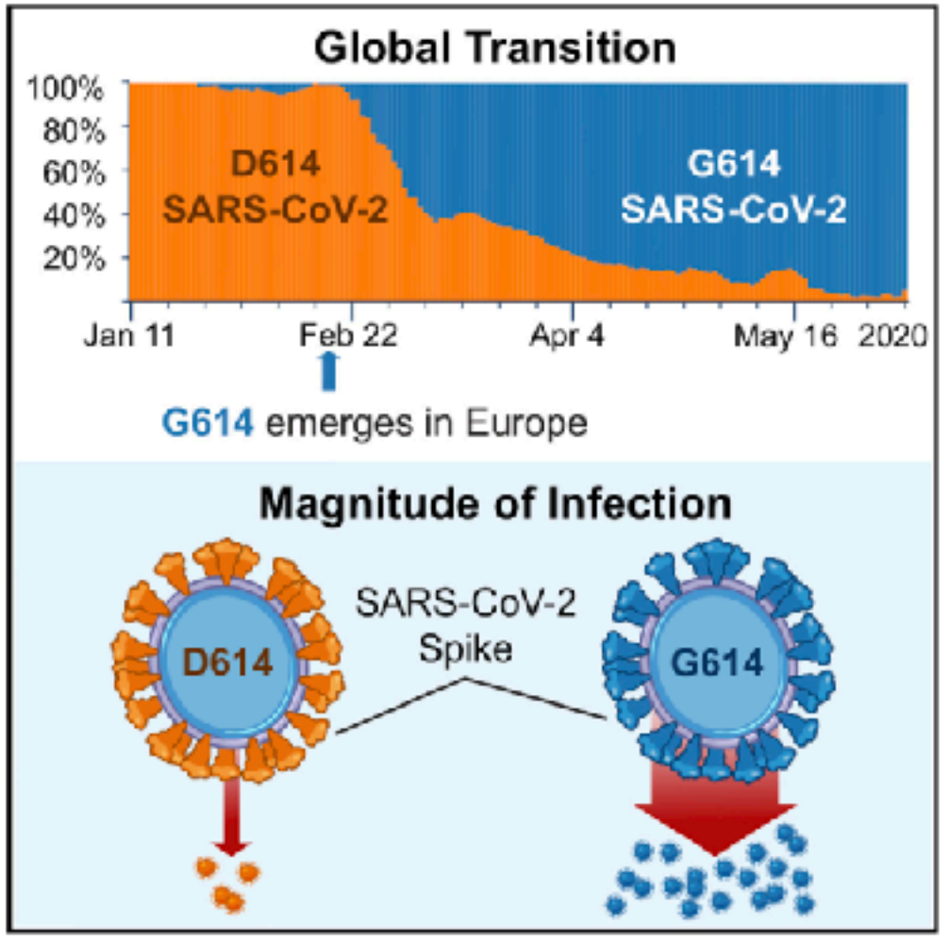
G614 asociada a mayor infectividad *in vitro* = ¿Más transmisible?

Cell

Article

Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus

Graphical Abstract



Authors

Bette Korber, Will M. Fischer, Sandrasegaram Gnanakaran, ..., Celia C. LaBranche, Erica O. Saphire, David C. Montefiori

Correspondence

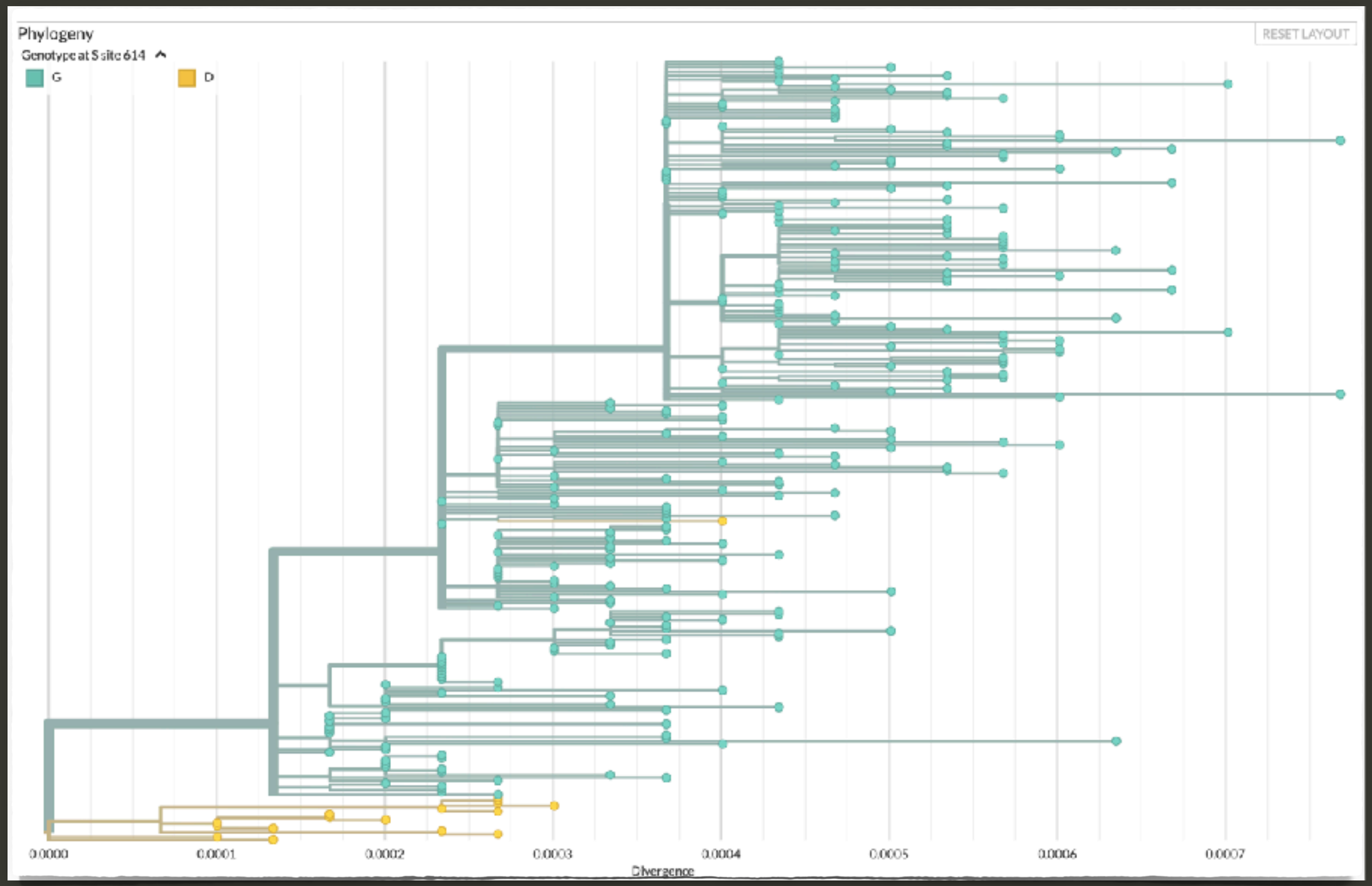
btk@lanl.gov

In Brief

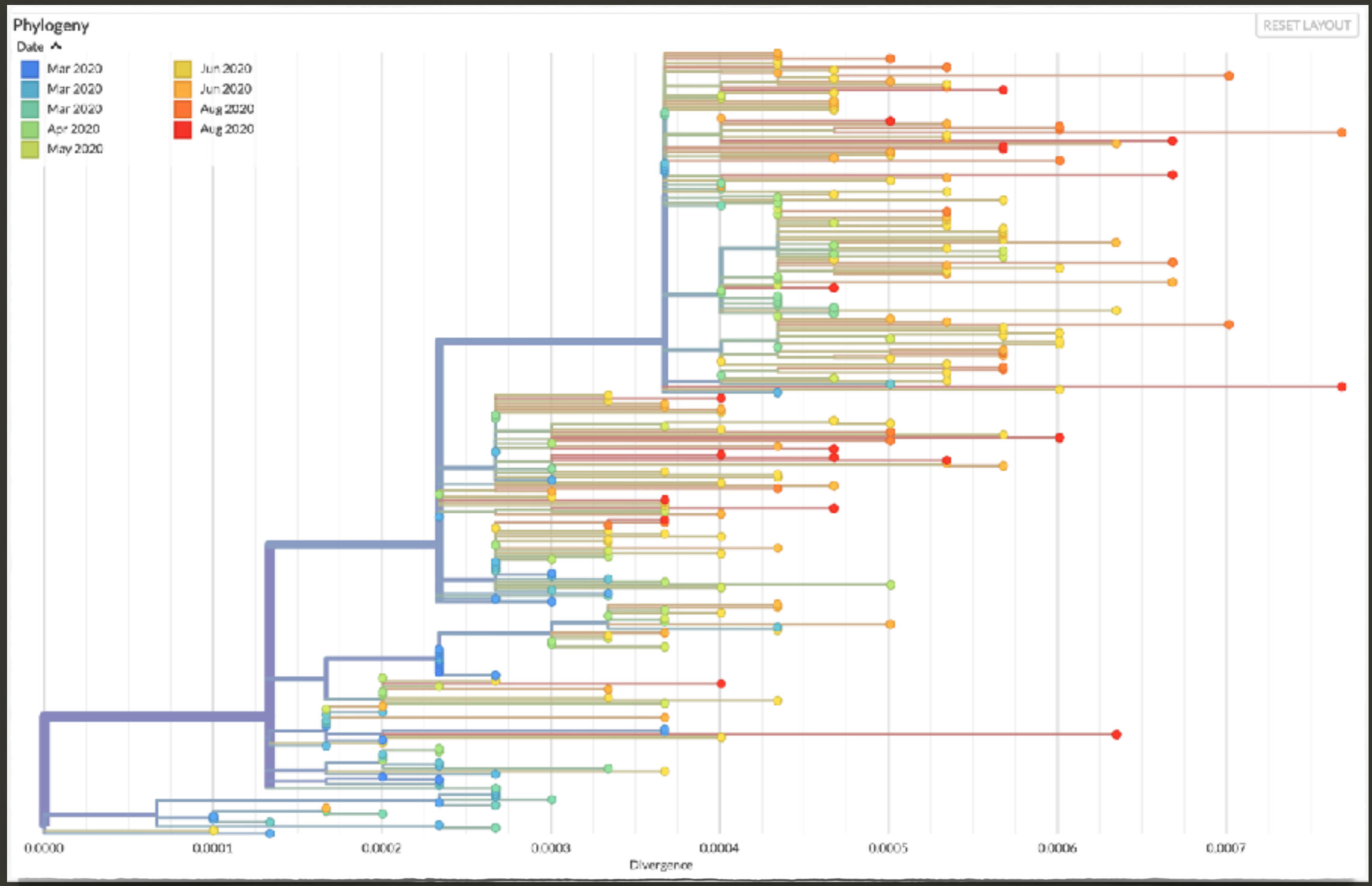
Korber et al. present evidence that there are now more SARS-CoV-2 viruses circulating in the human population globally that have the G614 form of the Spike protein versus the D614 form that was originally identified from the first human cases in Wuhan, China. Follow-up studies show that patients infected with G614 shed more viral nucleic acid compared with those with D614, and G614-bearing viruses show significantly higher infectious titers *in vitro* than their D614 counterparts.

Highlights

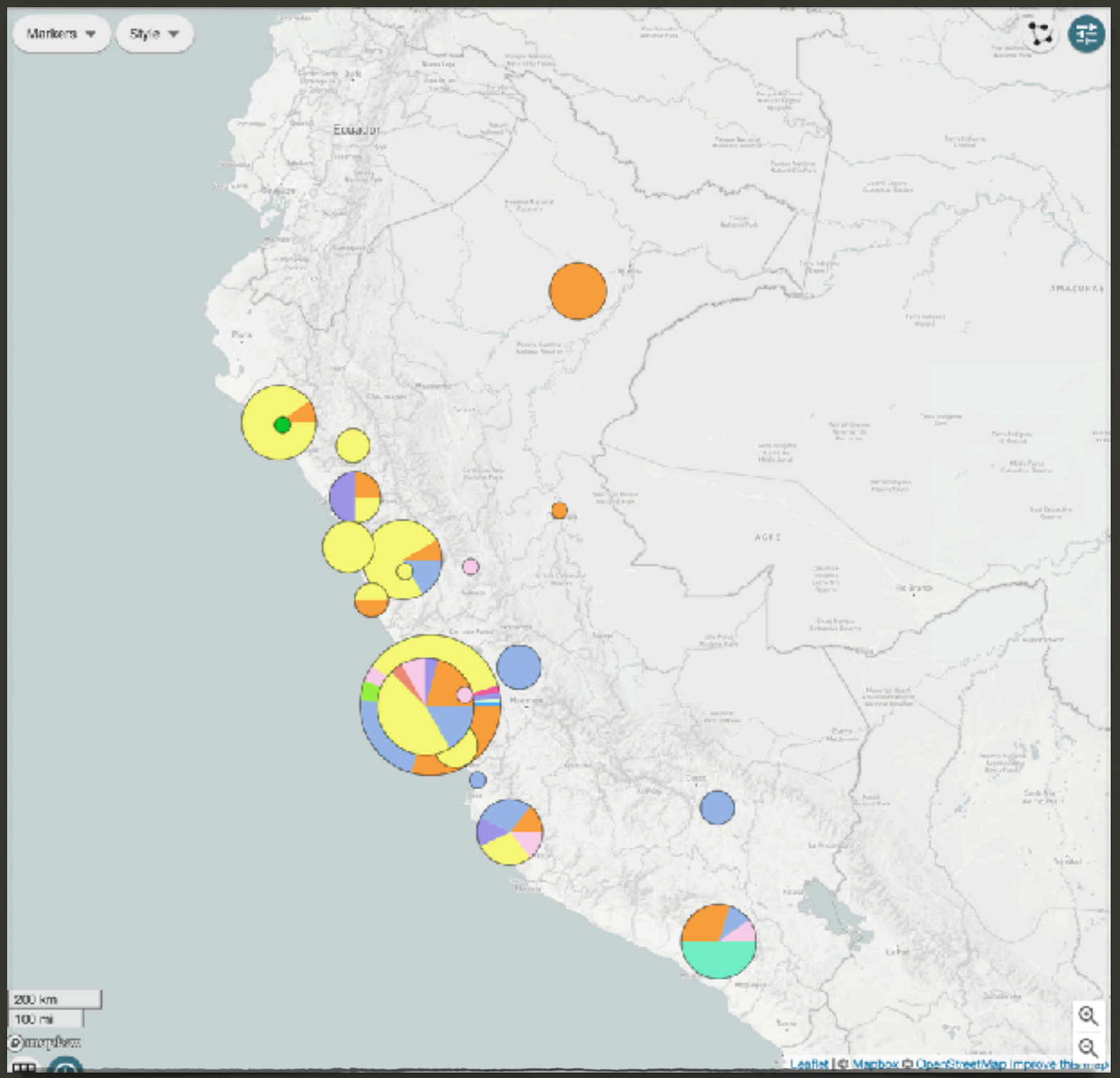
G614 en la mayoría de aislados peruanos



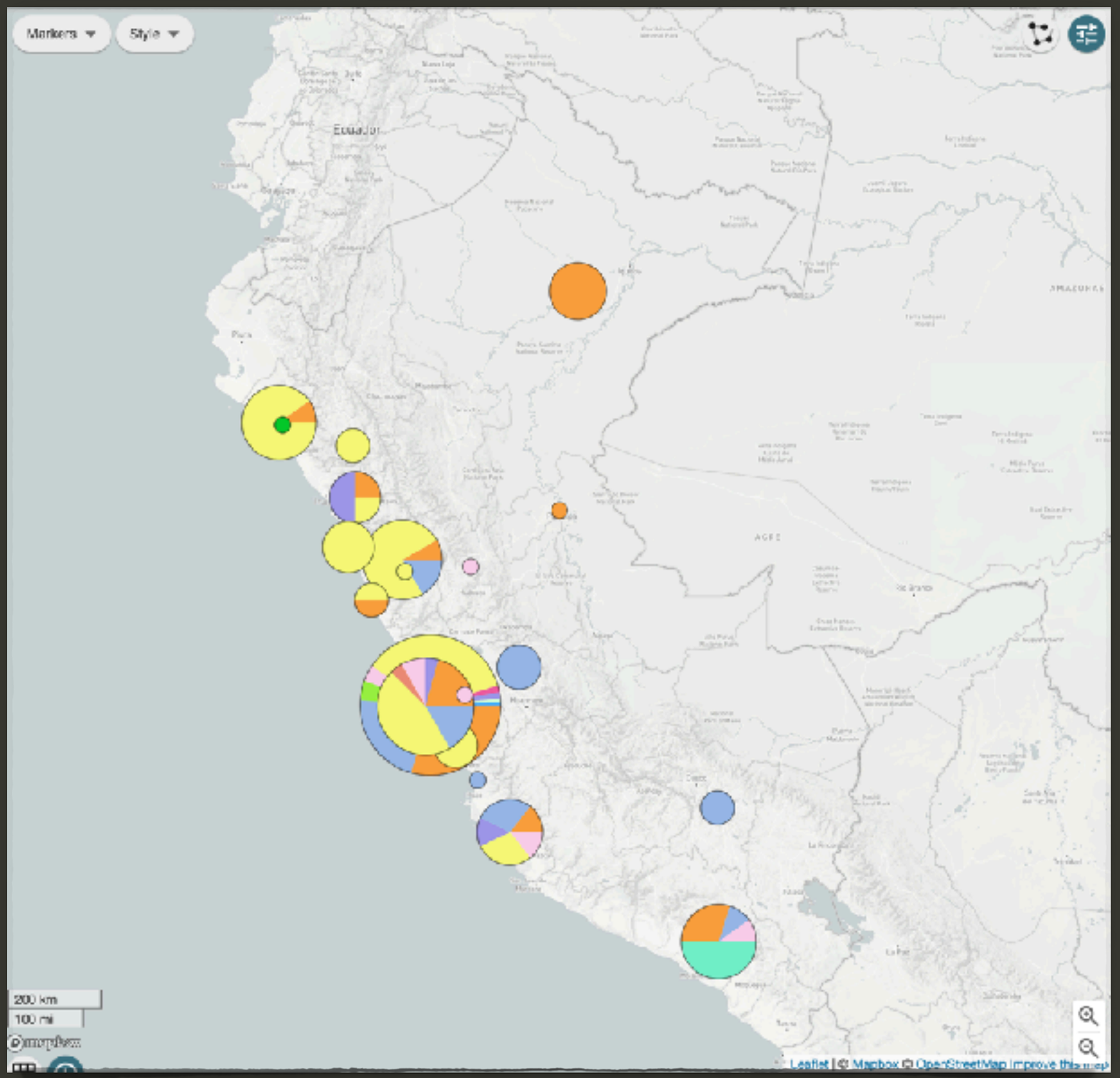
Aislados más recientes acumulan más mutaciones



Lima y Callao presentan la mayor diversidad genética (porque son el origen)



Pero hay varias regiones que requieren mayor muestreo



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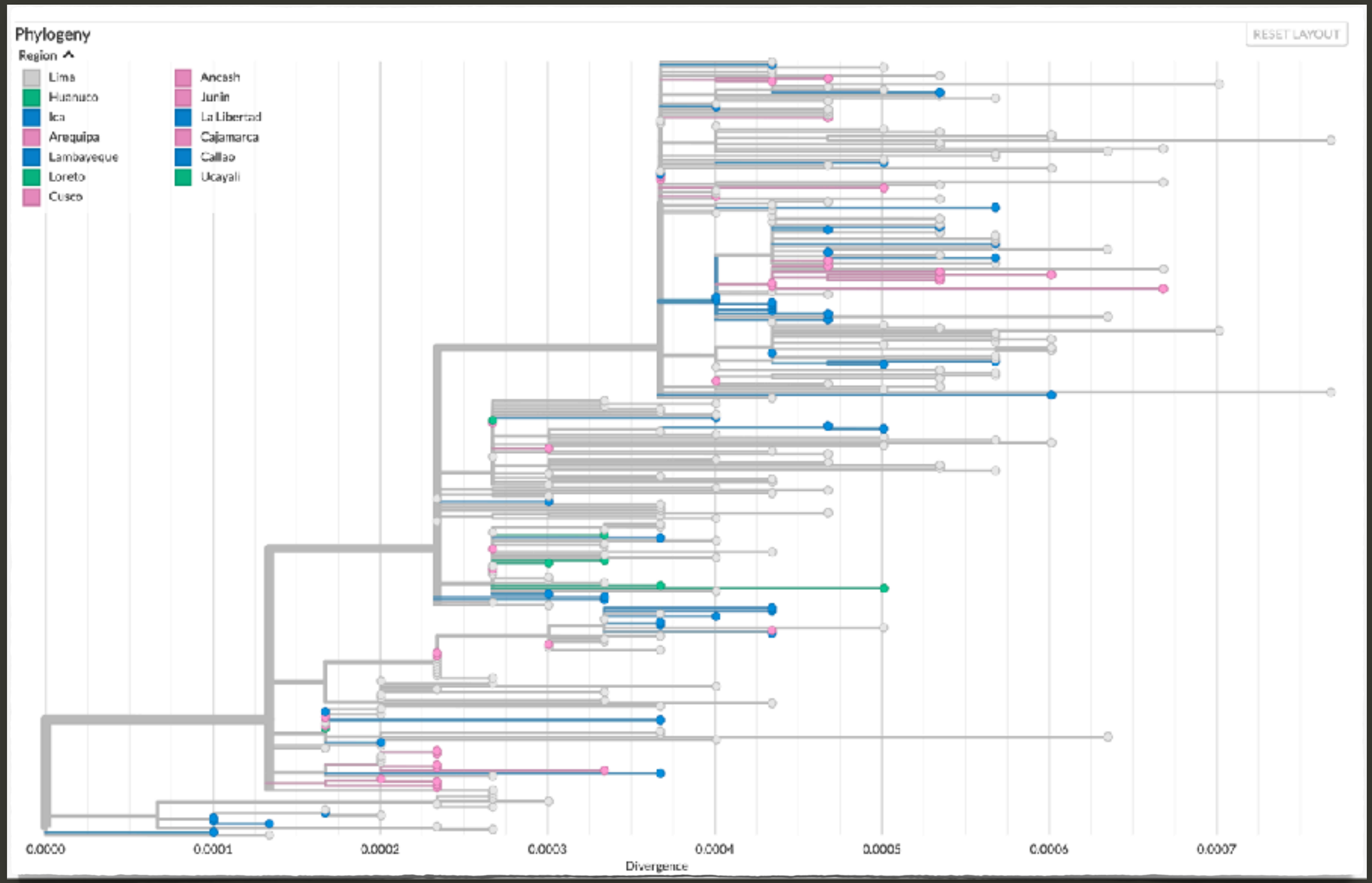
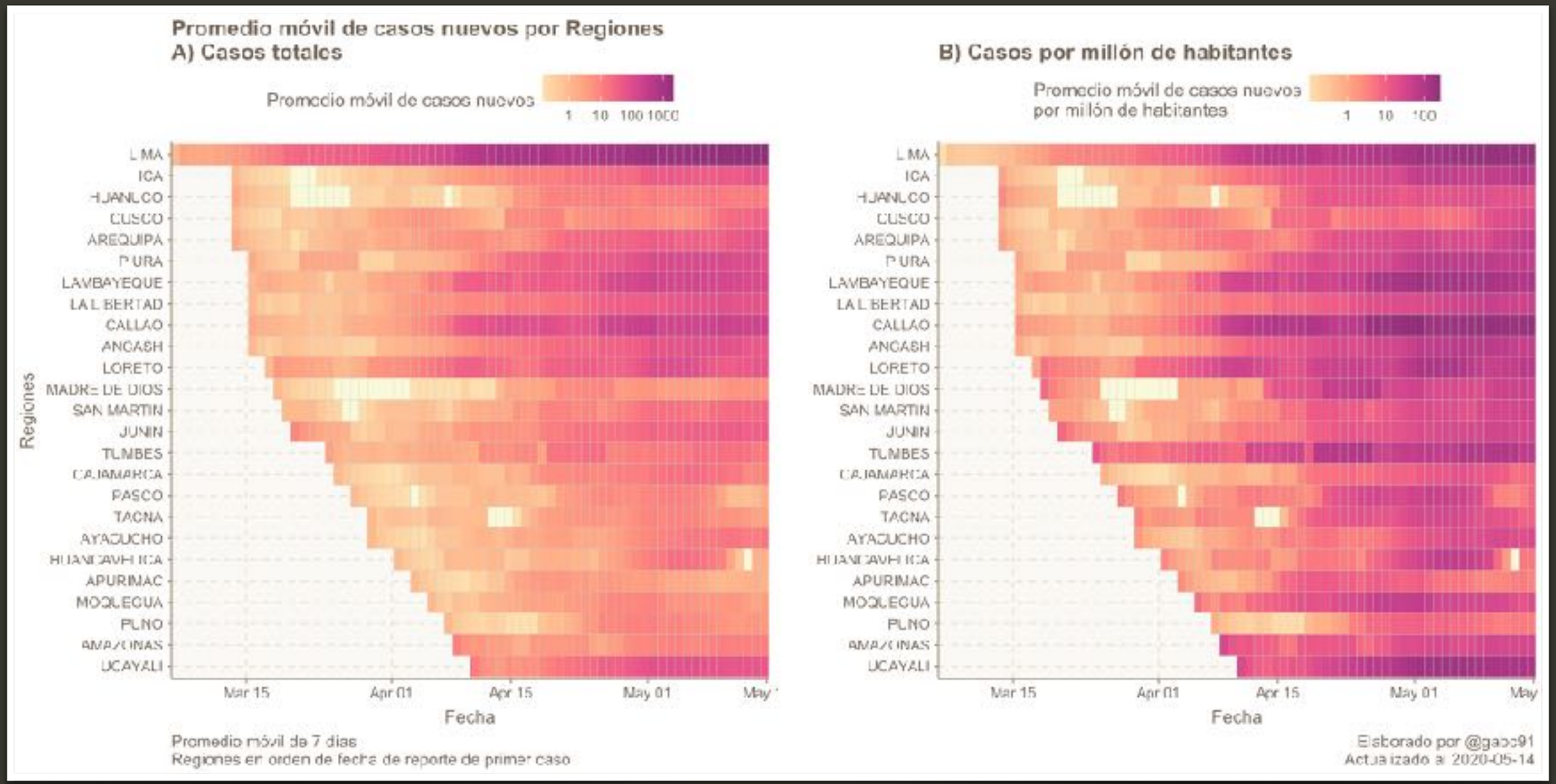
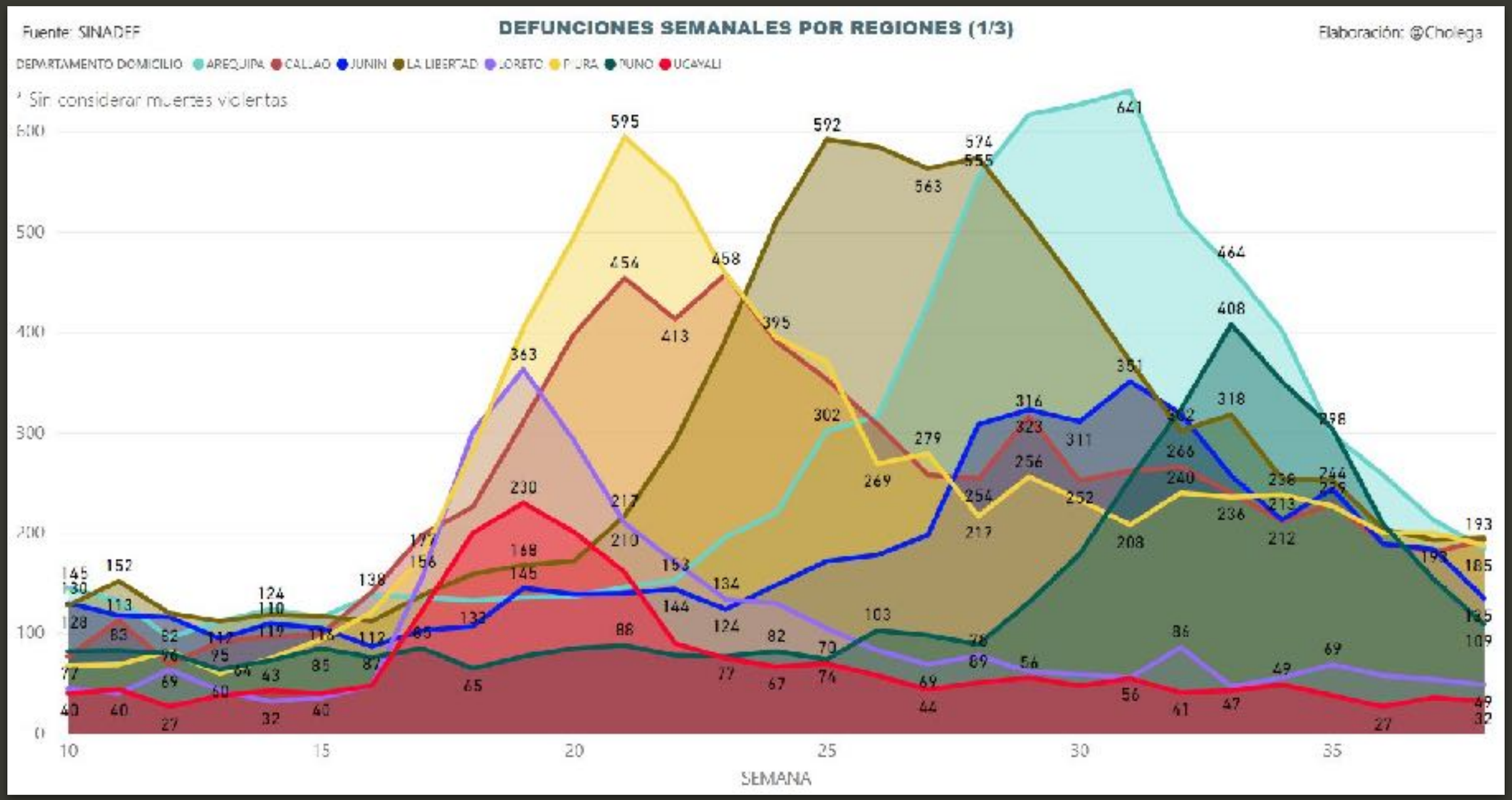


Recordemos que en Perú hay 25 epidemias regionales ocurriendo en paralelo



Elaboración: Gabriel Carrasco (UPCH + UCSD)

Recordemos que en Perú hay 25 epidemias regionales ocurriendo en paralelo



Elaboración: @Cholega

Aprovechemos la red de laboratorios de diagnóstico molecular de INS

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UNIVERSIDAD PERUANA CAYETANO HEREDIA

LABORATORIO DE GENÓMICA MICROBIANA

FONDECYT
Becas y financiamiento del Concytec

PONTIFICIA UNIVERSIDAD CATÓLICA DEL PERÚ

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vliruos
SHARING MINDS, CHANGING LIVES

TUMI Genomics

BID LAB

Entrenamiento en secuenciamiento y análisis de genomas

- Noviembre: Workshop de 5 días en UPCH. 10 participantes (y muestras!) de instituciones colaboradoras. Financia VLIR-UOS.

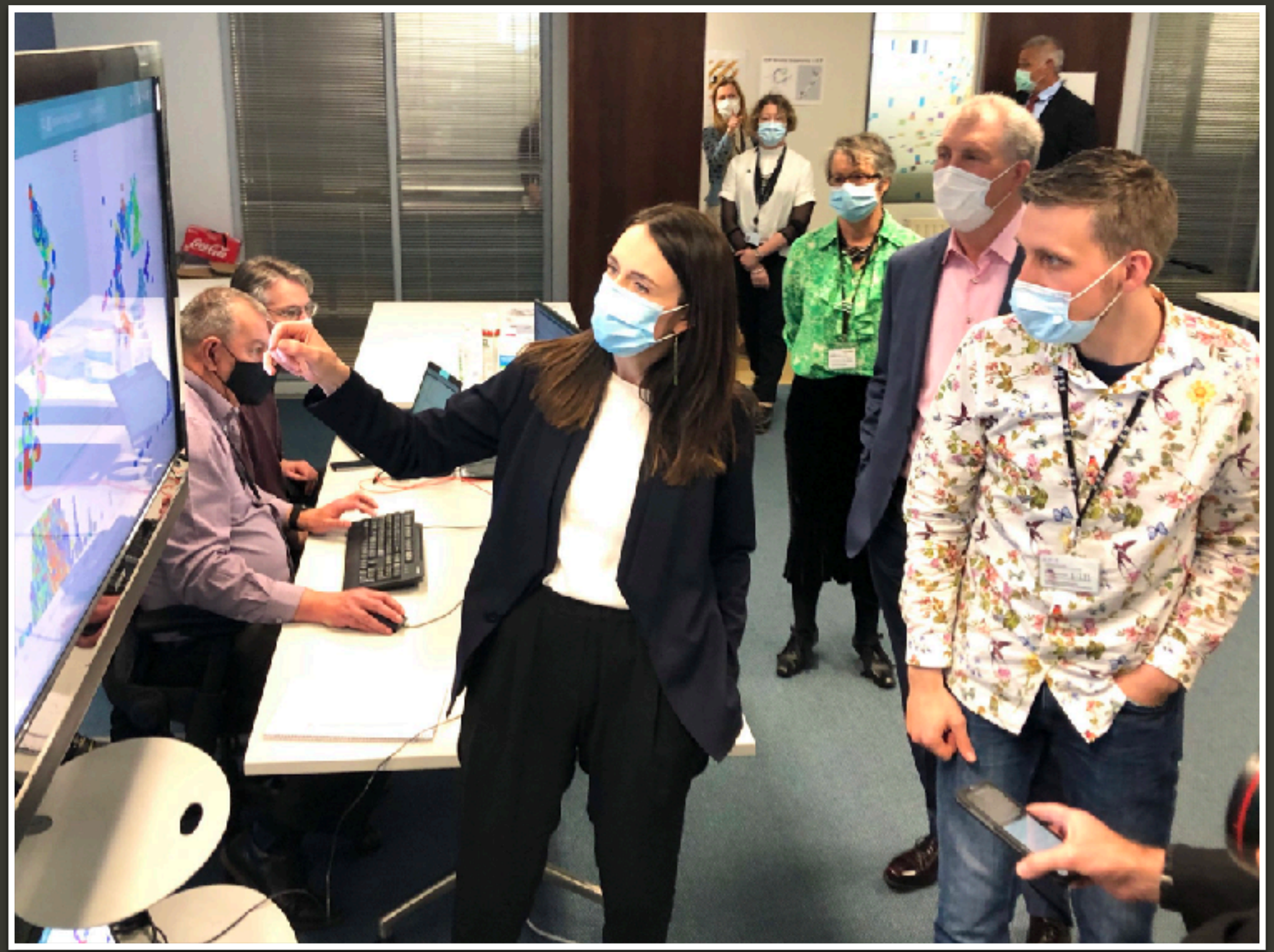
- Diciembre: CABANA workshop en análisis bioinformático.

- Diciembre / enero: Visitas de 5 días a Arequipa y Chachapoyas para apoyar en implementación de laboratorios y procesamiento de muestras. (VLIR-UOS)

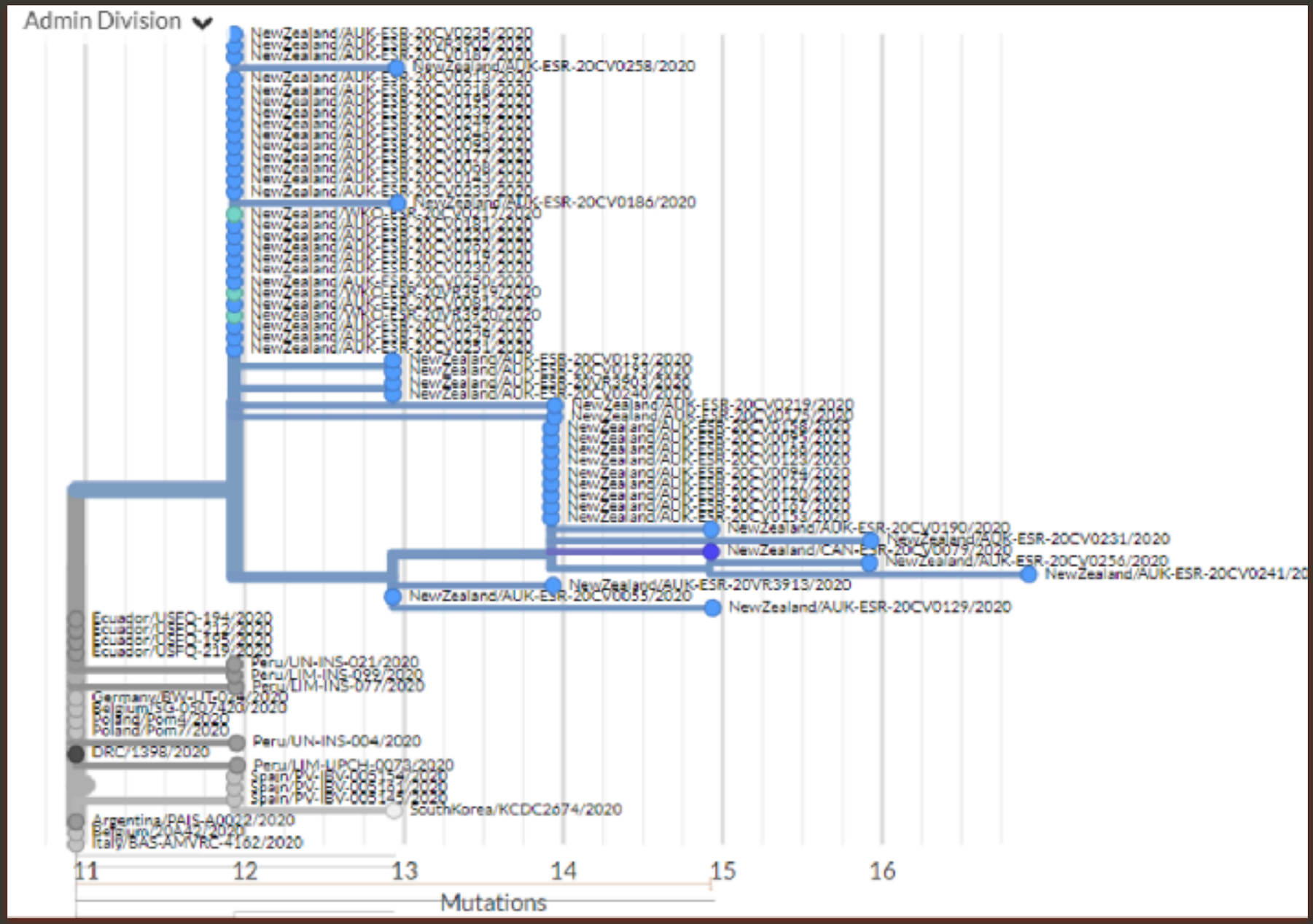
¿Qué puede hacer esta red de vigilancia en los siguientes meses?

1. Análisis de cadenas de transmisión y rastreo de contactos en la segunda ola de casos
2. Identificar re-introducciones desde otros países
3. Vigilancia de variantes de riesgo (vacunas, fármacos, sistema inmune)
4. Vigilancia del nuevos patógenos con potencial pandémico.

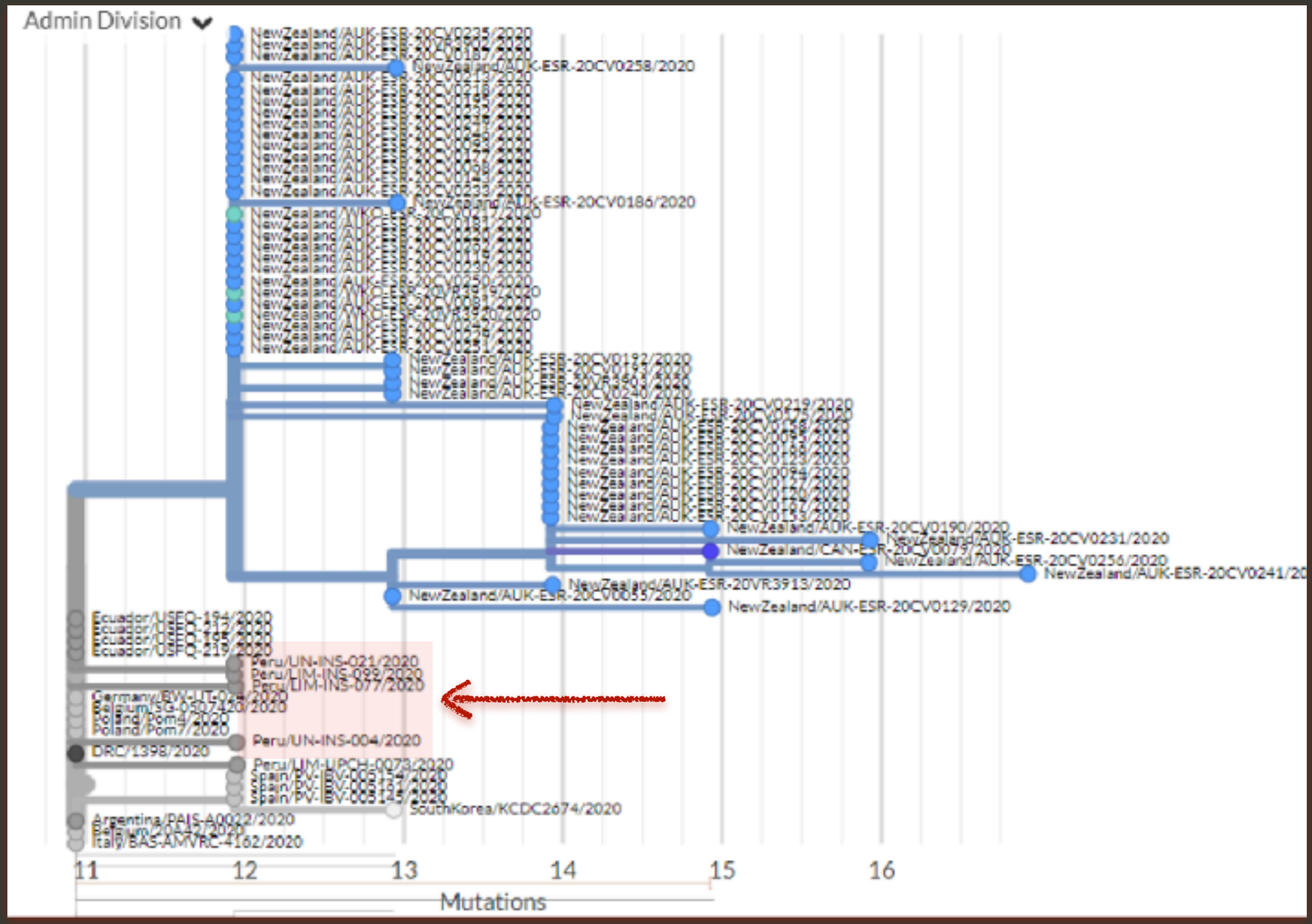
Seamos con Nueva Zelanda



Secuencias del brote reciente en NZ
(todas son parte del mismo cluster)



Secuencias de NZ son similares a secuencias peruanas (no significa que los casos estén asociados)



#SinCienciaNoHayFuturo

Laboratorio de Genómica Microbiana UPCH (est. 2017)

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Gracias

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