Global Influenza
Hospital Surveillance
Network

GIHSN 9TH ANNUAL MEETING

25-26 October 2021

Foundation for
Influenza
Epidemiology

Sous l’égide de

Fondation
de
France

Global Influenza
Hospital Surveillance
Network

www.gihsn.org

GIHSN 9TH ANNUAL MEETING, 25-26 OCTOBER 2021

WELCOME & OPENING OF THE MEETING

Catherine COMMAILLE-CHAPUS, GIHSN Coordination

Foundation for
Influenza
Epidemiology

Sous l'égide de
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de
France

WELCOME TO THE GIHSN COMMUNITY!

Global Influenza
Hospital Surveillance
Network

9th ANNUAL MEETING
2020-2021 SEASON

25-26 October 2021

ORGANISATION OF THE MEETING

- **25 OCTOBER 2pm-4pm CET – PLENARY SESSION**
  - GIHSN update & perspectives
  - External speeches from WHO, GISAID and the Global Virus Network
  - 2020-2021 season results

- **26 OCTOBER 9am-12am & 2pm–5pm CET – 2 REGION SPECIFIC SESSIONS**
  - 2020-2021 season results by site
  - Implementation challenges for the coming season
  - Publication update

PLENARY SESSION 25 OCTOBER 2PM-4PM CET AGENDA

MONDAY 25th OCT **2pm - 4pm CET: PLENARY SESSION *(ALL)***

2:00 - 2:05	**Welcome & Opening of the Meeting**	C Commaille-Chapus
2:05 - 2:15	**GIHSN Update & Perspectives**	C Mahé
2:15 - 2:30	**The Global Virus Network** *Presentation and Q&A*	Dr C Bréchot
2:30 - 2:45	**GISAID: Update on Covid-19** *Presentation and Q&A*	S Maurer-Stroh
2:45 - 3:00	**GISRS and Covid-19 Impact** *Presentation and Q&A*	Dr V Cozza
3:00 - 3:15	**Lyon center of excellence on respiratory pathogens** *Presentation and Q&A*	Pr B Lina
3:15 - 3:35	**GIHSN 2020-2021: Descriptive Analysis & Results** **Sequencing Update**	C Commaille-Chapus Pr B Lina
3:35 - 3:55	**GIHSN 2021-2022: Participating sites** **Protocol Highlights**	L Torcel-Pagnon S Chaves
3:55 - 4:00	**Closing of the Plenary Session**	

WEBINAR RULES

- Please do not forget to switch off your microphone when you are not speaking.
- Questions will be discussed after the presentations. Please raise your hand or use the chat/discussion button.
- A dedicated on-boarding meeting will be proposed to new sites to answer all their questions.
- Speakers are kindly asked to stick to the speaking time allotted!
- Please note that the session will be recorded.

Thank you all for your cooperation.

Global Influenza Hospital Surveillance Network

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GIHSN UPDATE & PERSPECTIVES 2021-2022

Cédric MAHE, President, Foundation for Influenza Epidemiology

Foundation for Influenza Epidemiology

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ASSETS OF THE NETWORK

- Network of **sentinel hospitals** identifying **acute respiratory infection** cases according to a **similar protocol**
- 100+ hospitals in 20+ sites worldwide collecting **clinical data , virological data and virus genome sequencing**.
- **Co-funded** by local authorities and by the Foundation for Epidemiology which provides **private sector catalytic funding** under the format of grants

Assets of the network

- Empowered community of motivated sites owning their data
- Use of existing infrastructures combined with capacity building
- Severe respiratory disease surveillance (potentially multi-pathogens)
- Link between clinicals outcome and virus genome sequencing

North America
- Canada
- Mexico

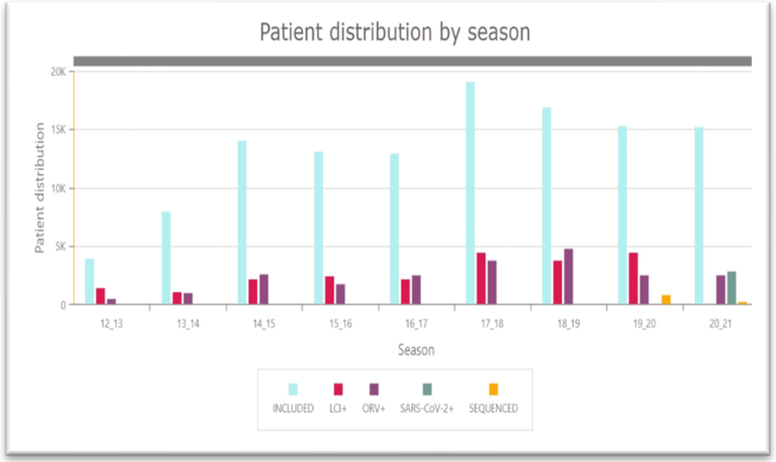
South America
- Brazil
- Peru

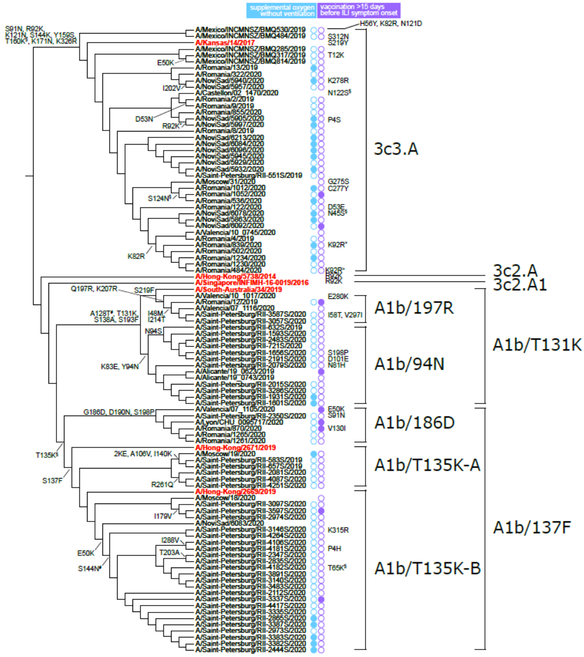
Eurasia
- France
- Romania
- Russia-Moscow
- Russia-St Pet
- Spain
- Ukraine

Africa
- Kenya
- Morocco
- South Africa
- Ivory Coast

Middle East
- Lebanon
- Turkey

Asia/Pacific
- China-Fudan
- India
- Nepal





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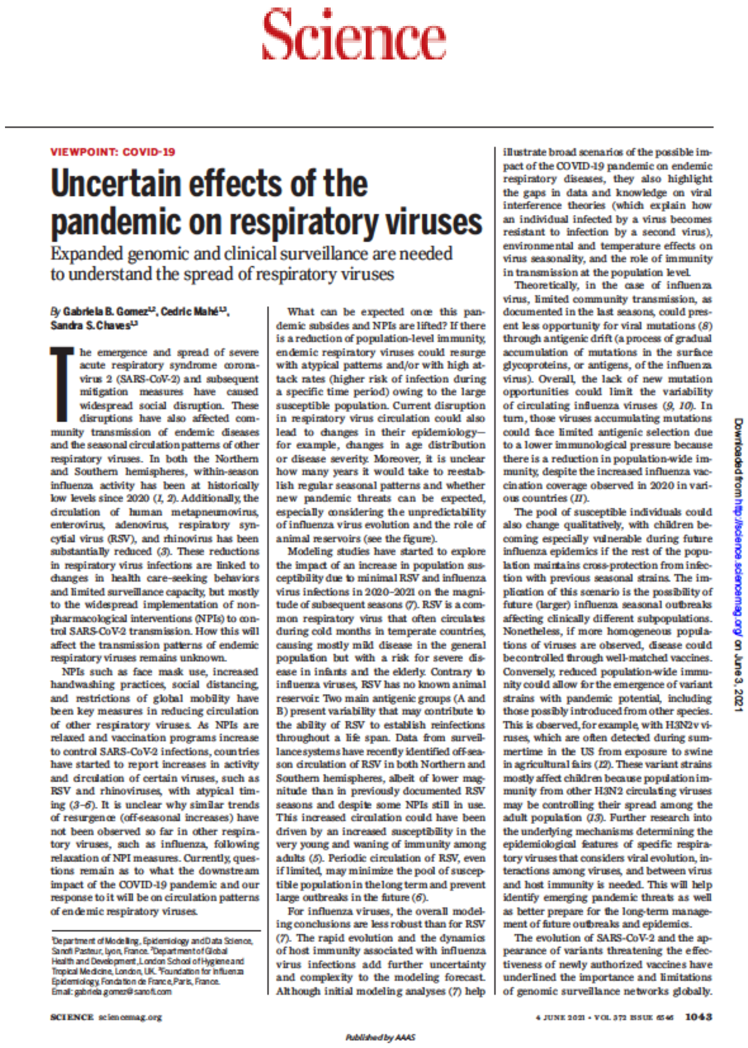
More information on www.gihsn.org

RELEVANCE IN A POST-PANDEMIC WORLD

- ❖ COVID-19 pandemic has stressed the weakness of the current systems
  - Disruption of existing systems > need for a targeted genetic sequencing scale up and resilient surveillance system
  - Alternative tools involving both public and private sector have emerged (COVAX, GISAID, CEPI) > need for a multi-stakeholders approach. Private sector could play an important role
- ❖ The uncertainly about other respiratory virus circulation timing and impact post SARS-CoV-2 (including potential pandemic threats) make such surveillance even more important
- ❖ The GISHN offers a capable instrument and a community which have shown resilience over 9 years including during the pandemic – it relies on existing national assets
- ❖ This sentinel platform can be scaled-up and leverage to be part of a larger pandemic preparedness system
- ❖ A governance system is already place to allow for private sector catalytic funding, minimizing risk of conflicts of interest (no earmarking, independent scientific committee, grant format/data access)



Science

VIEWPOINT: COVID-19

Uncertain effects of the pandemic on respiratory viruses

Expanded genomic and clinical surveillance are needed to understand the spread of respiratory viruses

By **Gabriela B. Gomez**[1,2], **Cedric Mahé**[1,3], **Sandra S. Chaves**[1,3]

The emergence and spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and subsequent mitigation measures have caused widespread social disruption. These disruptions have also affected community transmission of endemic diseases and the seasonal circulation patterns of other respiratory viruses. In both the Northern and Southern hemispheres, within-season influenza activity has been at historically low levels since 2020 (*1*, *2*). Additionally, the circulation of human metapneumovirus, enterovirus, adenovirus, respiratory syncytial virus (RSV), and rhinovirus has been substantially reduced (*3*). These reductions in respiratory virus infections are linked to changes in health care–seeking behaviors and limited surveillance capacity, but mostly to the widespread implementation of nonpharmacological interventions (NPIs) to control SARS-CoV-2 transmission. How this will affect the transmission patterns of endemic respiratory viruses remains unknown.

NPIs such as face mask use, increased handwashing practices, social distancing, and restrictions of global mobility have been key measures in reducing circulation of other respiratory viruses. As NPIs are relaxed and vaccination programs increase to control SARS-CoV-2 infections, countries have started to report increases in activity and circulation of certain viruses, such as RSV and rhinoviruses, with atypical timing (*3*–*6*). It is unclear why similar trends of resurgence (off-seasonal increases) have not been observed so far in other respiratory viruses, such as influenza, following relaxation of NPI measures. Currently, questions remain as to what the downstream impact of the COVID-19 pandemic and our response to it will be on circulation patterns of endemic respiratory viruses.

What can be expected once this pandemic subsides and NPIs are lifted? If there is a reduction of population-level immunity, endemic respiratory viruses could resurge with atypical patterns and/or with high attack rates (higher risk of infection during a specific time period) owing to the large susceptible population. Current disruption in respiratory virus circulation could also lead to changes in their epidemiology—for example, changes in age distribution or disease severity. Moreover, it is unclear how many years it would take to reestablish regular seasonal patterns and whether new pandemic threats can be expected, especially considering the unpredictability of influenza virus evolution and the role of animal reservoirs (see the figure).

Modeling studies have started to explore the impact of an increase in population susceptibility due to minimal RSV and influenza virus infections in 2020–2021 on the magnitude of subsequent seasons (*7*). RSV is a common respiratory virus that often circulates during cold months in temperate countries, causing mostly mild disease in the general population but with a risk for severe disease in infants and the elderly. Contrary to influenza viruses, RSV has no known animal reservoir. Two main antigenic groups (A and B) present variability that may contribute to the ability of RSV to establish reinfections throughout a life span. Data from surveillance systems have recently identified off-season circulation of RSV in both Northern and Southern hemispheres, albeit of lower magnitude than in previously documented RSV seasons and despite some NPIs still in use. This increased circulation could have been driven by an increased susceptibility in the very young and waning of immunity among adults (*5*). Periodic circulation of RSV, even if limited, may minimize the pool of susceptible population in the long term and prevent large outbreaks in the future (*6*).

For influenza viruses, the overall modeling conclusions are less robust than for RSV (*7*). The rapid evolution and the dynamics of host immunity associated with influenza virus infections add further uncertainty and complexity to the modeling forecast. Although initial modeling analyses (*7*) help illustrate broad scenarios of the possible impact of the COVID-19 pandemic on endemic respiratory diseases, they also highlight the gaps in data and knowledge on viral interference theories (which explain how an individual infected by a virus becomes resistant to infection by a second virus), environmental and temperature effects on virus seasonality, and the role of immunity in transmission at the population level.

Theoretically, in the case of influenza virus, limited community transmission, as documented in the last seasons, could present less opportunity for viral mutations (*8*) through antigenic drift (a process of gradual accumulation of mutations in the surface glycoproteins, or antigens, of the influenza virus). Overall, the lack of new mutation opportunities could limit the variability of circulating influenza viruses (*9*, *10*). In turn, those viruses accumulating mutations could face limited antigenic selection due to a lower immunological pressure because there is a reduction in population-wide immunity, despite the increased influenza vaccination coverage observed in 2020 in various countries (*11*).

The pool of susceptible individuals could also change qualitatively, with children becoming especially vulnerable during future influenza epidemics if the rest of the population maintains cross-protection from infection with previous seasonal strains. The implication of this scenario is the possibility of future (larger) influenza seasonal outbreaks affecting clinically different subpopulations. Nonetheless, if more homogeneous populations of viruses are observed, disease could be controlled through well-matched vaccines. Conversely, reduced population-wide immunity could allow for the emergence of variant strains with pandemic potential, including those possibly introduced from other species. This is observed, for example, with H3N2v viruses, which are often detected during summertime in the US from exposure to swine in agricultural fairs (*12*). These variant strains mostly affect children because population immunity from other H3N2 circulating viruses may be controlling their spread among the adult population (*13*). Further research into the underlying mechanisms determining the epidemiological features of specific respiratory viruses that considers viral evolution, interactions among viruses, and between virus and host immunity is needed. This will help identify emerging pandemic threats as well as better prepare for the long-term management of future outbreaks and epidemics.

The evolution of SARS-CoV-2 and the appearance of variants threatening the effectiveness of newly authorized vaccines have underlined the importance and limitations of genomic surveillance networks globally.

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THE GLOBAL VIRUS NETWORK

Dr Christian BRECHOT, MD, PhD, President of the Global Virus Network

Foundation for
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France

GIHSN Annual Meeting 2021
Overview of Global Virus Network

Christian Brechot, MD, PhD
President, Global Virus Network
Senior Associate Dean for Research in Global Affairs
Associate Vice President for International Partnerships and Innovation
Professor in the Division of Infectious Disease, Department of Internal Medicine
Morsani College of Medicine, University of South Florida, USA

What went wrong?

- **Lack of coordination:** national vs international strategies
  Global cooperation; interconnection of every personal health
  Ex: COVAX

- **Health care system organizations**

- **Science/Medicine/Public Health-driven political decisions:** EXPERTIZE
  ex: Virus sequenced on Jan 5th in China. Immediately made public
    Masks
    Diagnostics

- **Communication:** fake news/social networks

Global Virus Network

- The GVN was co-founded in 2011
- A non-profit global organization based in Baltimore, Maryland, USA
- A coalition comprised of leading virologists working to:
  - Advance discovery and knowledge on how viruses cause disease
  - Develop drugs and vaccines to prevent illness and death


NEWS

New organization pledges scientific expertise for viral outbreaks

First responders: Global Virus Network co-founders Reinhard Kurth (left), Robert Gallo (center) and William Hall (right).

WASHINGTON, DC — The next time a viral outbreak like H1N1 influenza or the SARS virus threatens the world, Robert Gallo wants the scientific community to be ready. To make that happen, last month Gallo launched the Global Virus Network (GVN), an international group of leading virologists and medical researchers tasked with providing scientific expertise to government agencies in the face of emerging infectious viral agents.

"An independent voice of medical laboratory scientists would be a great addition to the surveillance world," says Gallo, who co-discovered the HIV retrovirus in 1984 and is currently director of the Institute of Human Virology at the University of Maryland School of Medicine in Baltimore.

At a meeting here in early March, representatives from 16 countries gathered to determine the network's mandate and mission. As envisioned by its members, the GVN will serve as a clearinghouse for rapid data collection and disease containment. In response to an outbreak, the organization would send researchers from one of its many international academic centers into the field to collect samples and help local officials diagnose and treat infected people.

The GVN, which hopes to secure a budget of at least $25 million per year with donations from governments, research centers, charitable organizations and private companies, would agencies such as the World Health Organization (WHO) and the US Centers for Disease Control and Prevention (CDC). Both of these agencies, which have ongoing discussions with GVN officials about how the groups can best work together, are also involved in controlling viral pathogens but are often more constrained by political considerations and region-specific funding support.

"We're not saying that the WHO or CDC can't do this. But because of our totally scientific approach, maybe we can get to it quicker," says GVN cofounder William Hall, a medical microbiologist at University College Dublin.

In addition to providing first-responder scientific know how, the network also plans researchers about how to counter emerging infectious diseases. "We have to cultivate and nurture a younger generation of virologists with a keen motivation to deal with public health issues," says Jonathan Gershoni, a molecular immunologist at Tel Aviv University and the Israeli representative to the GVN.

Nathan Wolfe, a Stanford University virologist who directs the Global Viral Forecasting Initiative, a San Francisco–based infectious disease outbreak research and advocacy organization, welcomes the arrival of another group with a similar mandate. "What's being done now is just a drop in the bucket of what needs to be done in order to stop pandemics before they occur," he says.

Research

EXPERTIZE

Reactivity

Academic-Industrial Partnerships

Education/Training

Advocacy Communication

Regional GVNs

- **65 Centers of Excellence**
- **12 Affiliated Institutions**
- **In 35 Countries**

The Global Virus Network

Vision

“A world prepared to prevent, contain and control viral epidemic threats, through the collaboration of a global network of expert virus laboratories.”

Mission

“To strengthen medical research and response to current viral cases of human disease and to prepare for new viral pandemic threats.”

Research	Promoting development of better diagnostics, antiviral drugs, and vaccines
Training and Education	For the next generation of virologists
Advocacy and Public Education	Advocate for public health policies and research in response to emerging viruses worldwide

GLOBAL VIRUS NETWORK

Regional GVN Meetings

- Latin America & Caribbean in March, June, Sep, and Dec 2021
- Africa Regional Meeting in July and Oct 2021
- Southeast Asia in 2021 or 2022

Past:

- Africa in 2019

Programs & Initiatives Overview

RESEARCH

- Hepatitis B Database
- Joint Grant Applications
- Annual Meetings
- Regional Meetings
- Zika Serum Bank
- Chikungunya Task Force
- Anticipation & Preparedness Task Force &Virus Watch Group
- HTLV-1 Task Force
- Zika Task Force
- SARS-CoV-2 Task Force
- SARS-CoV-2 Biobank

TRAINING AND EDUCATION

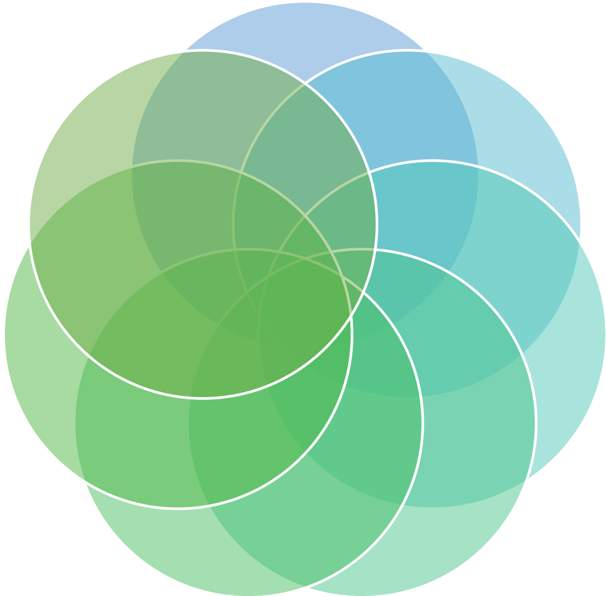
- GVN Short Course
- Hepatitis C Provider Training
- GVN Regional Chapters
- GVN Academy
- GVN Postdoctoral Fellowship
- GVN Online Medical Virology Class
- GVN Microbiome & Viral Infection Online Course

ADVOCACY, PUBLIC EDUCATION AND COMMUNICATIONS

- Ebola FAQs
- GVN Intranet
- Forefront COVID-19 Online Seminars
- GVN Viral Infection Preparedness Education and Resilience (VIPER) Advisory Group
- GVN Perspectives
- Weekly GVN Newsletter
- Press releases and Op-eds

GVN SARS-CoV-2 Activities Highlights

SARS-CoV-2 Task Force



Biobanking Project

GVN SARS-CoV-2 Perspectives

Research & Clinical Trials

GVN Center and Member Spotlights

Dr. Brechot's Health and Care Blog

GVN: Forefront of Virology COVID-19 Webinar Series

SARS-COV-2 RESPONSE EFFORT HIGHLIGHTS

DR. BRECHOT GVN-USF WEEKLY BLOG

Dr. Christian Bréchot

President, Global Virus Network

Professor, University of South Florida

Dr. Bréchot's Weekly Blog - June 24, 2020

GVN CENTER OF EXCELLENCE SPOTLIGHT

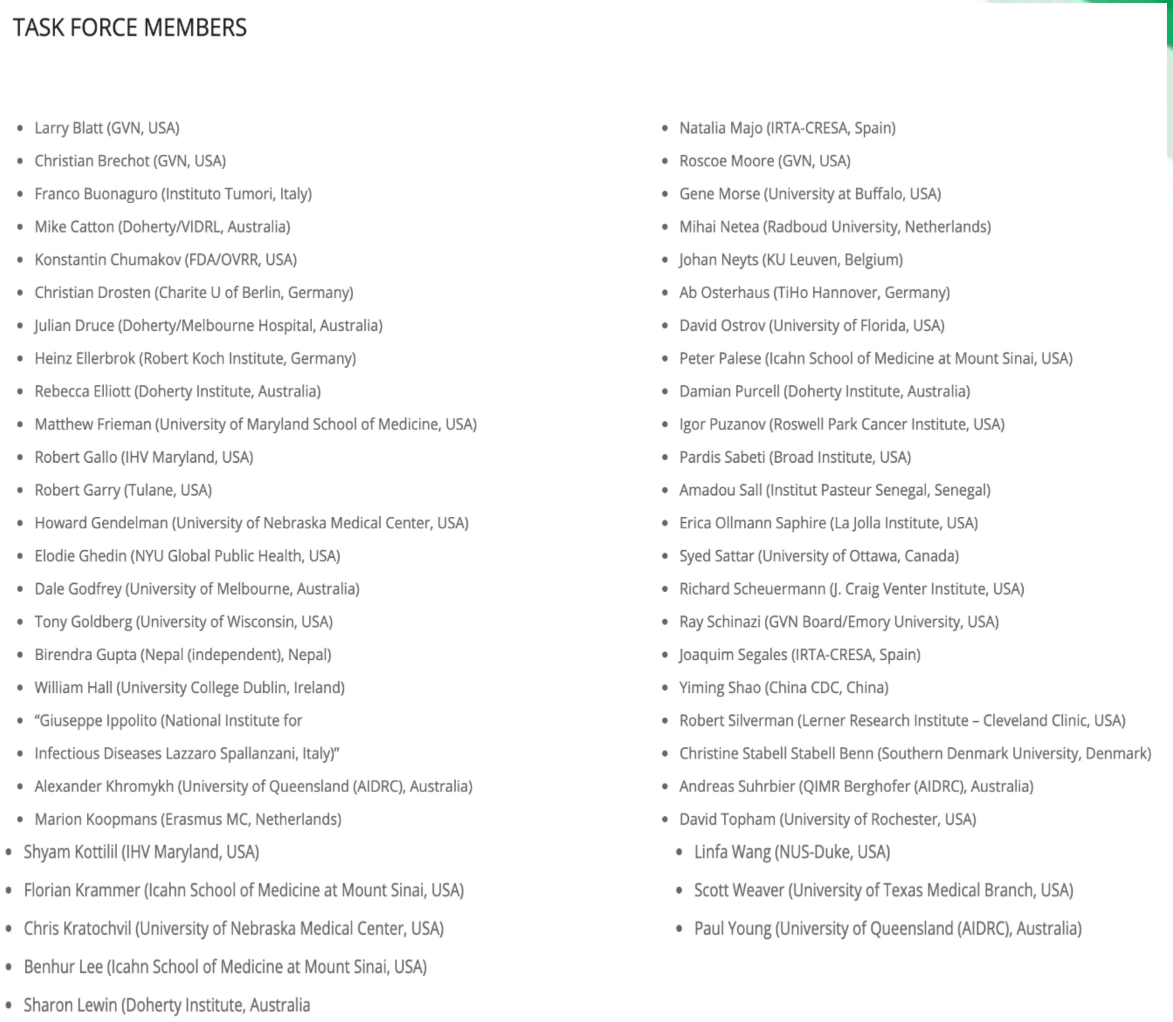
GVN Center Spotlight: Pontiano Kaleebu

View All GVN Center Spotlights

GVN: FOREFRONT OF VIROLOGY COVID-19 WEBINAR SERIES

SARS-CoV-2 Task Force

- Representatives from 32 GVN centers in 13 countries.
- Meet virtually biweekly-monthly to share the most recent and advanced research findings, and to discuss developments in diagnostic, serological tests, and vaccines
- To date: Hosted **24** meetings in total

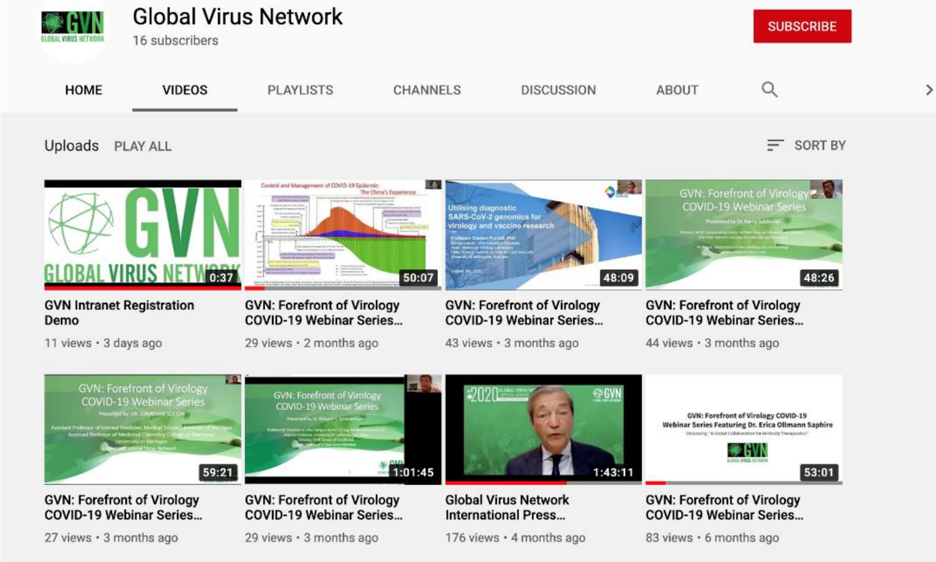


TASK FORCE MEMBERS

- Larry Blatt (GVN, USA)
- Christian Brechot (GVN, USA)
- Franco Buonaguro (Instituto Tumori, Italy)
- Mike Catton (Doherty/VIDRL, Australia)
- Konstantin Chumakov (FDA/OVRR, USA)
- Christian Drosten (Charite U of Berlin, Germany)
- Julian Druce (Doherty/Melbourne Hospital, Australia)
- Heinz Ellerbrok (Robert Koch Institute, Germany)
- Rebecca Elliott (Doherty Institute, Australia)
- Matthew Frieman (University of Maryland School of Medicine, USA)
- Robert Gallo (IHV Maryland, USA)
- Robert Garry (Tulane, USA)
- Howard Gendelman (University of Nebraska Medical Center, USA)
- Elodie Ghedin (NYU Global Public Health, USA)
- Dale Godfrey (University of Melbourne, Australia)
- Tony Goldberg (University of Wisconsin, USA)
- Birendra Gupta (Nepal (independent), Nepal)
- William Hall (University College Dublin, Ireland)
- "Giuseppe Ippolito (National Institute for
- Infectious Diseases Lazzaro Spallanzani, Italy)"
- Alexander Khromykh (University of Queensland (AIDRC), Australia)
- Marion Koopmans (Erasmus MC, Netherlands)
- Shyam Kottilil (IHV Maryland, USA)
- Florian Krammer (Icahn School of Medicine at Mount Sinai, USA)
- Chris Kratochvil (University of Nebraska Medical Center, USA)
- Benhur Lee (Icahn School of Medicine at Mount Sinai, USA)
- Sharon Lewin (Doherty Institute, Australia
- Natalia Majo (IRTA-CRESA, Spain)
- Roscoe Moore (GVN, USA)
- Gene Morse (University at Buffalo, USA)
- Mihai Netea (Radboud University, Netherlands)
- Johan Neyts (KU Leuven, Belgium)
- Ab Osterhaus (TiHo Hannover, Germany)
- David Ostrov (University of Florida, USA)
- Peter Palese (Icahn School of Medicine at Mount Sinai, USA)
- Damian Purcell (Doherty Institute, Australia)
- Igor Puzanov (Roswell Park Cancer Institute, USA)
- Pardis Sabeti (Broad Institute, USA)
- Amadou Sall (Institut Pasteur Senegal, Senegal)
- Erica Ollmann Saphire (La Jolla Institute, USA)
- Syed Sattar (University of Ottawa, Canada)
- Richard Scheuermann (J. Craig Venter Institute, USA)
- Ray Schinazi (GVN Board/Emory University, USA)
- Joaquim Segales (IRTA-CRESA, Spain)
- Yiming Shao (China CDC, China)
- Robert Silverman (Lerner Research Institute – Cleveland Clinic, USA)
- Christine Stabell Stabell Benn (Southern Denmark University, Denmark)
- Andreas Suhrbier (QIMR Berghofer (AIDRC), Australia)
- David Topham (University of Rochester, USA)
- Linfa Wang (NUS-Duke, USA)
- Scott Weaver (University of Texas Medical Branch, USA)
- Paul Young (University of Queensland (AIDRC), Australia)

GVN: Forefront of Virology COVID-19 Webinar Series

- COVID-19 related science sharing, featuring expert virologists from GVN centers around the world.
- Previous seminars are posted on our YouTube channel:



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Global Virus Network International Press...
176 views • 4 months ago

GVN: Forefront of Virology COVID-19 Webinar Series...
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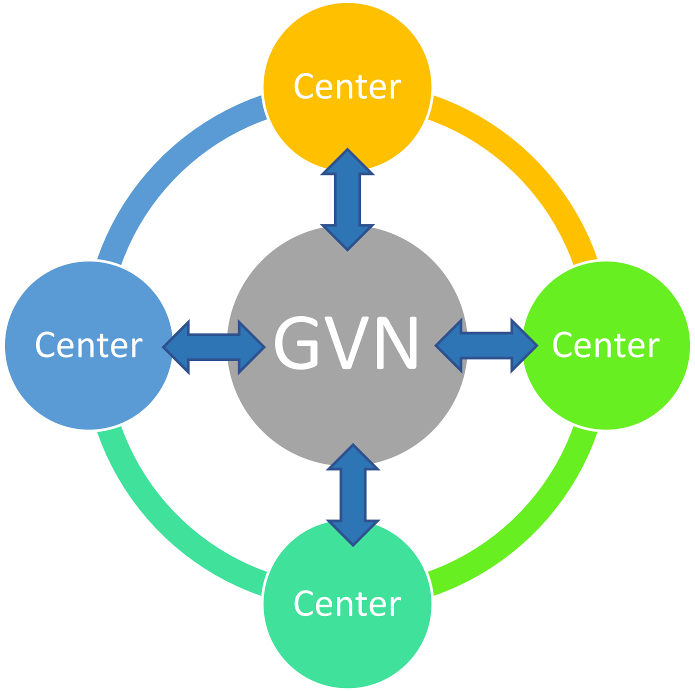
GVN Biobank Program

- Global collaboration efforts to assist with the development of diagnostics, vaccines, and therapeutics
- Efficient control of epidemics/pandemics by sharing clinical samples and data



- ○ **<u>GVN:</u>** providing oversight and coordination; platforms and protocols for research projects
- ○ **<u>Centers:</u>** conducting clinical sample collection; analyses and data collection
- ○ **<u>Outcomes:</u>** establishment of a database system by storing analytical and clinical data; evaluation of therapeutical and diagnostic protocols

GVN International Meetings

2011
Washington DC, USA &
Dublin, Ireland

2012
Naples, Italy
&
Baltimore, USA

2013
Munich, Germany
&
Moscow, Russia

2015
Beijing, China

2016
Sapporo, Japan

2017
Melbourne, Australia

2018
Annecy, France

2019
Barcelona, Spain

2020
Virtual Special Annual Meeting

GVN Academy Program

- GVN Postdoctoral Fellowship Training Program
- GVN Rising Star Mentorship Program
- GVN Short Course: Emerging Leaders in Virology
- GVN Online Short Course
- GVN Alumni Networking Series

GVN Postdoctoral Fellowship Training Program

Goal

- **Fostering global collaborations** and **increasing capacity building** of junior virologists globally

Program Details

- To recruit and train **three** postdoctoral trainees for a **2-year term**
- Rotate at **two** GVN Centers of Excellence during their 2-year program
- **Mentors-Mentee** match based on the research interests
- Participate in GVN annual/regional meetings
- Establish contact with industrial partners for further collaborations
- Meet and network with **senior GVN scientists**

Upcoming trainees:

- 3 trainees are supported

GVN Rising Stars Program

Overview

- The GVN rising star initiative is an investment in a small group of outstanding junior virologists/scientists to help promote their careers and increase the capacity building in their regions .

Program Details

- To recruit 5 junior scientists for Year 1 and 10 for Year 2
- Mentor-mentee match and interactions
- Participate in GVN annual/regional meetings
- Networking opportunities

Who Can Apply

- Ranking from Post-doctoral Research Associate to Associate Professors in the GVN Academic Centers
- Conducting research in a basic, medical or veterinary virology targeting vaccine, therapy, and diagnostics
- Research experience with a good track record of publications

Benefits of being a Rising Star

- Financial support to attend a GVN meetings and workshops
- Opportunity to get trained for grantsmanship
- Opportunity to identify research collaborators and strengthen research program and publications

GVN & USF Online Course: Microbiomes and their Impact on Viral Infections

- World-renowned Speakers
- 2 certificated noncredit courses
  - Introduction on the Microbiomes, 11 modules
  - Symbiotic Evolutions in the Microbiome World, 9 modules
- Self-paced, Online format
- GVN awarded four competitive scholarships to Africa based virologists working on the frontlines of the pandemic.

Expert Speakers From Around the World

JACQUES RAVEL, PHD
Professor, Microbiology and Immunology
Associate Director, Institute for Genome Sciences
Associate Director for Genomics, Institute for Genome Sciences
University of Maryland School of Medicine

LARRY DISHAW, PHD
Associate Professor, College of Medicine Pediatrics,
Assistant Professor, College of Medicine
Molecular Medicine
University of South Florida

SARKIS K. MAZMANIAN, PHD
Luis & Nelly Soux Professor of Microbiology
Investigator, Heritage Medical Research Institute
Division of Biology and Biological Engineering
California Institute of Technology

CAMILO ZALAMEA, PHD
Assistant Professor, Department of Integrative Biology
University of South Florida

KARINE CLÉMENT, MD, PHD
Sorbonne University, INSERM UMRS NutriOmics,
Faculty of Medicine

BENOIT CHASSAING, PHD
Team Leader
Mucosal Microbiota in Chronic Inflammatory Diseases
INSERM U1016

JOHN E. PARKINSON, PHD
Assistant Professor, Department of Integrative Biology
University of South Florida

LAURENCE ZITVOGEL, MD, PHD
Group Leader, Tumour Immunology and Immunotherapy of Cancer
Institut Gustave Roussy
European Academy of Tumor Immunology

MYA BREITBART, PHD
Professor, College of Marine Science
University of South Florida

MARIA CARLA SALEH, PHD
Principal Investigator, Viruses and RNAi Unit
Department of Virology, Institut Pasteur Paris

SARAH E. CLARK, PHD
Assistant Professor, Department of Otolaryngology
University of Colorado School of Medicine

RAMESH AKKINA, DVM, PHD
Professor, Department of Microbiology, Immunology and Pathology
Colorado State University

NICHOLE KLATT, PHD
Professor
Director, Surgical Outcomes and Precision Medicine Research Division
University of Minnesota Medical School and Department of Surgery

MATHILDE GENDRIN, PHD
Junior Group Leader, Microbiota of Insect Vectors Group
Institut Pasteur de la Guyane

MAUREEN GROER, PHD, RN, FAAAN
Gordon Keller Professor, Nursing
Executive Director, Bio-Behavioral Research Laboratory
Professor, College of Nursing
Professor, College of Medicine Internal Medicine
University of South Florida

LIPING ZHAO, PHD
Professor
Eveleigh-Fenton Chair of Applied Microbiology
Department of Biochemistry and Microbiology
School of Environmental and Biological Sciences
Rutgers University

GVN
GLOBAL VIRUS NETWORK

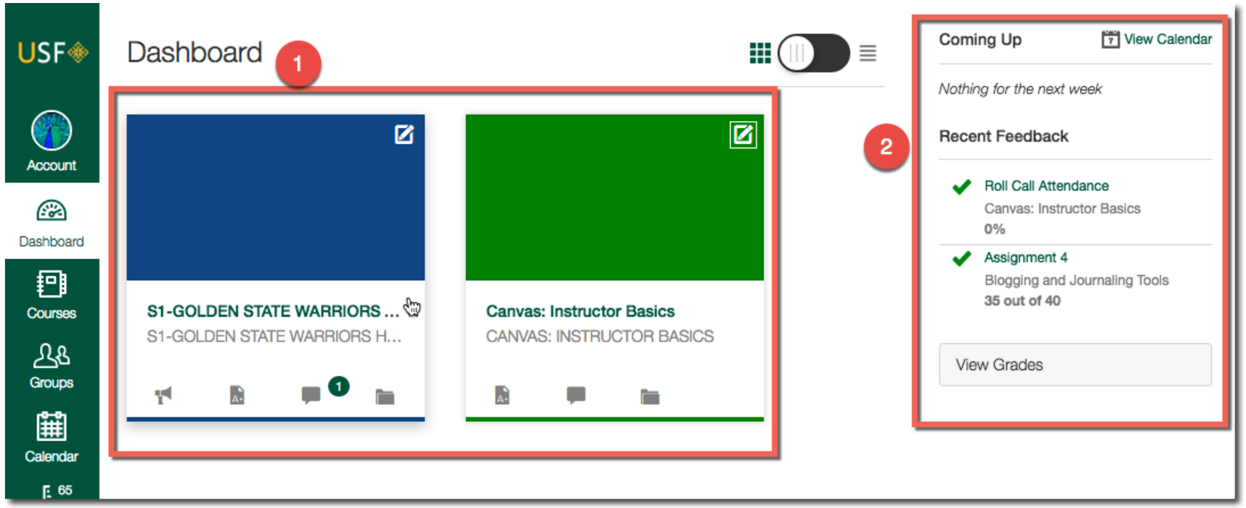
USF Initiative on MICROBIOMES

UNIVERSITY OF SOUTH FLORIDA

Online Short-Course for Emerging Leaders in Virology Part 1:

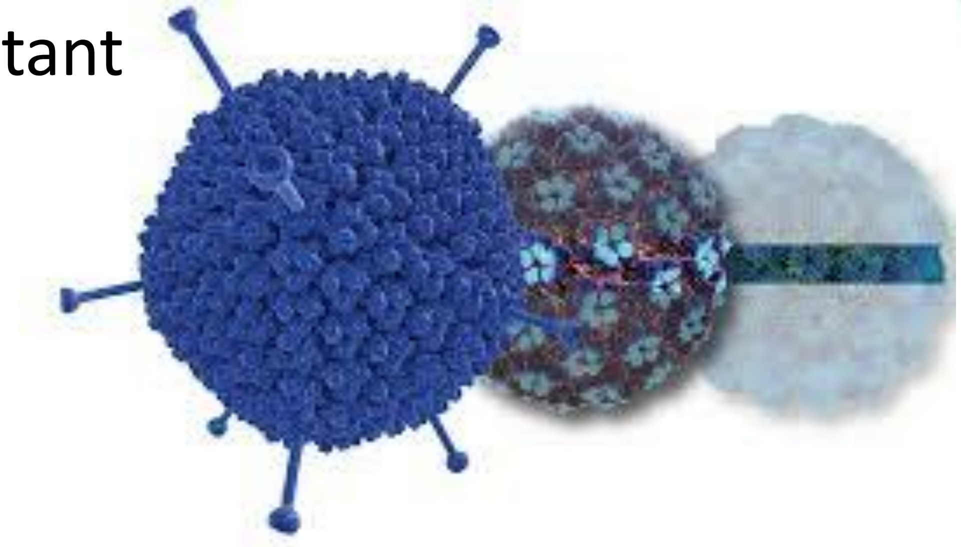
- Partner with University of South Florida, we are assembling an online version of the short-course to benefit **more** emerging leaders in virology, especially in middle- and low-income counties.

- **Estimated Completion Date:** Late 2021



Online Short-Course for Emerging Leaders in Virology Part 2: Oncology

- Sub course of the online short-course will focus on **cancer virology** - an increasingly important topic.



- **Estimated Completion Date:** Early 2022

GVN GLOBAL VIRUS NETWORK

UNIVERSITY OF SOUTH FLORIDA

GVN Corporate Partnership Program (GCCP)

- A **platform** for partnerships to strengthen international viral preparedness and response between business community and leading medical virologists
- To support research, training activities and increased awareness of medical virology issues, and address the risks and impacts of human viral diseases, including SARS- CoV -2.

Corporate Partnerships Activities Highlights

- Biobanking
- Emerging Pathogens Discovery Network Working Group
- Postdoctoral Fellowship Training Program
- Testing Product Effectiveness against SARS-CoV-2
- Developing Product Testing Protocols
- Clinical and Genome Sequencing
- Validation of Diagnostic Testing Kits

Unilever

BIOPROTECT

SANOFI PASTEUR

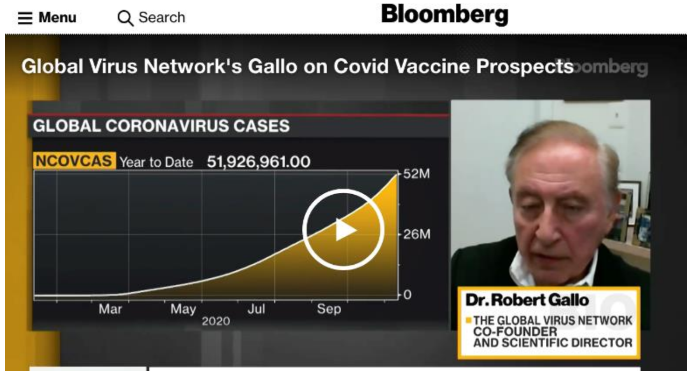
GILEAD

Abbott

NEKTAR

GVN Advocacy & Communication

- Getting accurate and timely information to our members and the general public is our primary goal during this pandemic.
- Since August 2020: 70,000 + pageviews of GVN website from around the world.
- IN 2020: GVN has been featured in
    - 25 Press Releases
    - 3 Op-eds & LTE: USA Today, WSJ, NYT
    - 1 International Press Conference
    - 116 News Articles
    - 30 TV Appearances
    - 10 Radio Appearances




Rollingstone

GVN Public Education

GVN: AN information hub for the dissemination and sharing of COVID-19 updates for scientists and the general public

- **GVN Weekly Brief**
  - Distribute the new insights of COVID-19 to the GVN scientists and the general public
  - To date: 33 issues
- **GVN SARS-CoV-2 Perspectives**
  - GVN scientific column about the latest scientific progress surrounding SARS-CoV-2.
  - To date, 24 posts
- **Dr. Brechot's Health and Care Blog**
  - Continuously updated resource by Dr. Brechot for novel insights into the current pandemic. To date: 26 posts
- **Global Health Conversation Series with USF Health International**

GVN to Become a Worldwide Information Resource for COVID-19 Vaccines and Variants

gvn.org

GVN
GLOBAL VIRUS NETWORK

Global Influenza
Hospital Surveillance
Network

www.gihsn.org

GIHSN 9TH ANNUAL MEETING, 25-26 OCTOBER 2021

GISAID: UPDATE ON COVID-19

Sebastian MAURER-STROH, GISAID

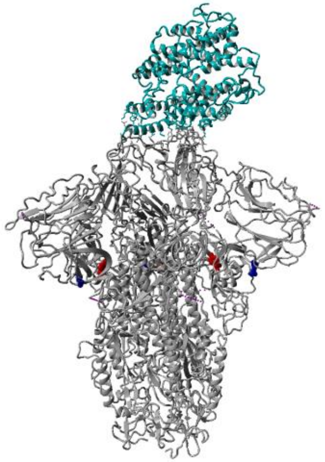
Foundation for
Influenza
Epidemiology

Sous l'égide de

Fondation
de
France

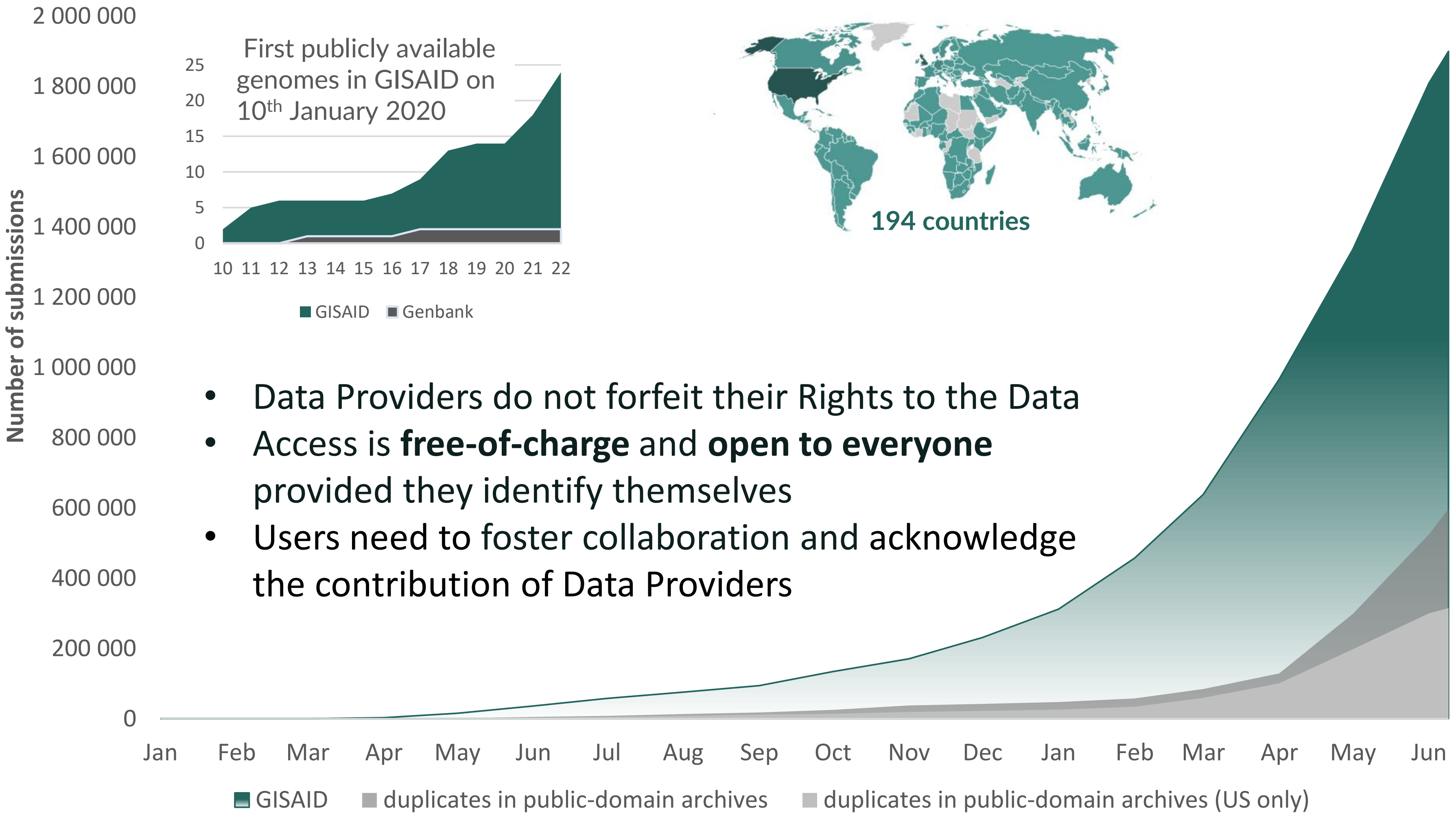
GISAID: Update on Covid-19

Sebastian Maurer-Stroh



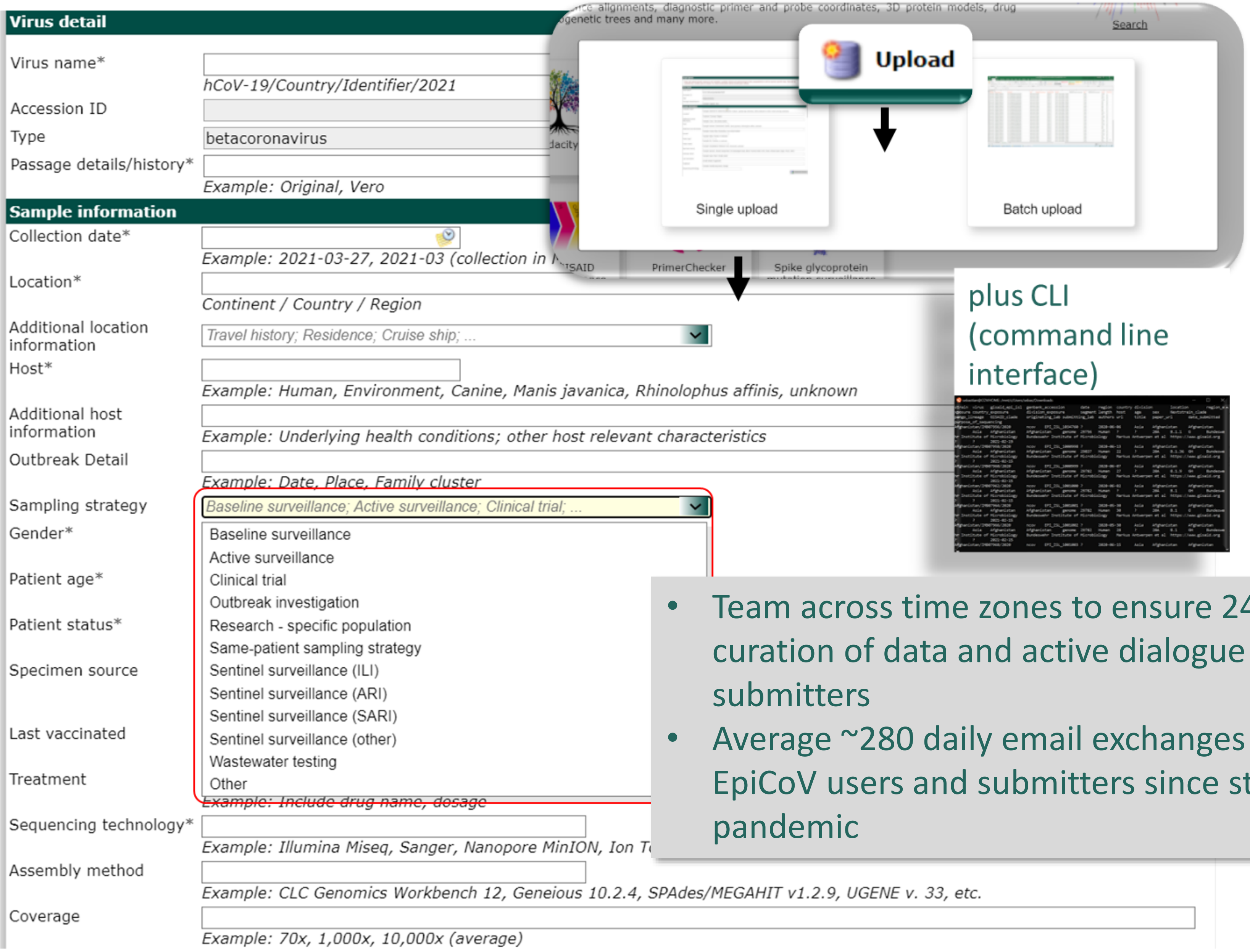
Real-time data sharing during the COVID-19 Pandemic => Trust

Submitters’ choice: GISAID's transparent sharing mechanism vs. anonymous access public-domain



- Data Providers do not forfeit their Rights to the Data
- Access is **free-of-charge** and **open to everyone** provided they identify themselves
- Users need to foster collaboration and acknowledge the contribution of Data Providers

GISAID submission modes and rich meta-data => Quality



Virus detail

Virus name*
hCoV-19/Country/Identifier/2021
Accession ID
Type: betacoronavirus
Passage details/history*
Example: Original, Vero

Sample information

Collection date*
Example: 2021-03-27, 2021-03 (collection in
Location*
Continent / Country / Region
Additional location information: *Travel history; Residence; Cruise ship; ...*
Host*
Example: Human, Environment, Canine, Manis javanica, Rhinolophus affinis, unknown
Additional host information
Example: Underlying health conditions; other host relevant characteristics
Outbreak Detail
Example: Date, Place, Family cluster
Sampling strategy: *Baseline surveillance; Active surveillance; Clinical trial; ...*
Gender*
Patient age*
Patient status*
Specimen source
Last vaccinated
Treatment
Example: Include drug name, dosage
Sequencing technology*
Example: Illumina Miseq, Sanger, Nanopore MinION, Ion To
Assembly method
Example: CLC Genomics Workbench 12, Geneious 10.2.4, SPAdes/MEGAHIT v1.2.9, UGENE v. 33, etc.
Coverage
Example: 70x, 1,000x, 10,000x (average)

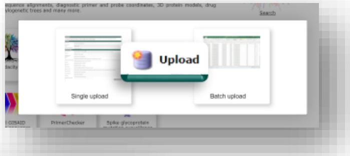
- Baseline surveillance
- Active surveillance
- Clinical trial
- Outbreak investigation
- Research - specific population
- Same-patient sampling strategy
- Sentinel surveillance (ILI)
- Sentinel surveillance (ARI)
- Sentinel surveillance (SARI)
- Sentinel surveillance (other)
- Wastewater testing
- Other

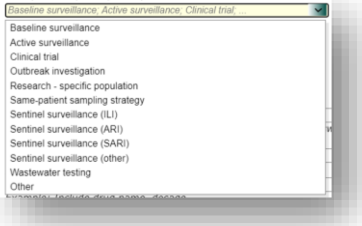
plus CLI (command line interface)

- Team across time zones to ensure 24/7 curation of data and active dialogue with submitters
- Average ~280 daily email exchanges with EpiCoV users and submitters since start of pandemic

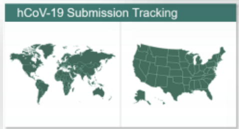
GISAID EpiCoV tools => Insights

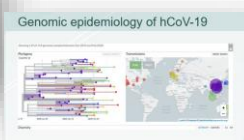
- Submission/Curation
  - New fields: sampling strategy
- Tools on the outside:
  - Submission tracker map
  - Genomic epidemiology
  - Variant tracking
- Tools on the inside:
  - Reporting:
    - Analysis reports and downloads
    - Audacity
    - PrimerChecker
    - EpiCoV search
  - New variants:
    - CoVsurver
    - Spike mutation surveillance
    - Emerging Variants
    - CoVizu
  - Contact Tracing:
    - Audacity Instant
    - BLAST



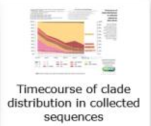

Baseline surveillance; Active surveillance; Clinical trial;

Baseline surveillance
Active surveillance
Clinical trial
Outbreak investigation
Research - specific population
Same-patient sampling strategy
Sentinel surveillance (ILI)
Sentinel surveillance (ARI)
Sentinel surveillance (SARI)
Sentinel surveillance (other)
Wastewater testing
Other

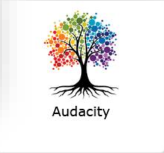

hCoV-19 Submission Tracking


Genomic epidemiology of hCoV-19


hCoV-19 Tracking of Variants

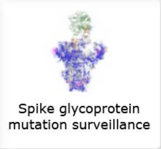

Timecourse of clade distribution in collected sequences


Regional clade distribution of new sequences

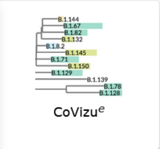

Audacity


PrimerChecker


Search

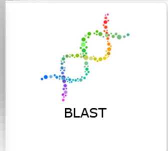

Spike glycoprotein mutation surveillance


Emerging Variants



CoVizu^e^

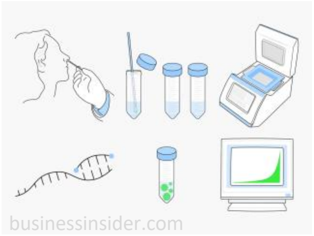

AudacityInstant


BLAST

Supported by BII/GIS, A*STAR Singapore

Insights: Value of real-time genomic surveillance

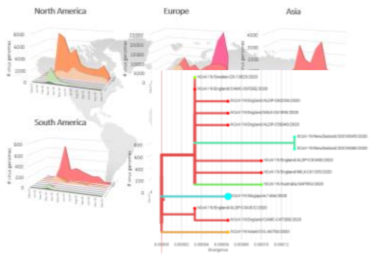
- Can you detect it?



businessinsider.com

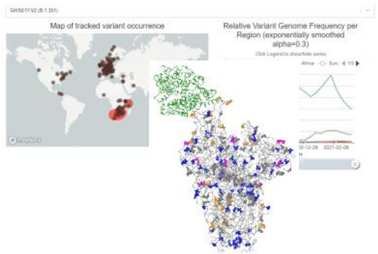
Check if mutations affect diagnostic kits

- How is it spreading?



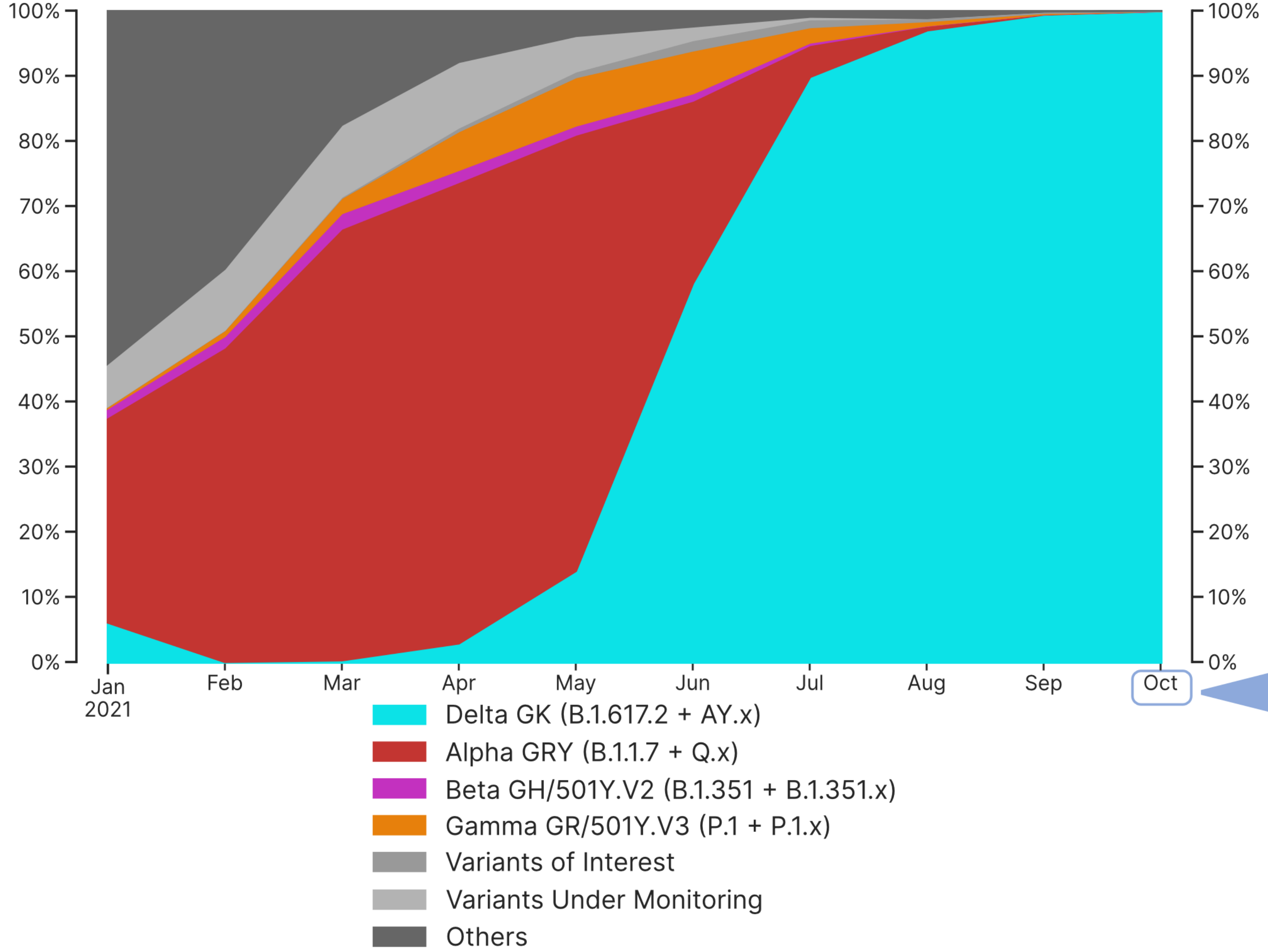
Global clade trends, Contact tracing

- Do vaccines work?



Variants with changes affecting receptor or antibody binding

Timecourse of variant distribution in all submitted sequences 2021-10-22



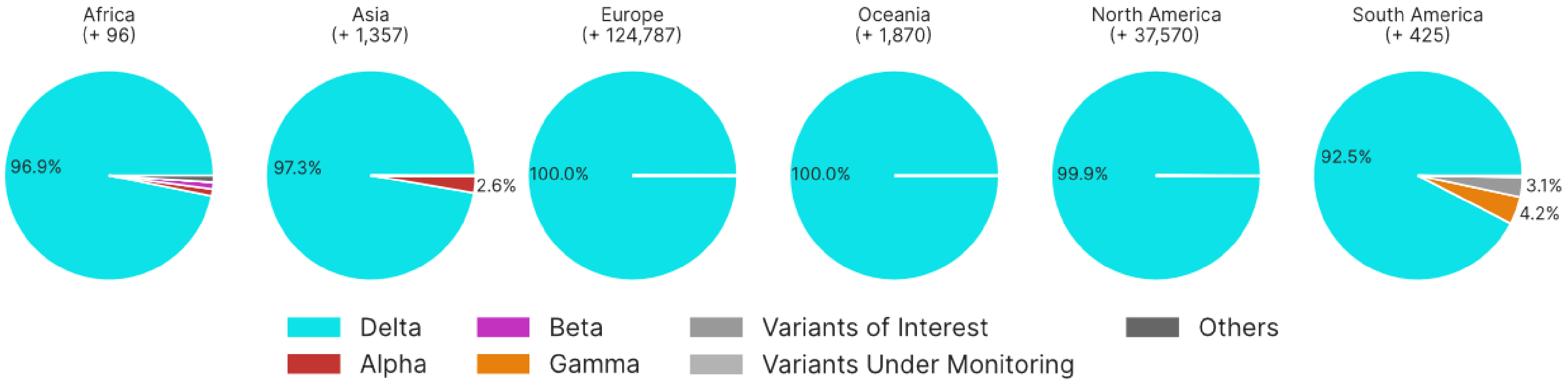
Small and/or Variable Sample Sizes

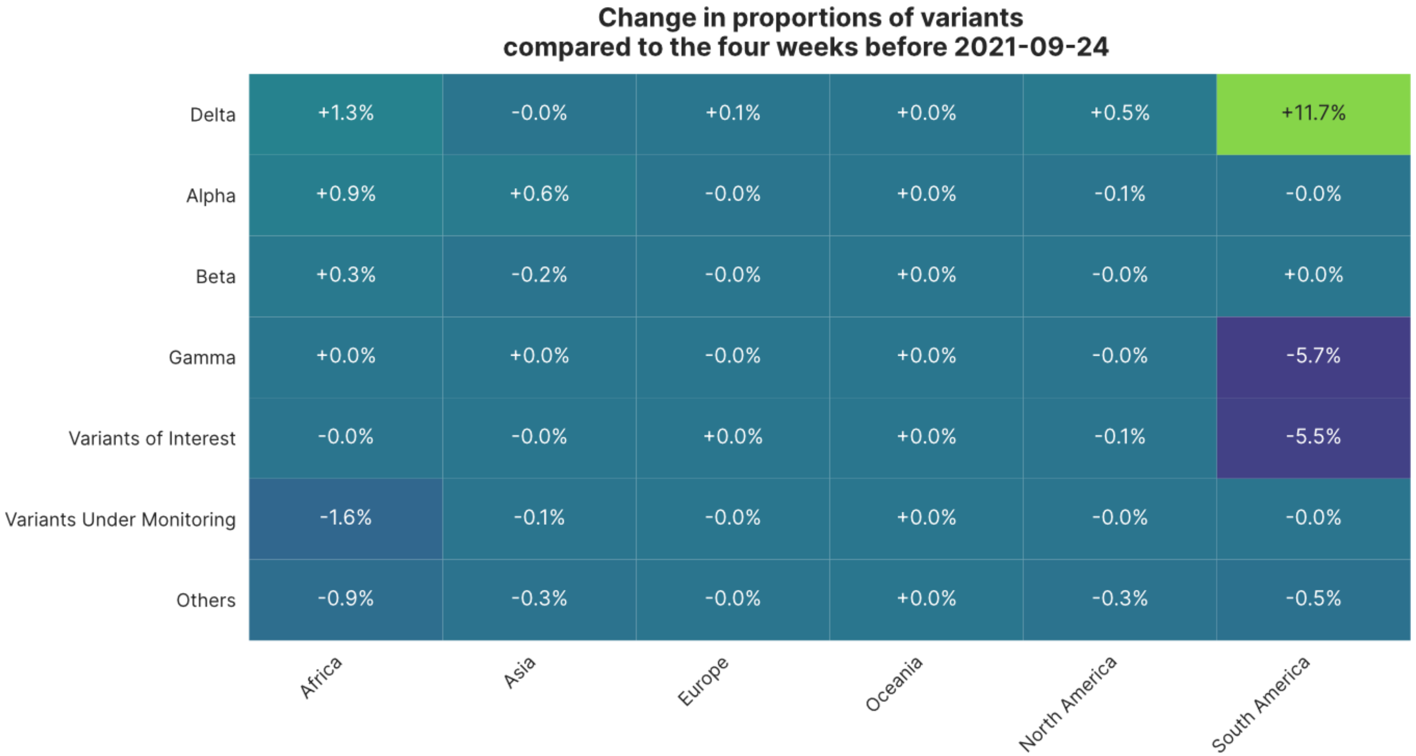
We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

GISAID

by BII/GIS, A*STAR Singapore

Regional distribution of variants in sequences collected from 2021-09-24 to 2021-10-22





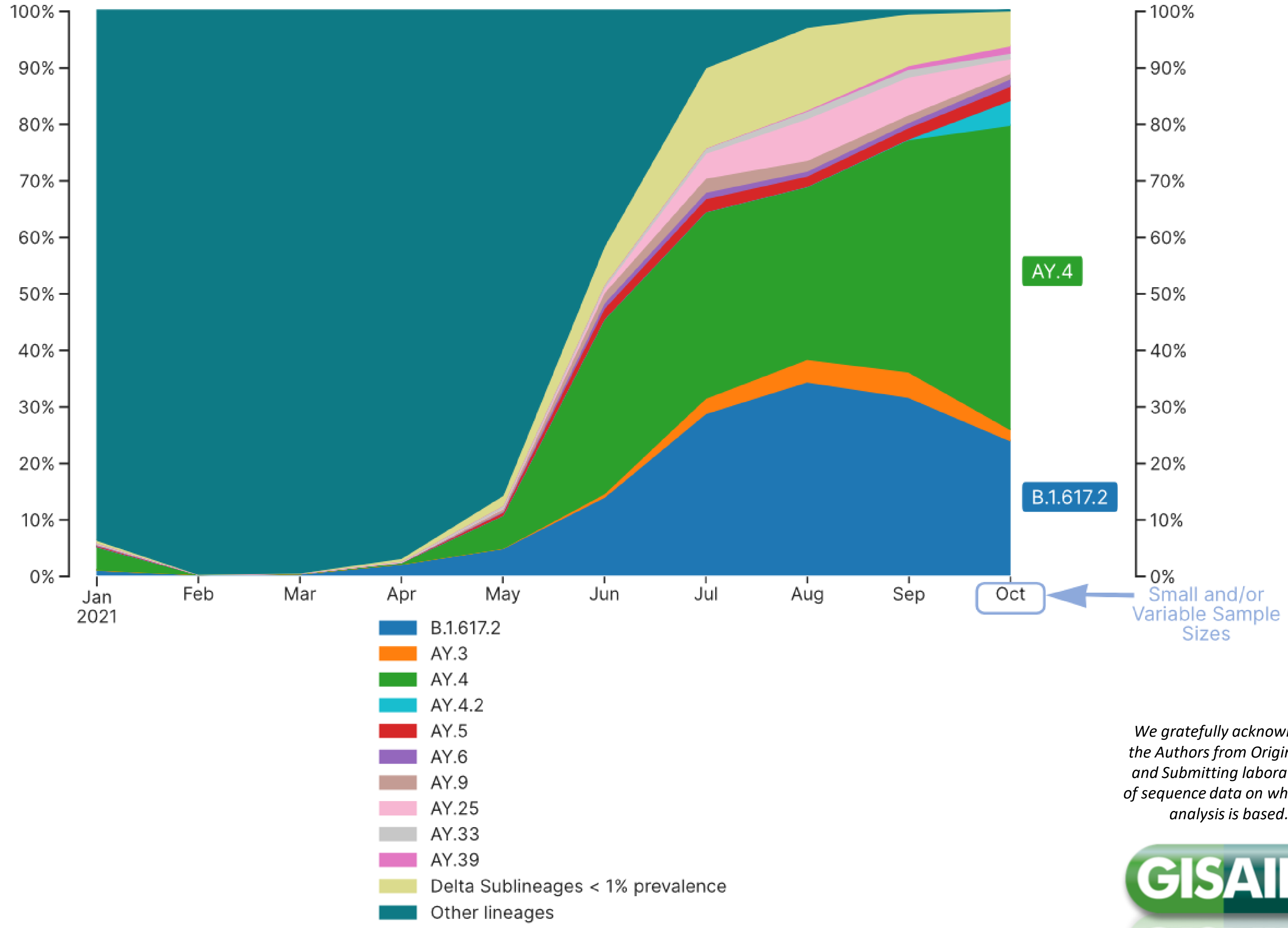
Change in proportions of variants compared to the four weeks before 2021-09-24

	Africa	Asia	Europe	Oceania	North America	South America
Delta	+1.3%	-0.0%	+0.1%	+0.0%	+0.5%	+11.7%
Alpha	+0.9%	+0.6%	-0.0%	+0.0%	-0.1%	-0.0%
Beta	+0.3%	-0.2%	-0.0%	+0.0%	-0.0%	+0.0%
Gamma	+0.0%	+0.0%	-0.0%	+0.0%	-0.0%	-5.7%
Variants of Interest	-0.0%	-0.0%	+0.0%	+0.0%	-0.1%	-5.5%
Variants Under Monitoring	-1.6%	-0.1%	-0.0%	+0.0%	-0.0%	-0.0%
Others	-0.9%	-0.3%	-0.0%	+0.0%	-0.3%	-0.5%

See https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ for variant information and definitions

by BII/GIS, A*STAR Singapore

Timecourse of Delta variant sublineage distribution in all submitted sequences 2021-10-22



See https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ for variant information and definitions

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GISAID

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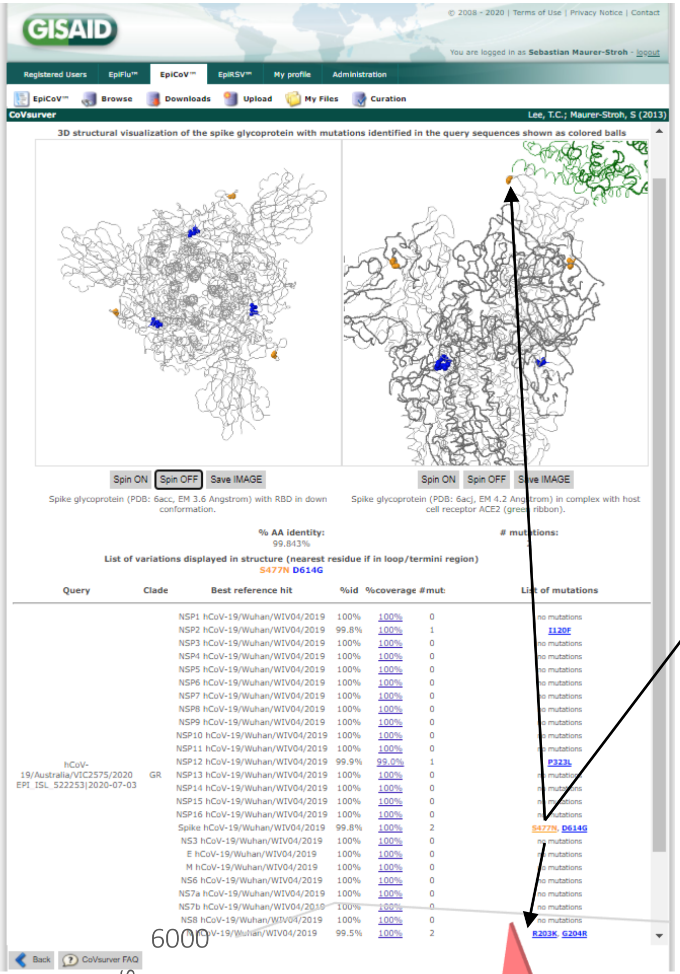
CoVsurver real-time surveillance for mutations that can affect vaccines



CoVsurver Lee, T.C.; Maurer-Stroh, S (2013)

3D structural visualization of the spike glycoprotein with mutations identified in the query sequences shown as colored balls

Spike glycoprotein (PDB: 6acc, EM 3.6 Angstrom) with RBD in down conformation.

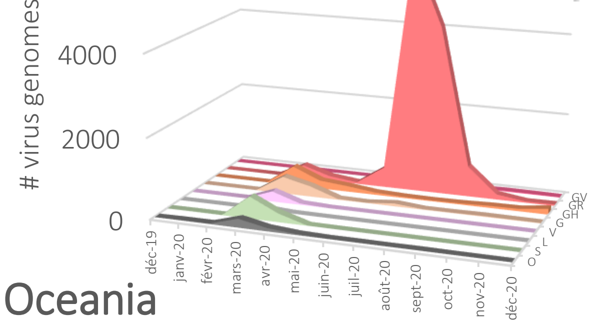
Spike glycoprotein (PDB: 6acj, EM 4.2 Angstrom) in complex with host cell receptor ACE2 (green ribbon).

% AA identity: 99.843%

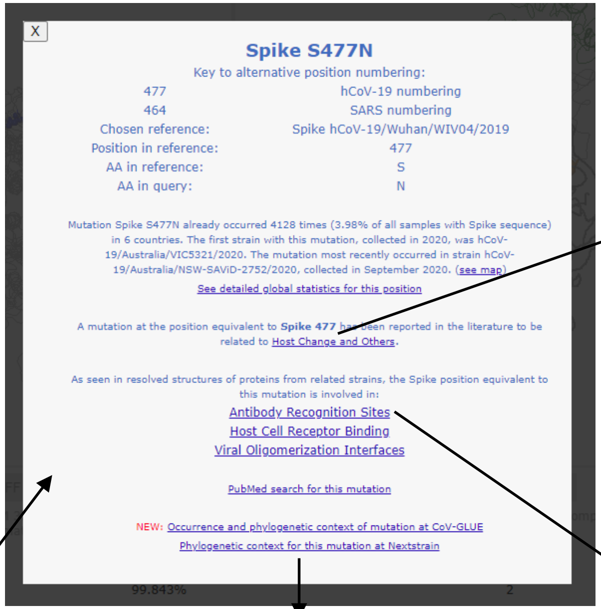
 # mutations:

List of variations displayed in structure (nearest residue if in loop/termini region)
S477N D614G

Query	Clade	Best reference hit	%id	%coverage	#mut:	List of mutations
hCoV-19/Australia/VIC2575/2020 EPI_ISL_522253|2020-07-03	GR	NSP1 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP2 hCoV-19/Wuhan/WIV04/2019	99.8%	100%	1	I120F
		NSP3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP4 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP5 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP7 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP9 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP10 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP11 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP12 hCoV-19/Wuhan/WIV04/2019	99.9%	99.0%	1	P323L
		NSP13 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP14 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP15 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NSP16 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		Spike hCoV-19/Wuhan/WIV04/2019	99.8%	100%	2	S477N, D614G
		NS3 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		E hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		M hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS6 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS7a hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS7b hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		NS8 hCoV-19/Wuhan/WIV04/2019	100%	100%	0	no mutations
		N hCoV-19/Wuhan/WIV04/2019	99.5%	100%	2	R203K, G204R



Oceania



Spike S477N

Key to alternative position numbering:

477	hCoV-19 numbering
464	SARS numbering
Chosen reference:	Spike hCoV-19/Wuhan/WIV04/2019
Position in reference:	477
AA in reference:	S
AA in query:	N

Mutation Spike S477N already occurred 4128 times (3.98% of all samples with Spike sequence) in 6 countries. The first strain with this mutation, collected in 2020, was hCoV-19/Australia/VIC5321/2020. The mutation most recently occurred in strain hCoV-19/Australia/NSW-SAViD-2752/2020, collected in September 2020. (see map)

See detailed global statistics for this position

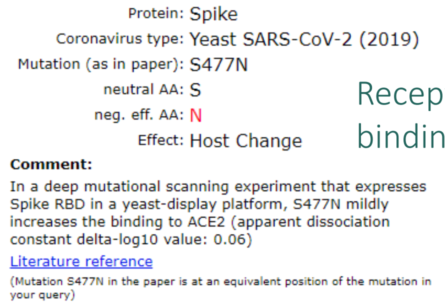
A mutation at the position equivalent to **Spike 477** has been reported in the literature to be related to Host Change and Others.

As seen in resolved structures of proteins from related strains, the Spike position equivalent to this mutation is involved in:

Antibody Recognition Sites
Host Cell Receptor Binding
Viral Oligomerization Interfaces

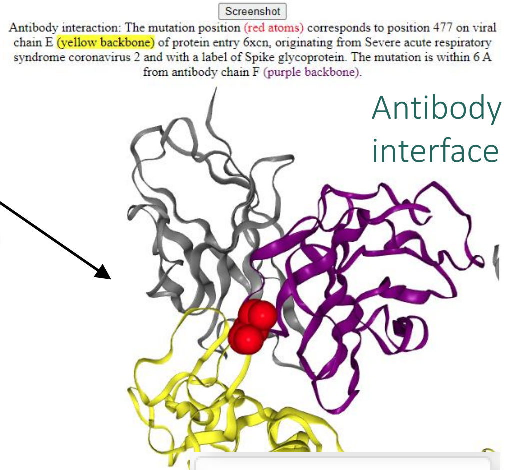
PubMed search for this mutation

NEW: Occurrence and phylogenetic context of mutation at CoV-GLUE
Phylogenetic context for this mutation at Nextstrain


Protein: Spike
Coronavirus type: Yeast SARS-CoV-2 (2019)
Mutation (as in paper): S477N
neutral AA: S
neg. eff. AA: N
Effect: Host Change

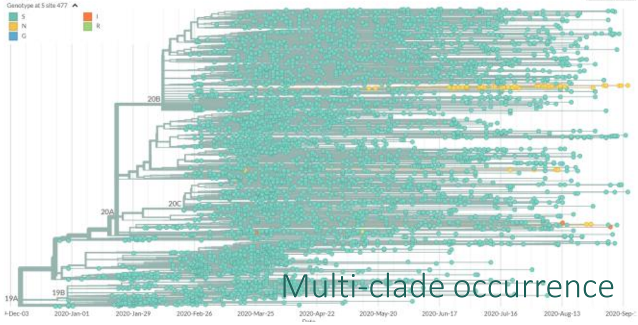
Comment:
In a deep mutational scanning experiment that expresses Spike RBD in a yeast-display platform, S477N mildly increases the binding to ACE2 (apparent dissociation constant delta-log10 value: 0.06)
Literature reference
(Mutation S477N in the paper is at an equivalent position of the mutation in your query)

Receptor binding



Antibody interaction: The mutation position (red atoms) corresponds to position 477 on viral chain E (yellow backbone) of protein entry 6xcn, originating from Severe acute respiratory syndrome coronavirus 2 and with a label of Spike glycoprotein. The mutation is within 6 A from antibody chain F (purple backbone).

Antibody interface

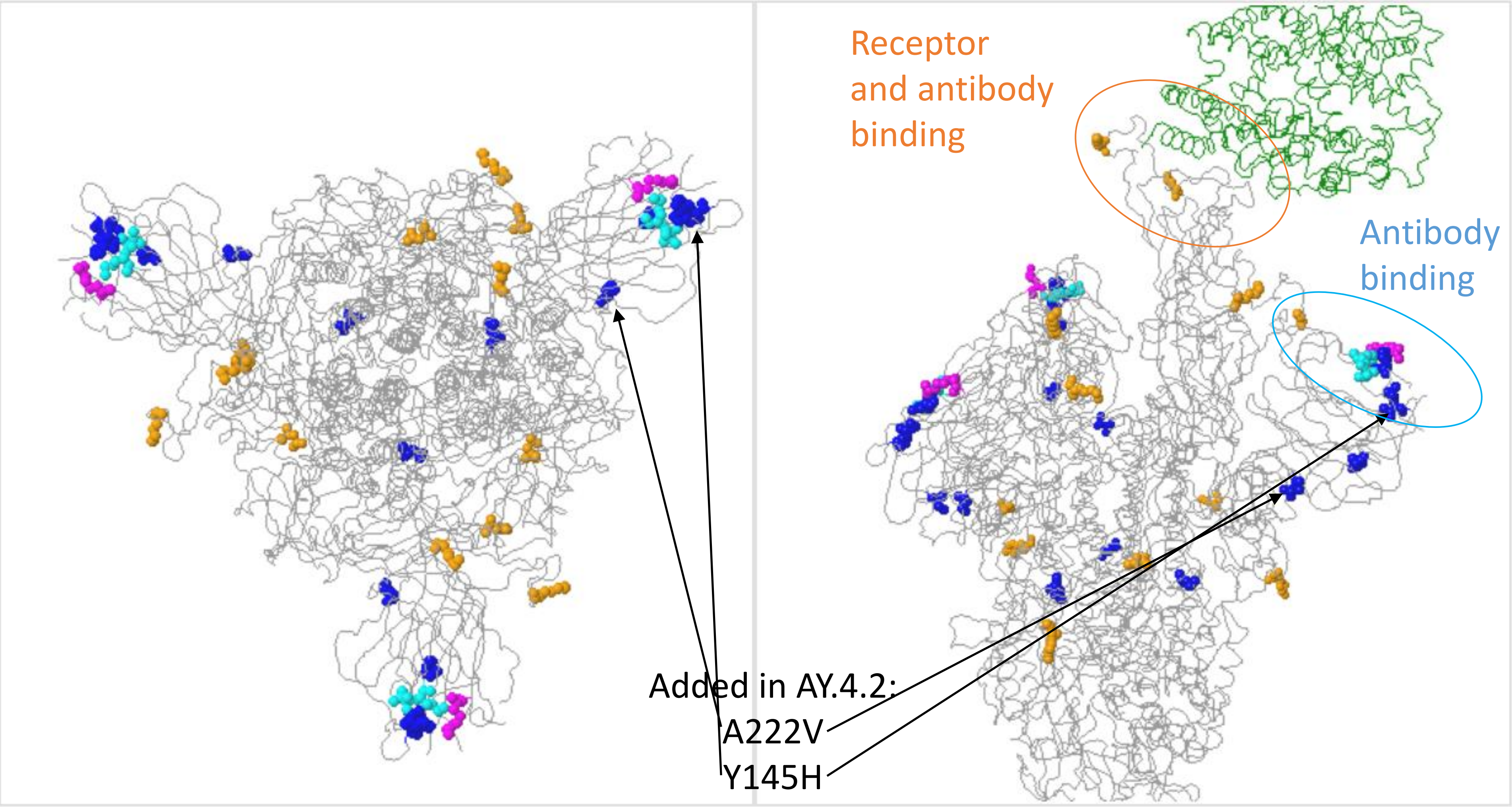


Multi-clade occurrence

1,680 variant phenotype annotations from literature plus 3,826 3D interactions

Supported by BII/GIS, A*STAR Singapore

Variation within Delta: AY.4.2



Receptor and antibody binding

Antibody binding

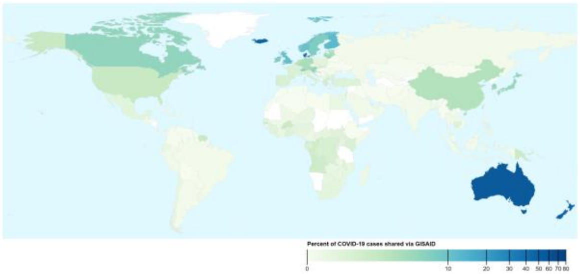
Added in AY.4.2:
A222V
Y145H

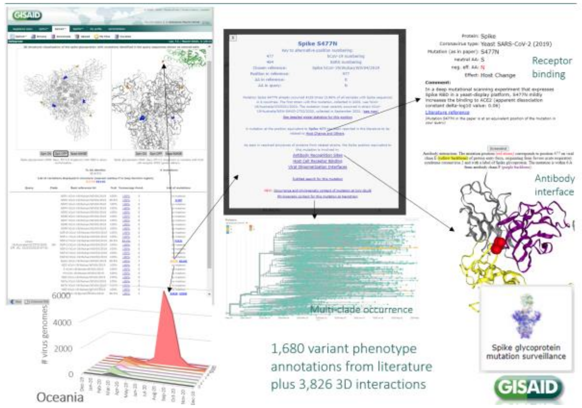
- A222V has been part of “summer variant” (clade GV) in 2020 and might have slight fitness effect through stability changes.
- Y145H is partially exposed to antibody binding sites in the NTD and might contribute mildly to vaccine efficacy changes. Y145H is sometimes missed through sequencing with the older Arctic 3 protocol.

Trust, Quality and Insights enable the value of real-time virus genomic surveillance

- Trusted sharing platform
- Global 24/7 quality checks
- The right analysis tools

Thank You!





1,680 variant phenotype annotations from literature plus 3,826 3D interactions

Global Influenza
Hospital Surveillance
Network

www.gihsn.org

GIHSN 9TH ANNUAL MEETING, 25-26 OCTOBER 2021

GISRS AND COVID-19 IMPACT

Dr Vanessa COZZA, Global Influenza Program, WHO

Foundation for
Influenza
Epidemiology

Sous l'égide de
Fondation
de
France

World Health
Organization

GISRS and COVID-19 impact

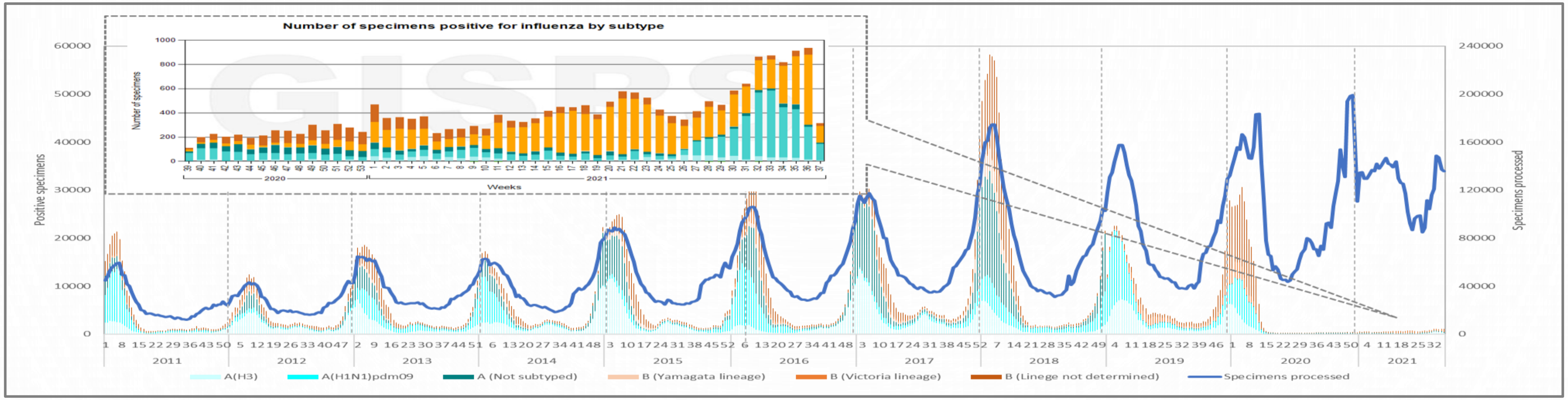
Global Influenza Programme

GIHSN Annual Meeting 2021
25 October 2021 • Virtual meeting

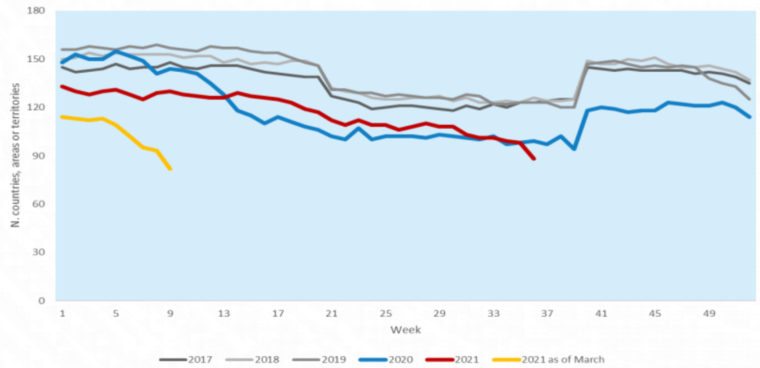
GLOBAL
INFLUENZA
STRATEGY
2019 – 2030
Prevent. Control. Prepare.

GISRS
GLOBAL INFLUENZA
SURVEILLANCE &
RESPONSE SYSTEM
Uniting the world in the fight against influenza

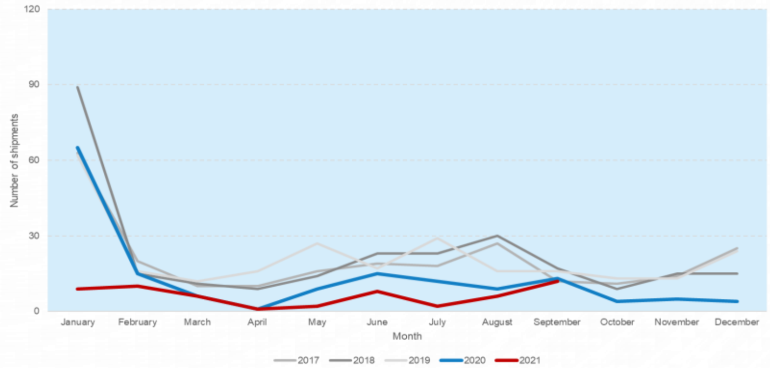
COVID-19 pandemic impacted on GISRS



Reporting flu data to FluNET



Virus shipments to WHO CCs – SFP



INFLUENZA PREPAREDNESS & RESPONSE

Integrated surveillance of influenza and SARS-CoV-2

Nov 2020

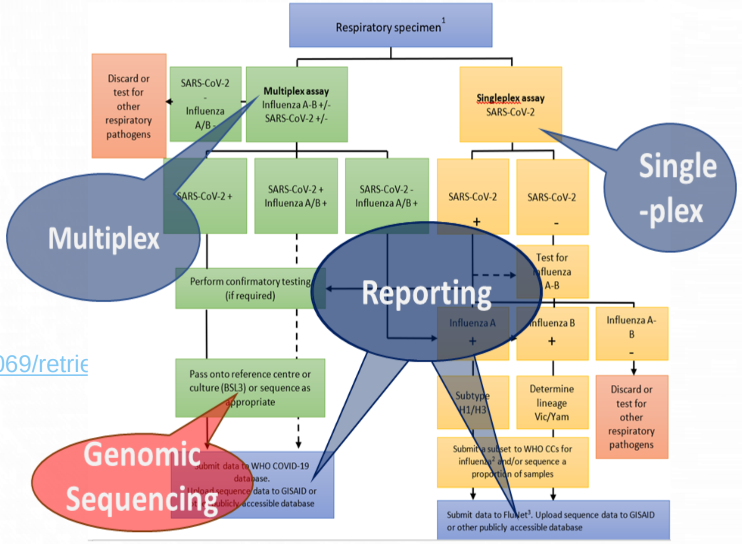

GLOBAL INFLUENZA PROGRAMME

Maintaining surveillance of influenza and monitoring SARS-CoV-2
adapting Global Influenza Surveillance and Response System (GISRS) and sentinel systems during the COVID-19 pandemic

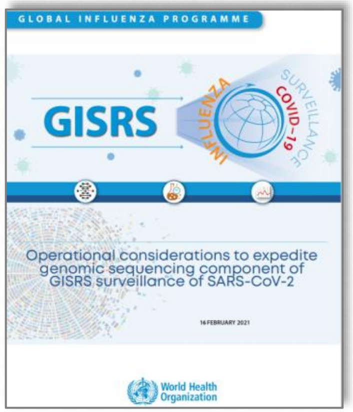
INTERIM GUIDANCE

6 NOVEMBER 2020

https://apps.who.int/iris/rest/bitstreams/1316069/retrie



Feb 2021


GLOBAL INFLUENZA PROGRAMME

Operational considerations to expedite genomic sequencing component of GISRS surveillance of SARS-CoV-2

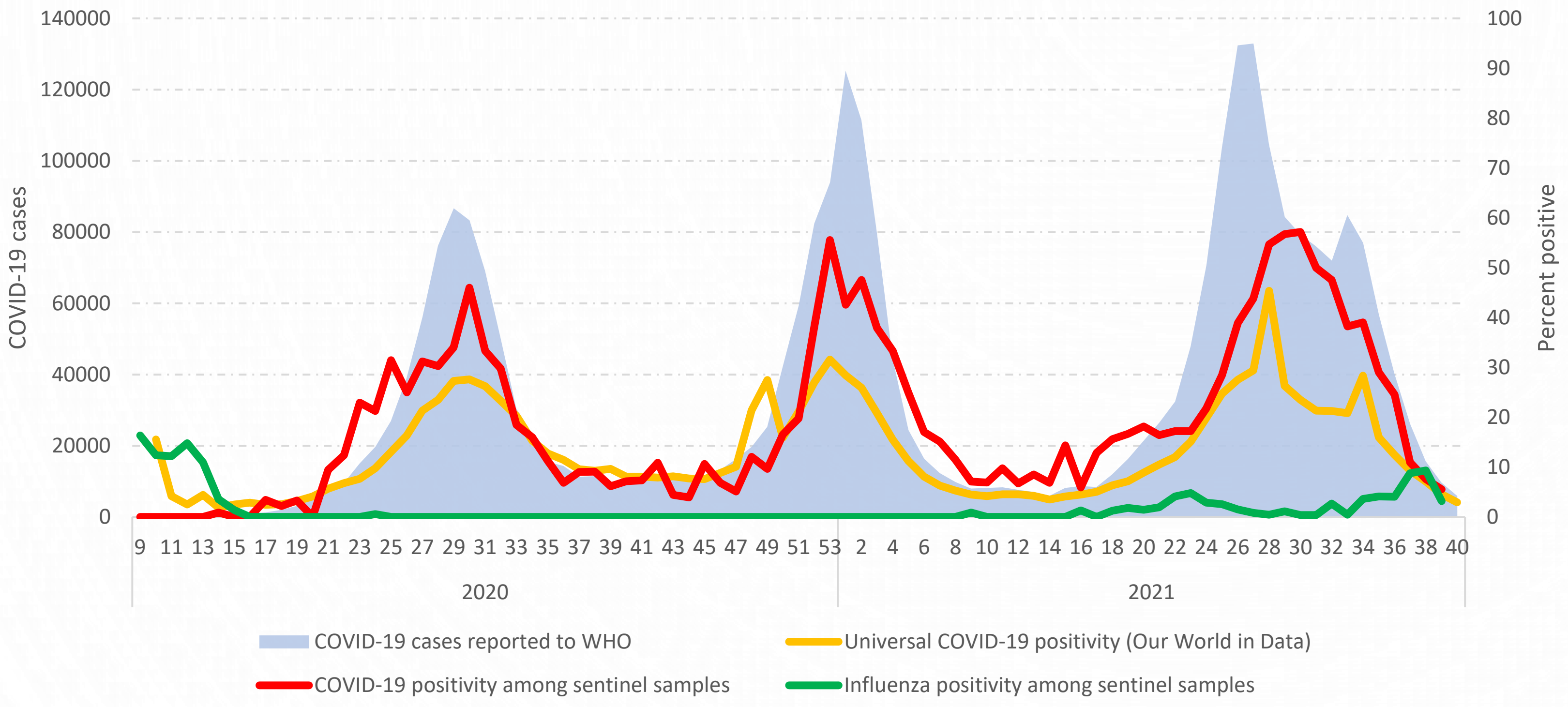
16 FEBRUARY 2021

https://www.who.int/publications/i/item/WHO-2019-nCoV-genomic-sequencing-GISRS-2021.1

- **Diagnostic support**
  - Flu – SARS-CoV-2 multiplex from WHO CC (US CDC) via influenza surveillance reagent resource channel – free of charge
- **Experience sharing webinars and trainings**
  - Bioinformatics, Multiplex, Reporting to FluMart
- **Demonstration project (27 countries: 23LMICs)**
  - To develop best practice models for the E2E integration of influenza and SARS-CoV-2 virologic and genomic surveillance
- **WHO EQA – 2021**
  - 20th WHO EQAP for influenza
  - 2nd WHO EQAP for SARS-CoV-2

Integrated sentinel surveillance of influenza & SARS-CoV-2

- a country example



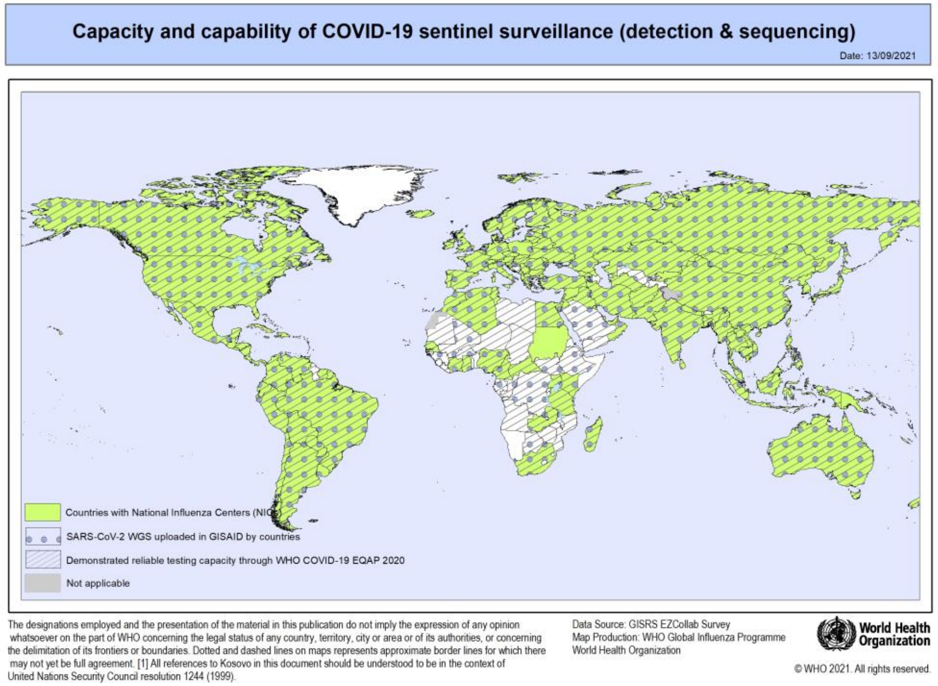
- COVID-19 **trends** from sentinel surveillance and universal testing **match** well
- Testing **~1500 times LESS** specimens in sentinel surveillance
- Testing an average of **142 specimens per week** from sentinel surveillance **monitors both** influenza and SARS-CoV-2 at the same time.

Every week:

Average number of sentinel samples tested for *COVID-19* and *influenza*	**142**
Average number of specimens in *COVID-19* universal testing	**209,794**

GISRS sentinel surveillance of influenza & SARS-CoV-2

- GISRS capacity for SARS-CoV-2 as of 19 Sep 2021

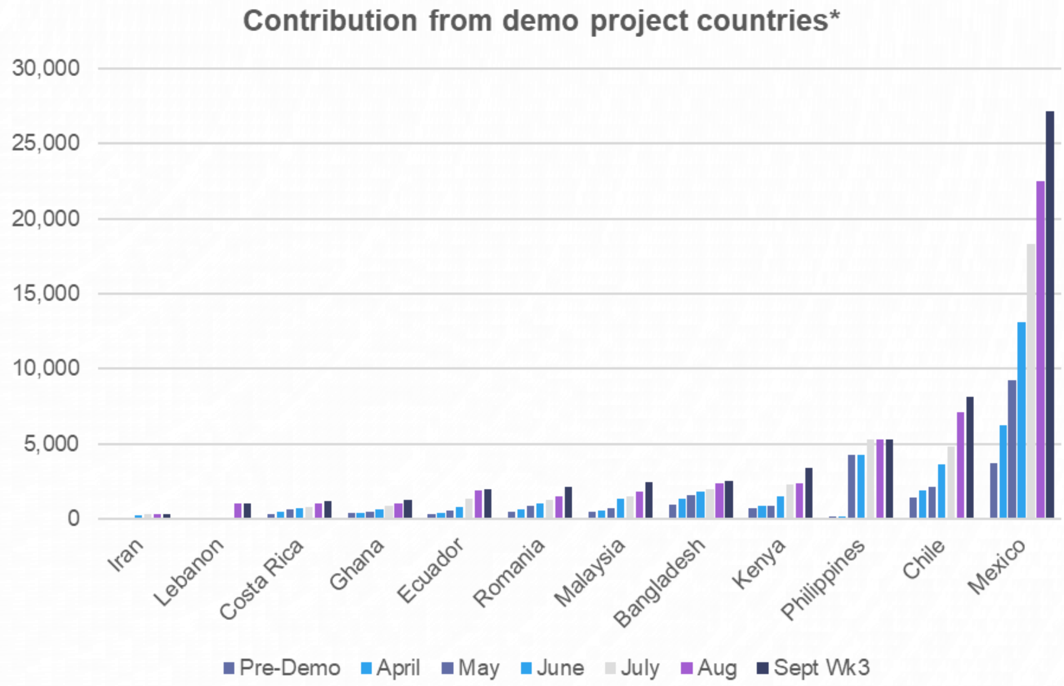


Capacity and capability of COVID-19 sentinel surveillance (detection & sequencing)

Date: 13/09/2021

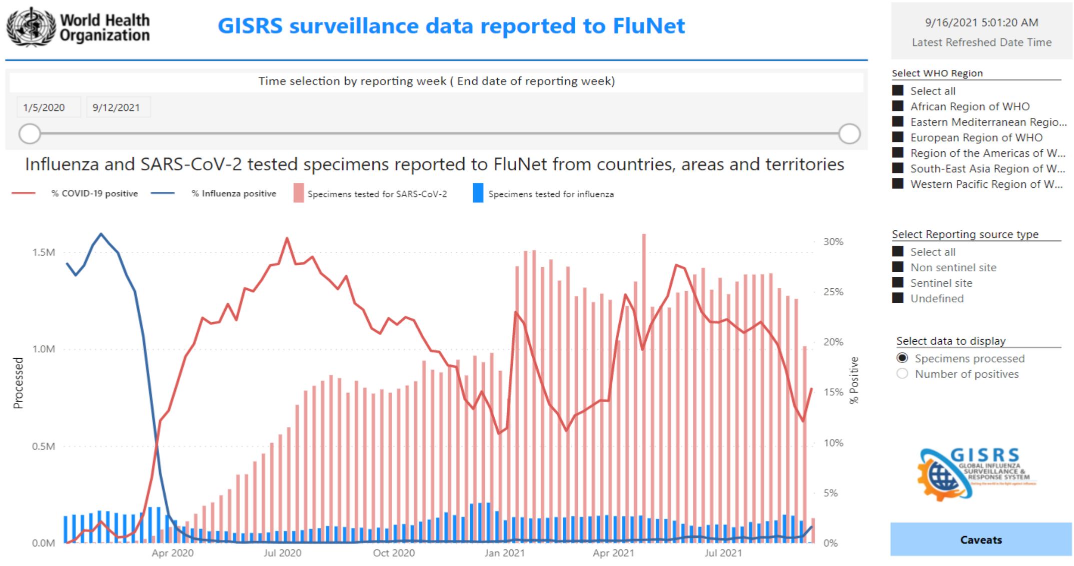
The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represents approximate border lines for which there may not yet be full agreement. [1] All references to Kosovo in this document should be understood to be in the context of United Nations Security Council resolution 1244 (1999).

Data Source: GISRS EZCollab Survey
Map Production: WHO Global Influenza Programme
World Health Organization



- At least 79**% GISRS labs** submitted WGS to GISAID
  - **123 labs from 104 countries**
- 68 **GISRS labs** support sequencing for other GISRS and non-GISRS labs

Influenza – SARS-CoV-2 outputs



World Health Organization

GISRS surveillance data reported to FluNet

9/16/2021 5:01:20 AM
Latest Refreshed Date Time

Time selection by reporting week (End date of reporting week)

1/5/2020 9/12/2021

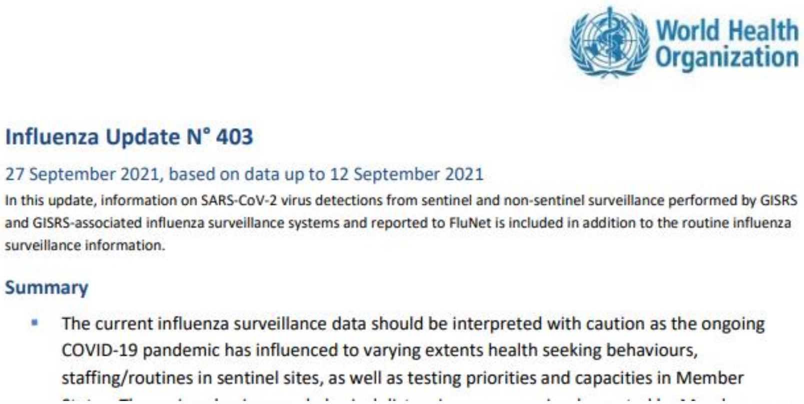
Influenza and SARS-CoV-2 tested specimens reported to FluNet from countries, areas and territories

Select WHO Region
- ■ Select all
- ■ African Region of WHO
- ■ Eastern Mediterranean Regio...
- ■ European Region of WHO
- ■ Region of the Americas of W...
- ■ South-East Asia Region of W...
- ■ Western Pacific Region of W...

Select Reporting source type
- ■ Select all
- ■ Non sentinel site
- ■ Sentinel site
- ■ Undefined

Select data to display
- ● Specimens processed
- ○ Number of positives

Dashboard: Influenza-SARS-CoV-2 dashboard



World Health Organization

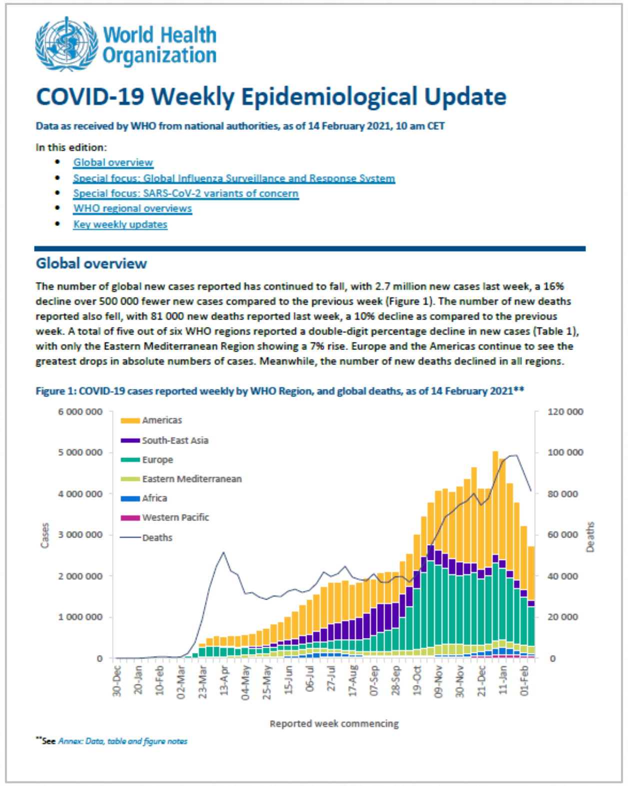
Influenza Update N° 403

27 September 2021, based on data up to 12 September 2021

In this update, information on SARS-CoV-2 virus detections from sentinel and non-sentinel surveillance performed by GISRS and GISRS-associated influenza surveillance systems and reported to FluNet is included in addition to the routine influenza surveillance information.

Summary

- The current influenza surveillance data should be interpreted with caution as the ongoing COVID-19 pandemic has influenced to varying extents health seeking behaviours, staffing/routines in sentinel sites, as well as testing priorities and capacities in Member



World Health Organization

COVID-19 Weekly Epidemiological Update

Data as received by WHO from national authorities, as of 14 February 2021, 10 am CET

In this edition:
- Global overview
- Special focus: Global Influenza Surveillance and Response System
- Special focus: SARS-CoV-2 variants of concern
- WHO regional overviews
- Key weekly updates

Global overview

The number of global new cases reported has continued to fall, with 2.7 million new cases last week, a 16% decline over 500 000 fewer new cases compared to the previous week (Figure 1). The number of new deaths reported also fell, with 81 000 new deaths reported last week, a 10% decline as compared to the previous week. A total of five out of six WHO regions reported a double-digit percentage decline in new cases (Table 1), with only the Eastern Mediterranean Region showing a 7% rise. Europe and the Americas continue to see the greatest drops in absolute numbers of cases. Meanwhile, the number of new deaths declined in all regions.

Figure 1: COVID-19 cases reported weekly by WHO Region, and global deaths, as of 14 February 2021**

**See *Annex: Data, table and figure notes*

https://www.who.int/teams/global-influenza-programme/influenza-covid19

Acknowledgement

- **WHO Global Influenza Programme**
- **WHO Regional Offices**

- **WHO GISRS** (Global Influenza Surveillance and Response System)
- GISRS associated **national/sub-national surveillance systems**
- **Countries** hosting GISRS institutions
- **GISAID**

Thank You

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LYON CENTER OF EXCELLENCE ON RESPIRATORY PATHOGENS (CERP)

Pr Bruno LINA, Lyon University

Foundation for
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CENTRE OF EXCELLENCE ON RESPIRATORY PATHOGENS (LYON)

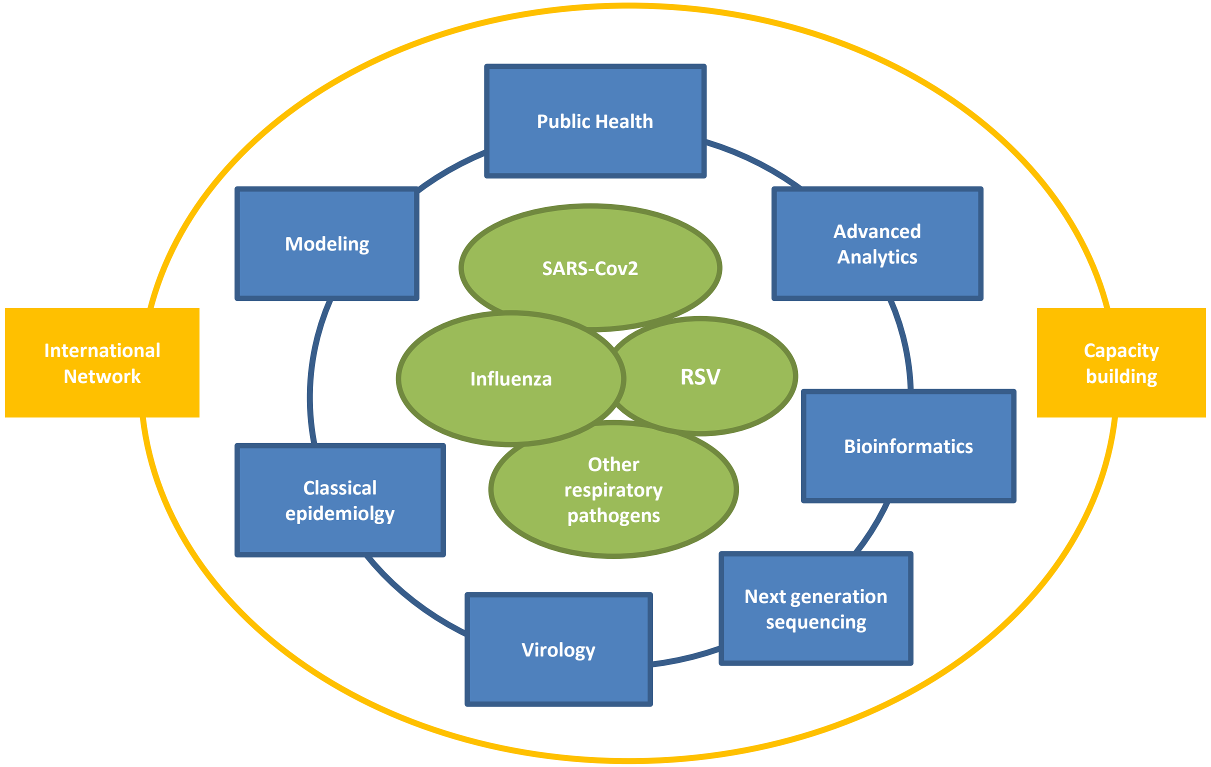
- Public – Private partnership between the Hospices Civils de Lyon (HCL) and SANOFI

- Build on existing competencies and collaborations
  - National reference centre for repiratory viruses (Incl. Influenza and emerging viruses)
  - GENEPII sequencing platform hosted by HCL
  - GIHSN sequencing facility (Staff and equipment)
  - DRIVE and CoviDRIVE european projects

THE VISION AND AMBITIONS

- Vision: To set up a global center of excellence in Lyon generating evidence to support decision making related to respiratory pathogens

- Mission
  - To create excellence in **multi-disciplinary research** combining virology, epidemiology, analytics, biocomputing and modeling.
  - To ensure a continuum from data collection (**surveillance** & capacity building) to **data use for policy making** (analytic, modeling and external engagement).
  - To be a **convener for the major stakeholders working on this thematic** and to develop public-private instruments to ensure synergies of the global investments.



NEXT STEPS

- Co-construction of a roadmap with the various local and global actors (by end 2021)

- Identification of an Industrial Chair to lead the center
    - Expertise in respiratory infectious diseases
    - Strong background in at least one of the following fields (epidemiology, virology, modeling, public health) and a strong entrepreneurship mindset. A clear appreciation for the other aspects and modern data science techniques are expected
    - Mid-level professional - associate professor experience including supervision of students and multi-functional research programs
    - International credibility and strong publication record
    - Leadership, good communication skills
    - Fluent in English and good command of French
    - Willing to relocate to Lyon
    - Previous experience working in collaboration with private sector/industry a plus

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GIHSN 2020-2021: DESCRIPTIVE ANALYSIS & RESULTS

Catherine COMMAILLE-CHAPUS, GIHSN Coordination

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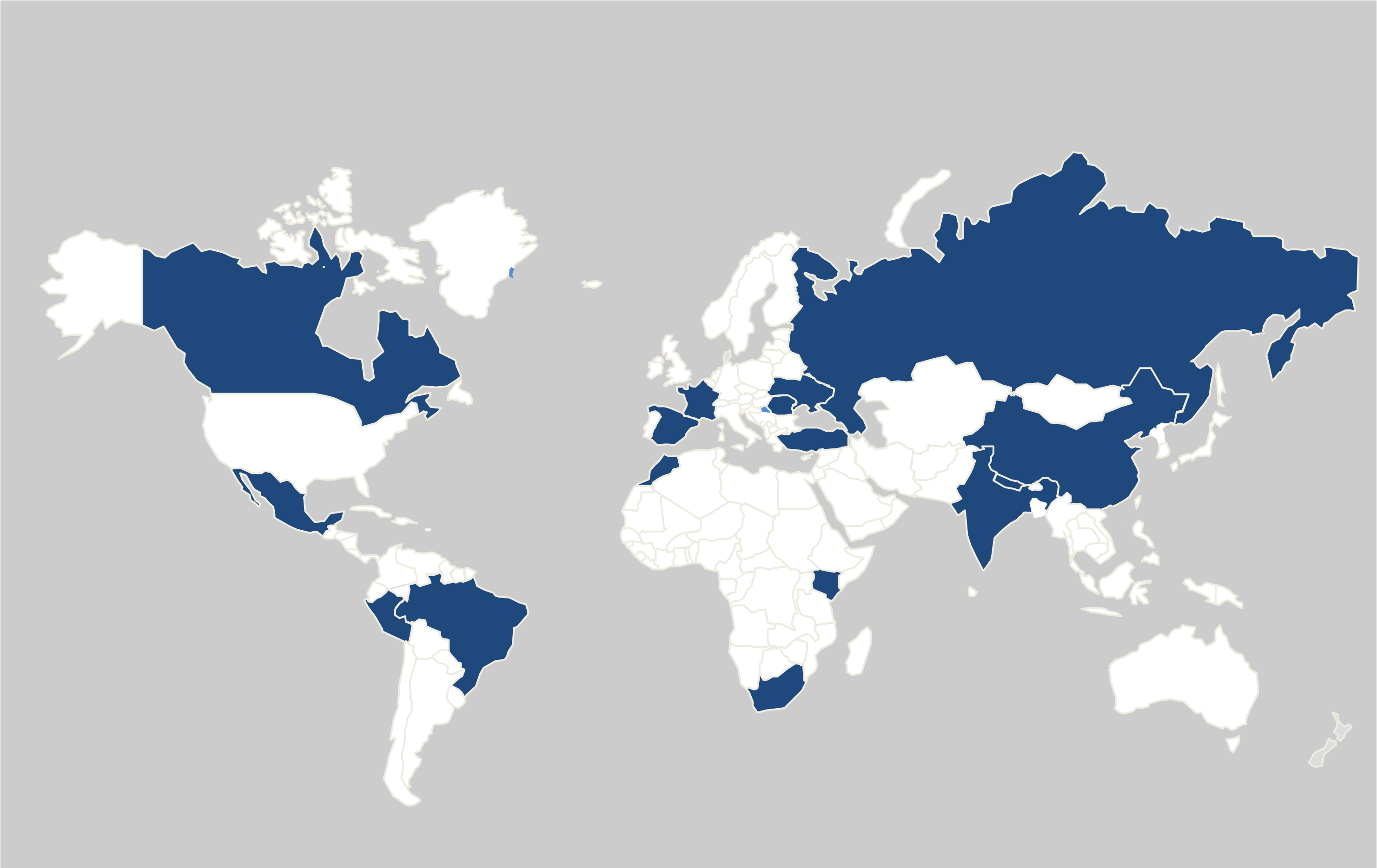
18 SITES (+1) HAVE BEEN PARTICIPATING IN THE GIHSN FOR THE 2020/21 SEASON

North America
Canada
Mexico

South America
Brazil
Peru

Eurasia
France
Romania
Russia-Moscow
Russia-St Pet
Spain
Ukraine



Africa
Kenya
Morocco
South Africa
Ivory Coast

Middle East
Lebanon
Turkey

Asia/Pacific
China-Fudan
India
Nepal

Data collection still on-going

Global Influenza Hospital Surveillance Network

REMINDER: GUIDELINES HAVE BEEN ADAPTED THIS YEAR IN THE CONTEXT OF A VERY LOW FLU ACTIVITY

- Clinical data were to be collected for all respiratory hospitalizations meeting case definition, irrespective of lab test results.
- PCR test were to be done for flu (Priority). If multiplex PCR and/or wet assay for COVID-19 (and RSV and other respiratory viruses) could be performed in addition, it was a strong added value.
- All COVID-19 data and SARS-COV2 testing results were to be entered in GIHSN database.
- All swab samples taken from participating patients were to be stored to allow for further testing if needed after the season.
- WGS was to be done in all flu+ samples at local level or sent to Lyon. If volume was low, sites were encouraged to complete if possible the shipment with SARS-CoV2 positive samples/RNA for sequencing at Lyon lab. The total number of 50-100 WGS per site was expected to be observed
- Sites were encouraged to upload WGS for SARS-COV2 identified in GIHSN participating patients in GISAID (when done locally) with the unique identifier (GIHSN tag)

GIHSN 2020-2021: OVERVIEW

(*DATA COLLECTION STILL ON-GOING*)

#included =
15 533

#LCI =
132

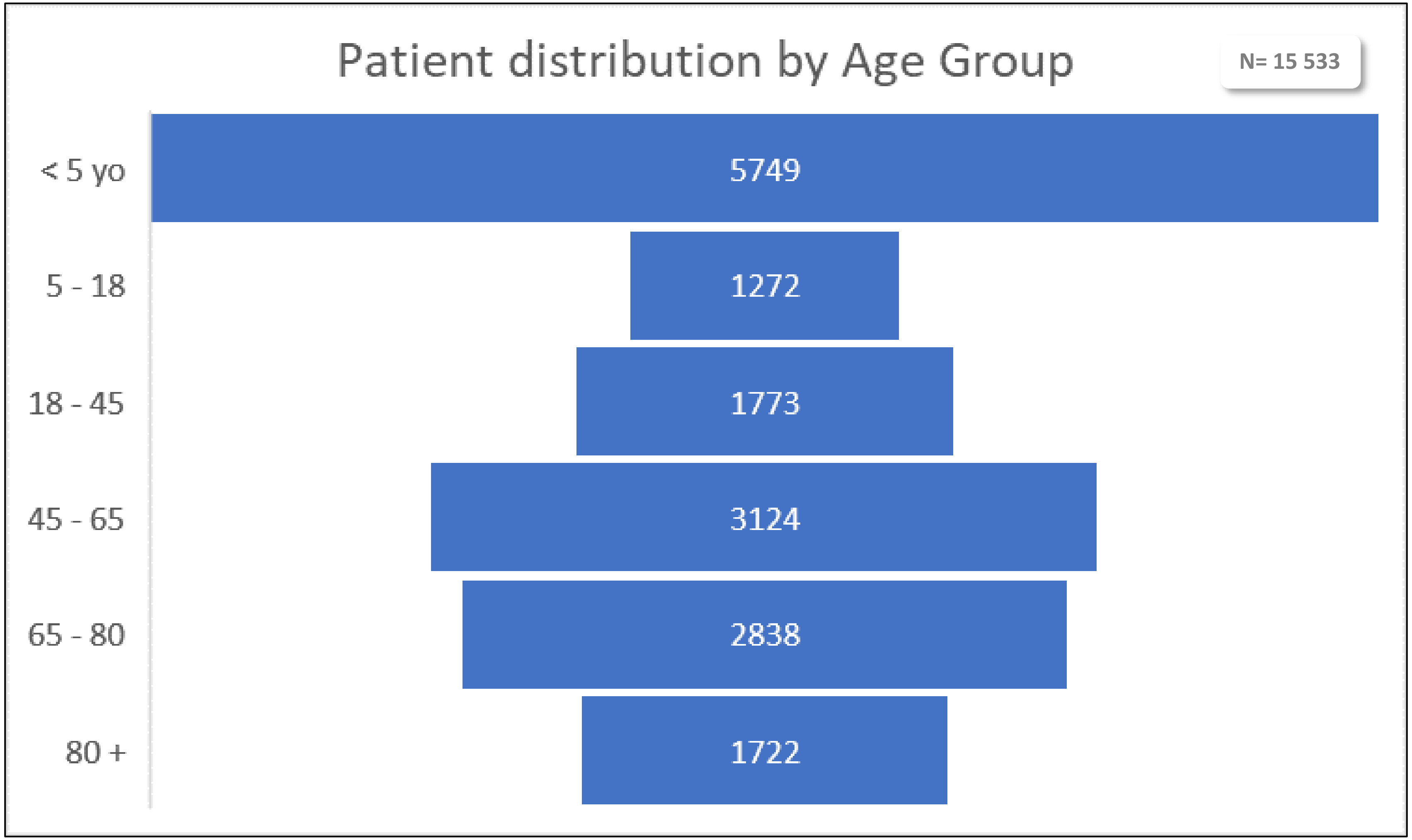
#SARS-CoV2+ =
2 858
(out of 10 029 tested – 28.5%)

#RSV+ =
597
(out of 7513 tested – 7.9%)

#ORV+ =
2 470
(out of 7908 tested – 31.2%)

#WGS (incl 2 flu+) =
273

GIHSN 2020-2021:
PATIENT DISTRIBUTION BY AGE GROUP



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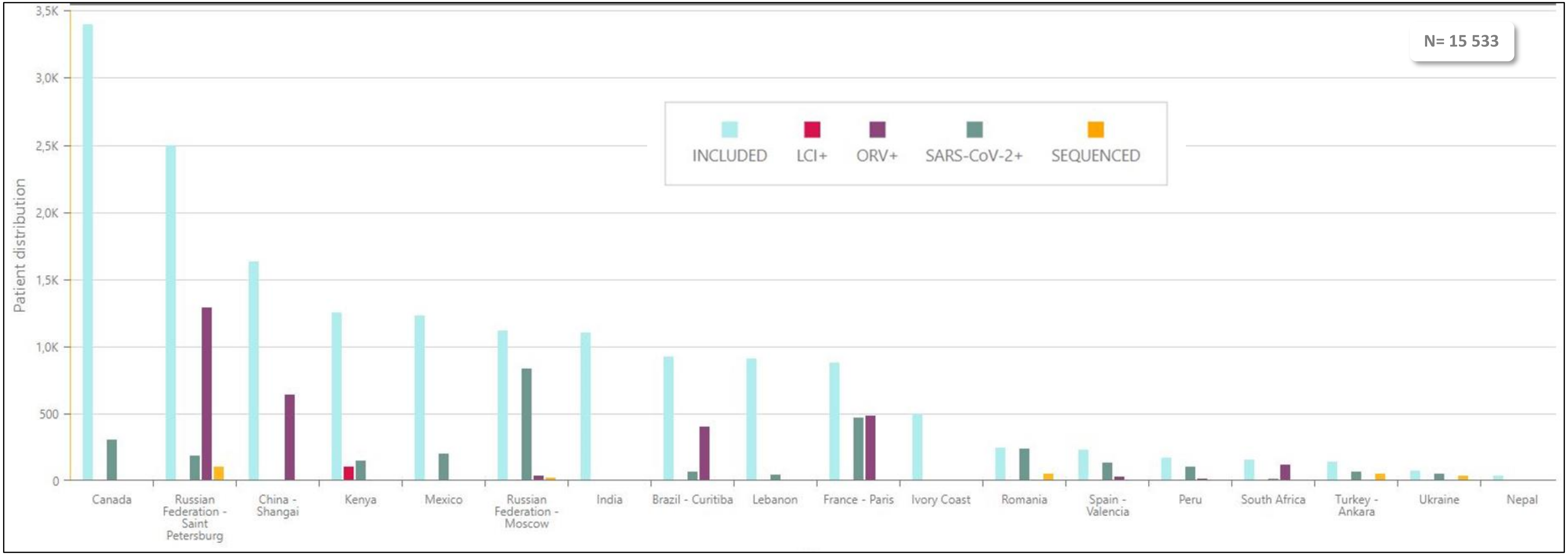
GIHSN 2020-2021:
PATIENT DISTRIBUTION BY SITE (ALL INCLUDED)

21 October 2021



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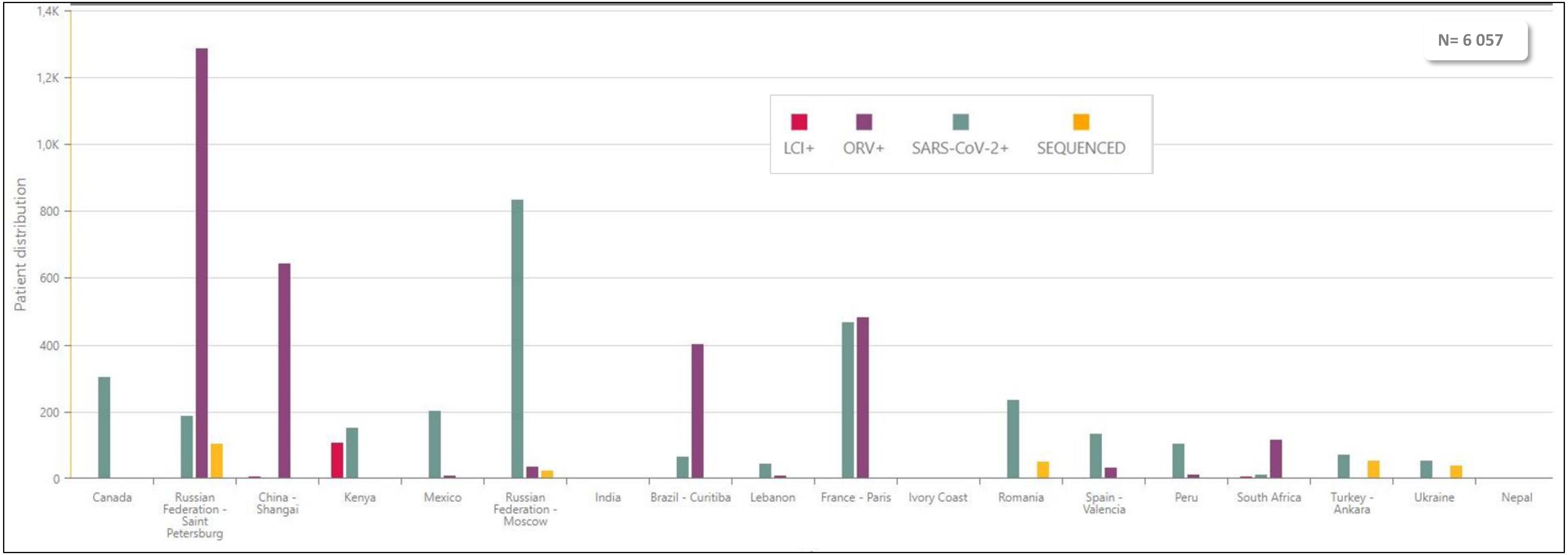
GIHSN 2020-2021:
PATIENT DISTRIBUTION BY SITE (+ CASES ONLY)

21 October 2021



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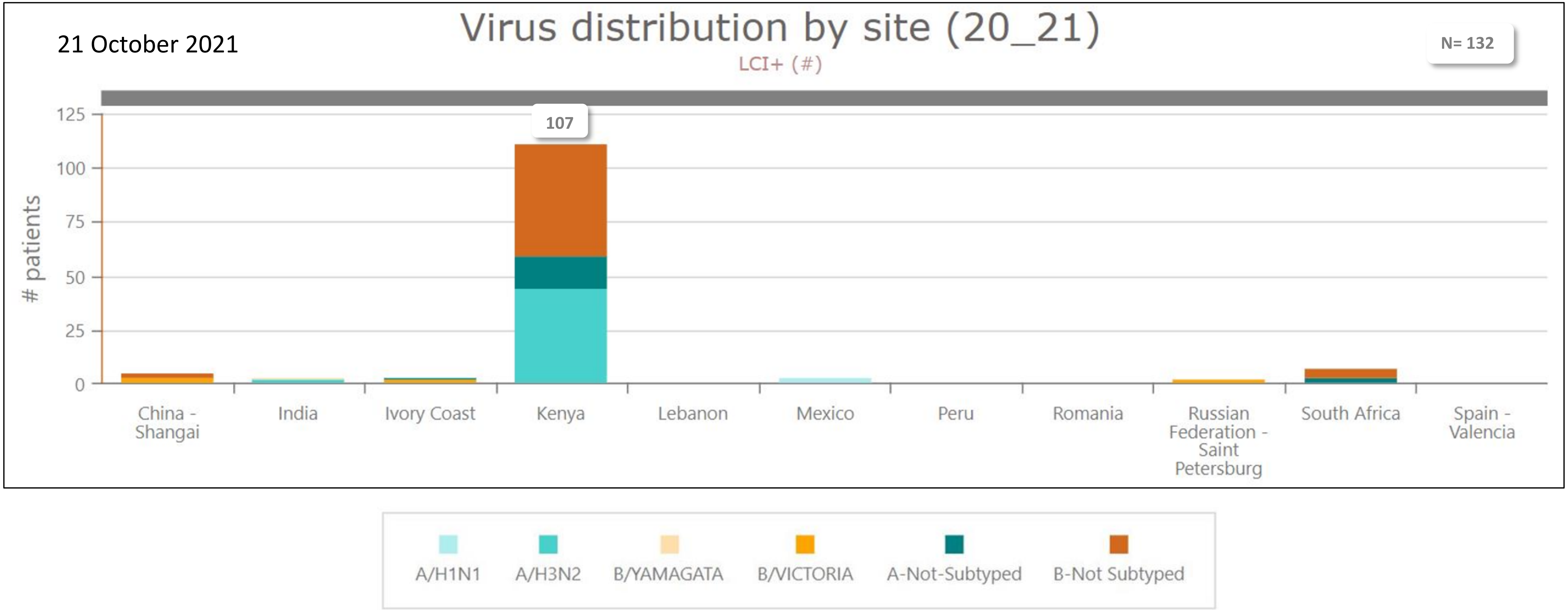
GIHSN 2020-2021:
LCI+: VIRUS DISTRIBUTION BY SITE



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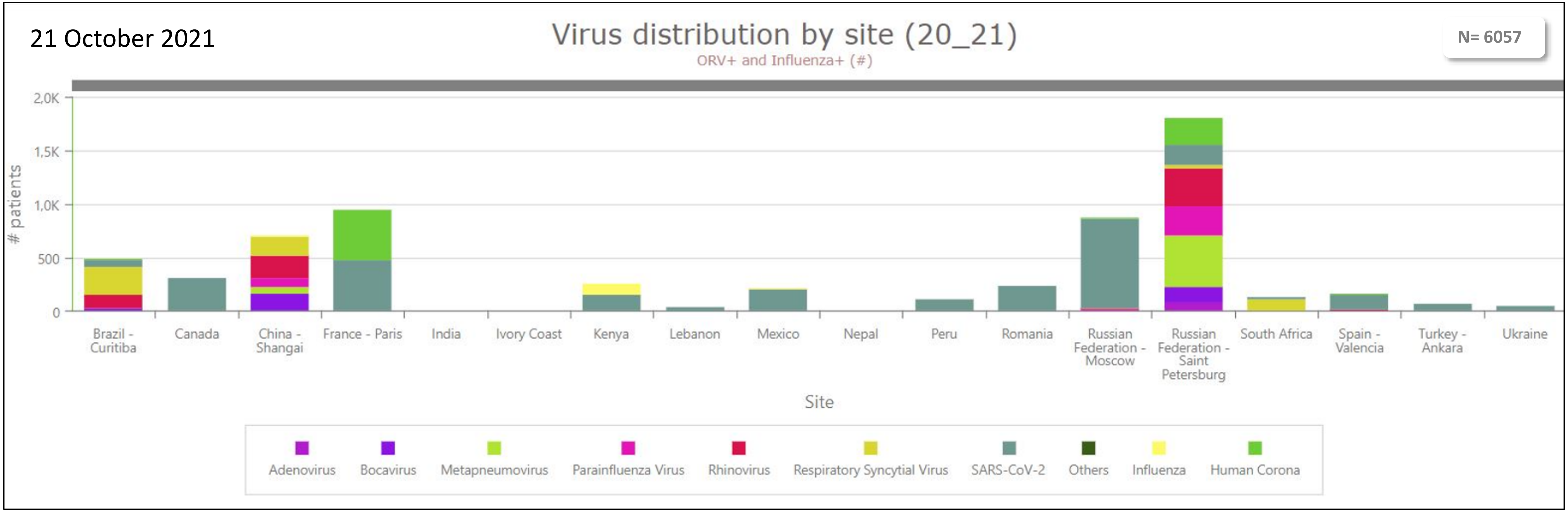
GIHSN 2020-2021:
VIRUS DISTRIBUTION BY SITE



21 October 2021

N= 6057

#LCI+ =
132

#RSV =
597

#SARS-CoV2+ =
2 858

#ORV+ =
2 470

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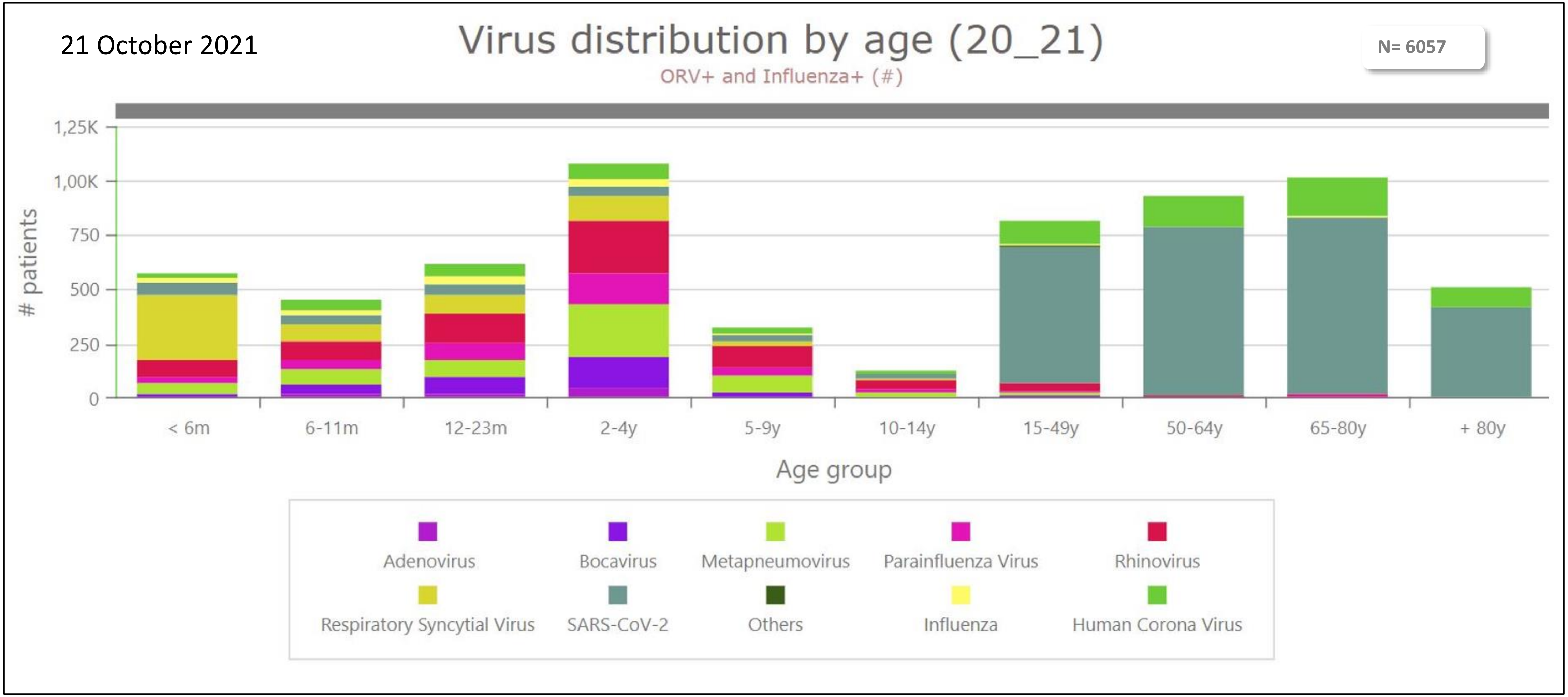
GIHSN 2020-2021:
VIRUS DISTRIBUTION BY AGE



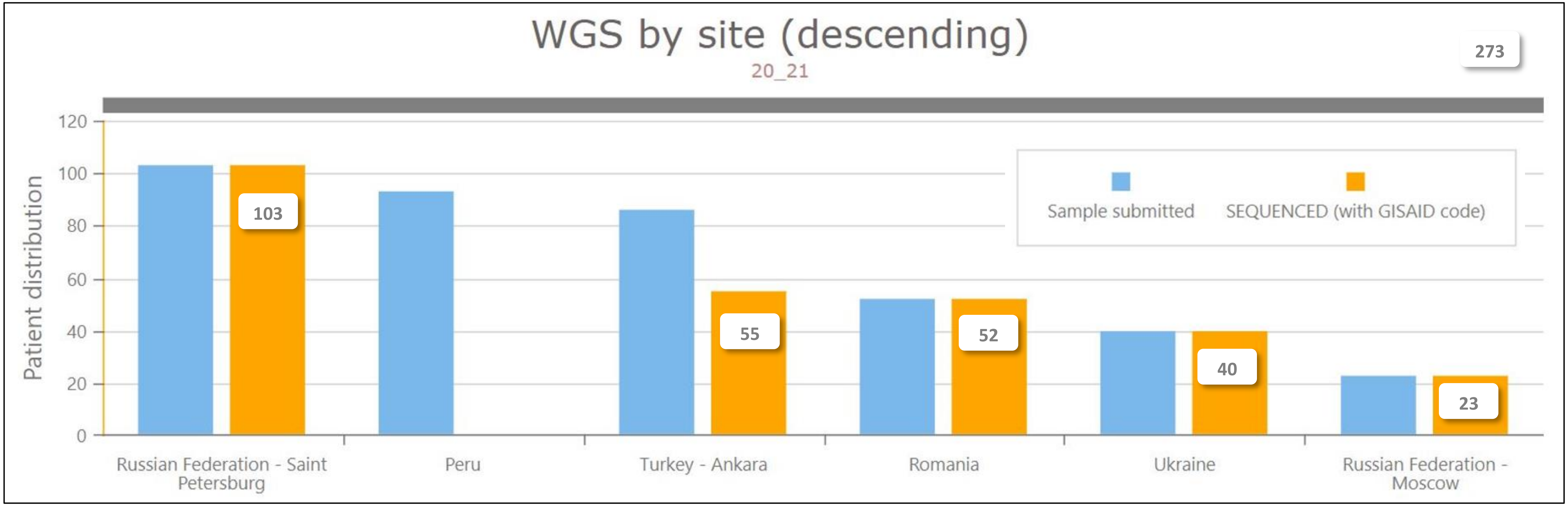
21 October 2021

Virus distribution by age (20_21)

ORV+ and Influenza+ (#)

N= 6057

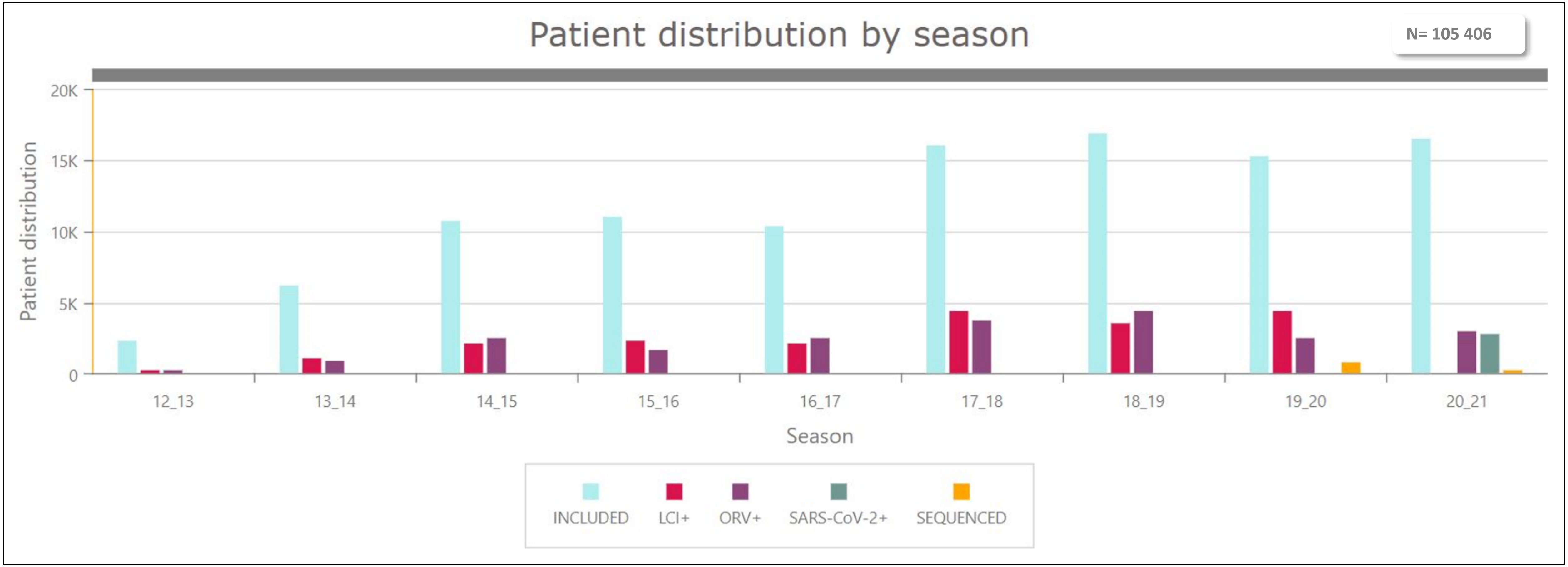
GIHSN 2020-2021:
6 SITES HAVE SUBMITTED WGS RESULTS TO DATE



❖ Additional WGS results are expected from the following sites:

- Spain
- Kenya (all flu specimens with strong ct values will be sequenced, results expected by end of October)
- Canada (expected)
- Lebanon (samples sent to lyon)

GIHSN (ALL SEASONS):
PATIENT DISTRIBUTION BY SEASON



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GIHSN 2020-2021: SEQUENCING UPDATE

Pr Bruno LINA, University of Lyon

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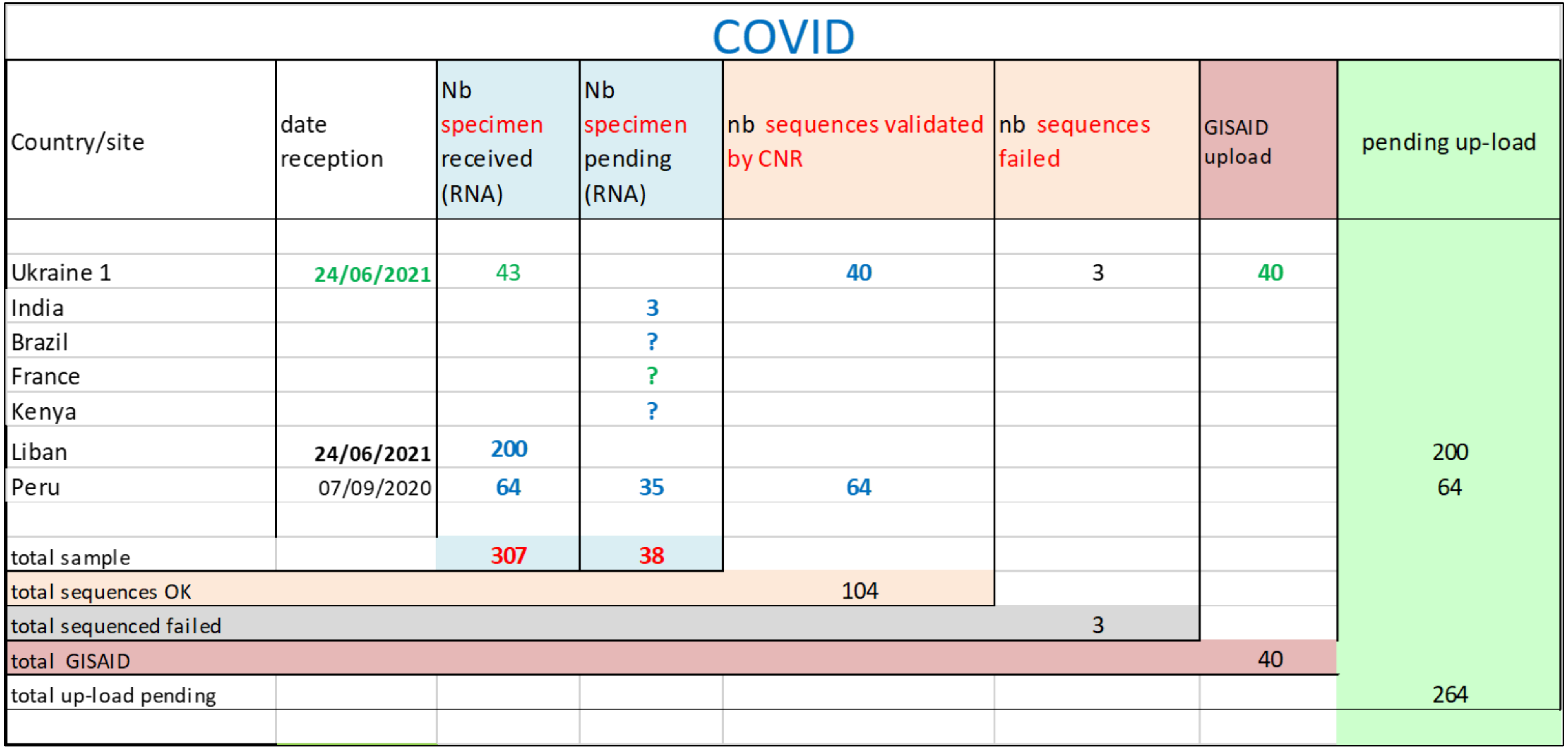
SEQUENCING UPDATE 2020-2021 – LYON LAB



COVID

Country/site	date reception	Nb specimen received (RNA)	Nb specimen pending (RNA)	nb sequences validated by CNR	nb sequences failed	GISAID upload	pending up-load
Ukraine 1	24/06/2021	43		40	3	40	
India			3				
Brazil			?				
France			?				
Kenya			?				
Liban	24/06/2021	200					200
Peru	07/09/2020	64	35	64			64
total sample		307	38				
total sequences OK				104			
total sequenced failed					3		
total GISAID						40	
total up-load pending							264

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GIHSN 9TH ANNUAL MEETING, 25-26 OCTOBER 2021

PARTICIPATING SITES FOR THE 2021-2022 SEASON

Laurence TORCEL-PAGNON, Executive Officer, Foundation for Influenza Epidemiology

Foundation for
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Epidemiology

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France

SITES SELECTION PROCESS

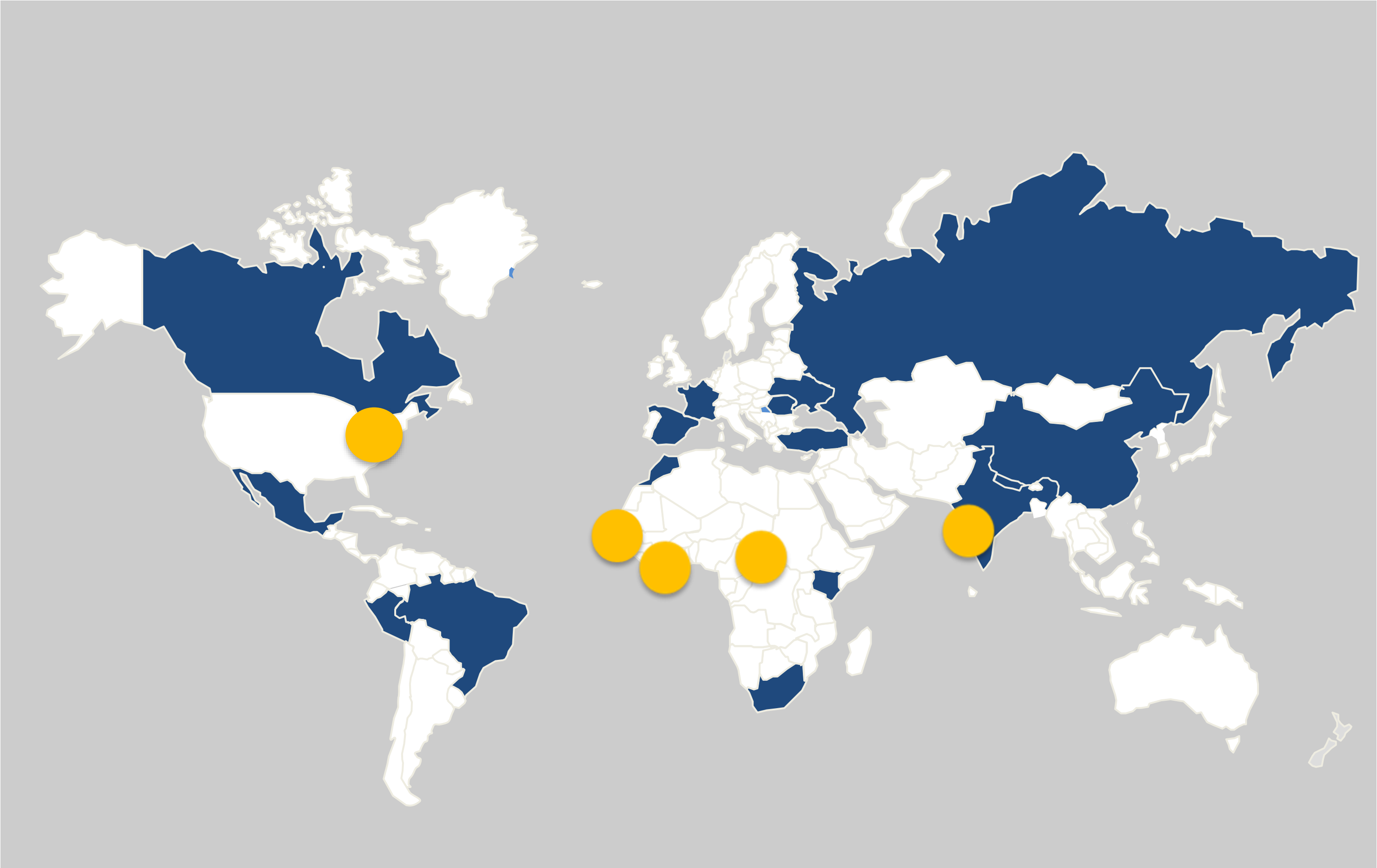
- The yearly Call for Proposals was published in May 2021 on the GIHSN website.
- Sites applied on-line following a GIHSN application template.
- All proposals have been reviewed and quoted by the experts from the Independent Scientific Committee according to the evaluation criteria
  - Experts did not quote proposals coming from their own country
- Grant allocations decision has been made by the Executive Committee of the Foundation based on experts grading, sites past contribution in the GIHSN, geographical representativeness and budget availability.
- 20 sites have been selected.

20 SITES IN 19 COUNTRIES WILL PARTICIPATE IN THE 2021/22 SEASON

North America
Canada
USA-NYC

South America
Brazil-Curitiba
Peru-Lima

Eurasia
France-Paris
Romania
Russia-Moscow
Russia-St Pet
Spain
Ukraine



🟦 2020-2021 🟨 New sites

Africa
Kenya
South Africa
Centre Afrique-Bangui
Ivory Coast
Senegal-Dakar

Middle East
Lebanon
Turkey

Asia/Pacific
China-Fudan
India-Pune
Nepal

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GIHSN PROTOCOL 2021-2022: HIGHLIGHTS

Sandra CHAVES, MD, MSc, Foundation for Influenza Epidemiology

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MAIN OBJECTIVES – REMINDER

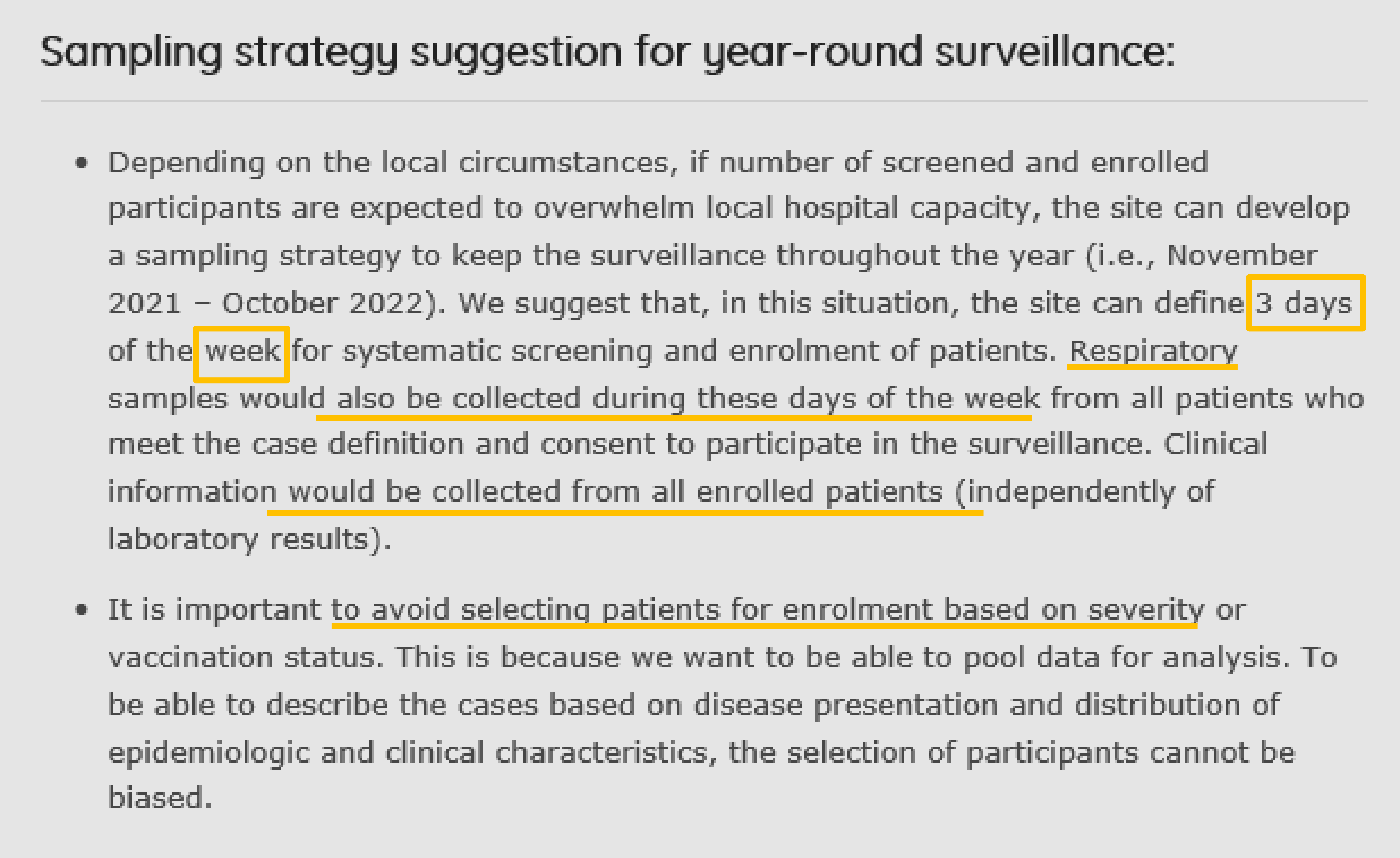
- Expand international laboratory and surveillance capacity and data sharing
- Support the biannual WHO vaccine strain selection process
- Link clinical and virologic (including whole genome sequence) data from hospitalized patients with acute respiratory illness

SPECIFIC ASPECTS UNDERSCORED IN THE 2021-22 SEASON CALL FOR TENDER

- Screening and inclusion of hospitalized patients with respiratory illness meeting protocol case definition year-round (**November 2021 to October 2022**)
- Collection of epidemiologic and clinical data for all participating patients (i.e., those who meet case definition and consent to participate), with a standardized questionnaire administered at enrolment and a chart abstraction at patient discharge/death
- Enrolled patients would have respiratory specimen collected shortly after hospital admission and sent for testing at the local and/or reference laboratory or National Influenza Centre

LABORATORY

- PCR test for influenza a priority. If **multiplex PCR and/or wet assay for SARS-COV-2** (and RSV and other respiratory viruses) can be performed in addition, it would be a strong added value
- Storage (-20C or -70C) of respiratory samples (swabs) from **all swabbed patients for a minimum of one year**. This can facilitate retrospective investigations on pathogen discovery, or evaluation of new diagnostic tools (ad hoc applications possible)
- WGS for a minimum of 50 to 100 influenza viruses will be expected. **If number of influenza positive cases are low, site is encouraged to complete WGS of SARS-COV-2**
    - WGS data uploaded to GISAID by site in a reasonable timeframe, so results are available for the WHO Vaccine Composition Meeting
    - Link between WGS data uploaded in GISAID and clinical data in GIHSN required



Sampling strategy suggestion for year-round surveillance:

- Depending on the local circumstances, if number of screened and enrolled participants are expected to overwhelm local hospital capacity, the site can develop a sampling strategy to keep the surveillance throughout the year (i.e., November 2021 – October 2022). We suggest that, in this situation, the site can define 3 days of the week for systematic screening and enrolment of patients. Respiratory samples would also be collected during these days of the week from all patients who meet the case definition and consent to participate in the surveillance. Clinical information would be collected from all enrolled patients (independently of laboratory results).
- It is important to avoid selecting patients for enrolment based on severity or vaccination status. This is because we want to be able to pool data for analysis. To be able to describe the cases based on disease presentation and distribution of epidemiologic and clinical characteristics, the selection of participants cannot be biased.

TOMORROW DISCUSSION

- Each site will present the data from previous season and highlight achievements and challenges
- Discuss surveillance implementation
  - Case ascertainment
  - Case definition
  - Sampling and testing strategies
- Suggestions for protocol and questionnaires based on previous experience
- Publication & Call for research updates

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CLOSING OF THE PLENARY SESSION

Cedric MAHE

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26 OCTOBER: 2 REGION SPECIFIC SESSIONS - DISCUSS SITE RESULTS & IMPLEMENTATION CHALLENGES

9am–12am CET

SITES SESSION 1

CHINA - FUDAN
INDIA - SRINAGAR
NEPAL
LEBANON
TURKEY
RUSSIA - ST PETERSBURG
RUSSIA - MOSCOW
UKRAINE
ROMANIA

2pm–5pm CET

SITES SESSION 2

CANADA
MEXICO
BRAZIL
PERU
SOUTH AFRICA
KENYA
SPAIN
FRANCE - PARIS

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THANK YOU!