



Global Influenza  
Hospital Surveillance  
Network

[www.gihsn.org](http://www.gihsn.org)



# GIHSN 12<sup>TH</sup> GLOBAL ANNUAL MEETING

25-26 November 2024

Cédric MAHE, President, Foundation for Influenza Epidemiology



Foundation for  
Influenza  
Epidemiology

Sous l'égide de

Fondation  
de  
France

Coordination  
**IMPACT**  
Healthcare

# WELCOME TO THE GIHSN GLOBAL ANNUAL MEETING! DOMAINE DE CHÂTEAUNEUF, 25-26 NOVEMBER 2024



50 participants - 25 countries





# 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 each new site to answer all questions.



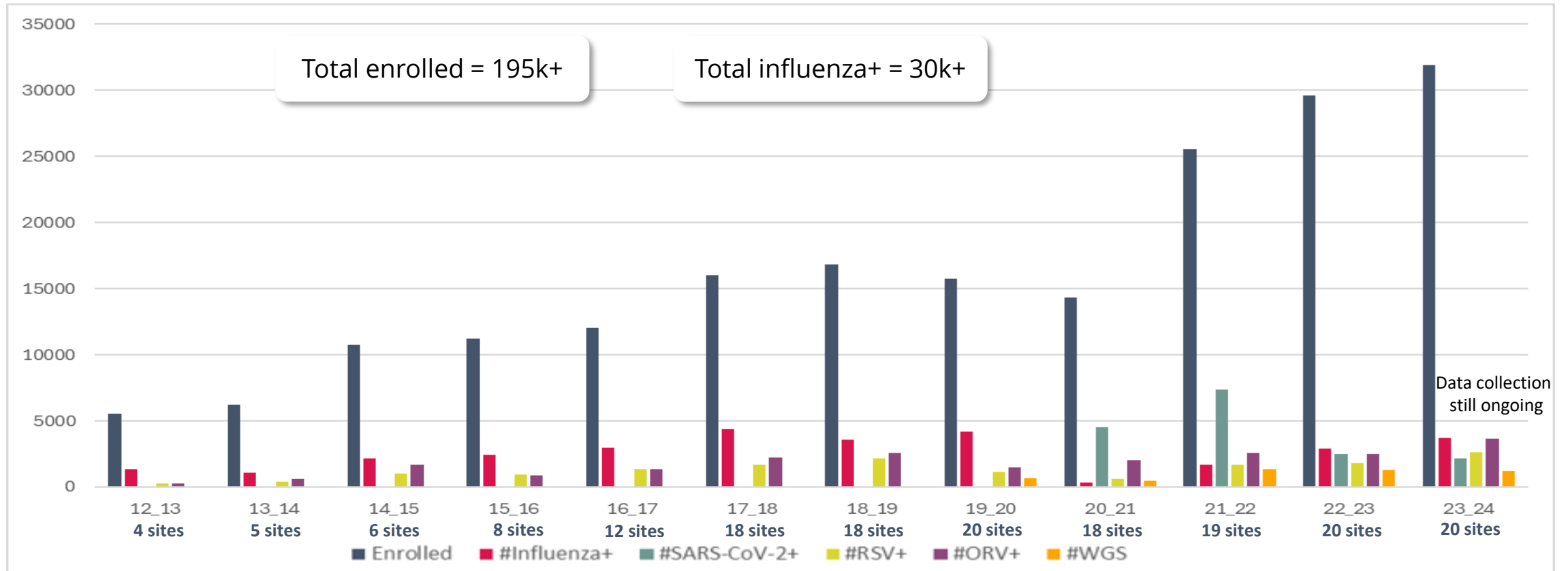
Speakers are kindly asked to stick to the speaking time allotted!



Please note that the meeting will be recorded.

**Thank you all for cooperation!**

# GIHSN HISTORY



Virus genome sequencing

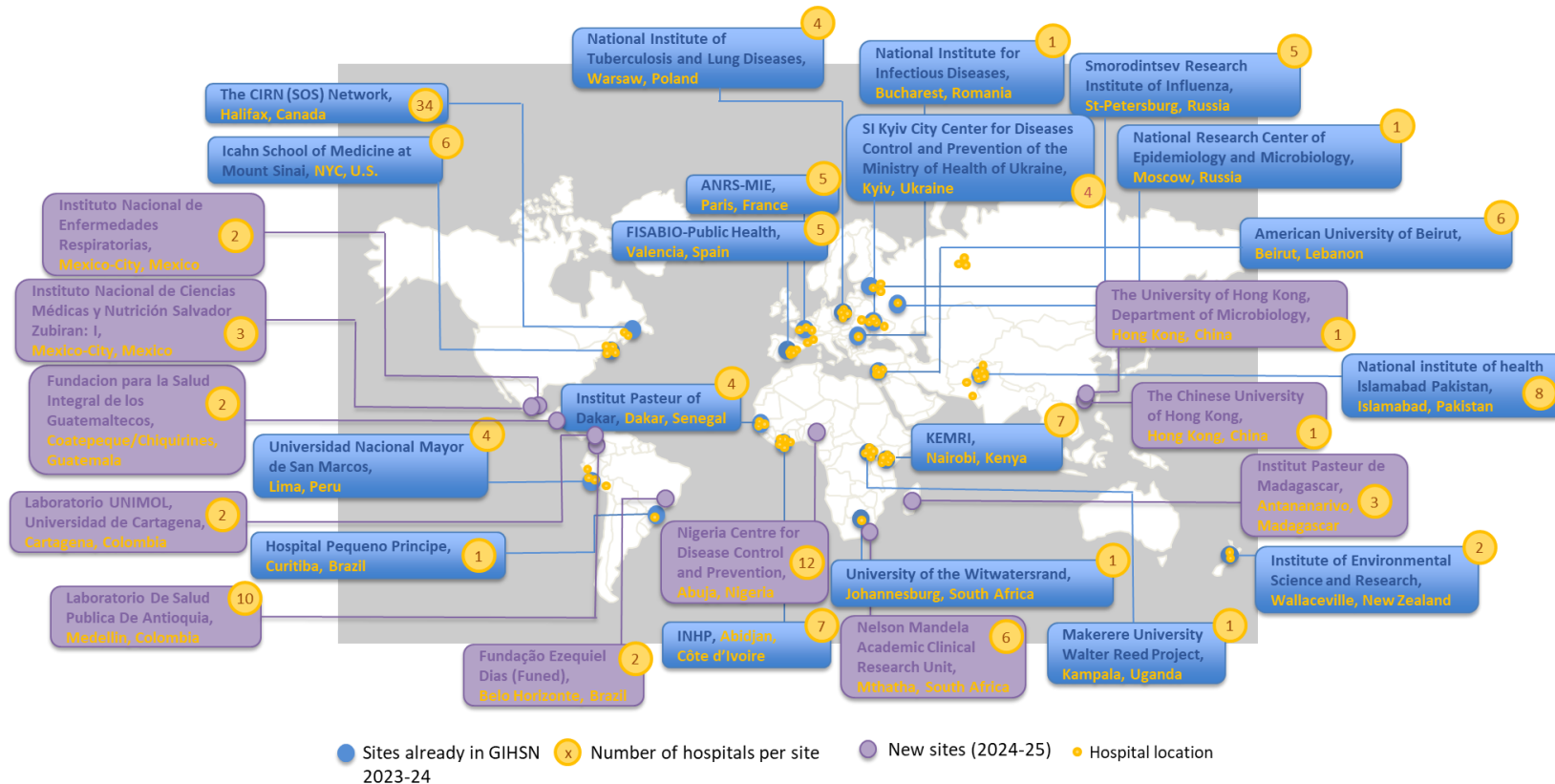
SARS-Cov2 circulation

Year round surveillance



# GIHSN TODAY

Network of sentinel hospitals (about 150 hospitals in 30 sites in 2025) conducting **active surveillance year-round** of **acute respiratory infections**



## Key features

- Use of a standardized protocol and questionnaire
- Strong links between clinical sites and laboratories
- Use of existing infrastructures combined with capacity building through the network and catalytic funding by the Foundation
- Interface with WHO and local authorities
- Sites own their data. Consolidated datawarehouse for research purpose



# VIRUSES TESTED BY SITES 2023-24

Increased use of multiplex-PCR > expansion to all respiratory viruses

Testing in 2022-23 included :

Country	Site/Institution	Influenza	SARS-CoV2	RSV	HCoV	HMPV	AdV	HBoV	HPIV	RhV	ORV
<b>Africa</b>											
Kenya	Kenya Medical Research Institute (KEMRI), Nairobi	█	█								
Côte d'Ivoire	Institut National d'Hygiène Publique (INHP), Abidjan	█	█	█	█	█	█	█	█	█	
Senegal	Institut Pasteur of Dakar (IPD), Dakar	█	█	█	█	█	█	█	█	█	█
South Africa	University of the Witwatersrand, Johannesburg	█	█	█		█					
<b>Asia/Pacific</b>											
China*	School of Public Health, Fudan University, Shanghai	█		█	█	█	█	█	█	█	
India	Sher-i-Kashmir Institute, Srinagar	█									
Nepal	Patan Academy of Health Sciences	█	█	█	█						
Pakistan	National institute of health, Islamabad	█	█	█	█	█	█	█	█	█	█
<b>Middle East</b>											
Türkiye	Turkish Society of Internal Medicine, Ankara	█	█	█	█	█	█	█	█	█	█
Lebanon	American University of Beirut, Beirut	█	█	█	█	█	█	█	█	█	█

Testing in 2022-23 included :

Country	Site/Institution	Influenza	SARS-CoV2	RSV	HCoV	HMPV	AdV	HBoV	HPIV	RhV	ORV
<b>Eurasia</b>											
Russia - St Petersburg	Smorodintsev Research Institute of Influenza, St Petersburg, Russia	█	█	█	█	█	█	█	█	█	
Russia - Moscow	FSBI "N.F. Gamaleya NRCEM" Ministry of Health, Moscow	█	█	█	█	█	█	█	█	█	█
Ukraine	L.V.Gromashevsky Institute of Epidemiology & Infectious Diseases, Kyiv	█	█								
Spain	FISABIO, Valencia	█	█	█	█	█	█	█	█	█	
Romania	National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest	█	█	█	█	█	█	█	█	█	█
France*	I-REIVAC (Innovative clinical research network in vaccinology), Paris	█	█	█	█	█	█	█	█	█	█
<b>North America</b>											
Canada	The CIRN Serious Outcomes Surveillance (SOS) Network, Halifax	█	█	█	█	█	█	█	█	█	█
USA	Icahn School of Medicine at Mount Sinai, NYC	█	█	█		█	█		█	█	█
<b>South America</b>											
Brazil	Hospital Pequeno Principe, Curitiba	█	█	█	█	█	█	█	█	█	
Peru	Instituto de Medicina Tropical, Lima	█	█	█		█	█				█



# GIHSN: A Scientific Community

A meeting organized each year to discuss results

Yearly GIHSN publication(s) in addition to individual site papers



The Journal of Infectious Diseases

MAJOR ARTICLE



## Predictors of Severity of Influenza-Related Hospitalizations: Results From the Global Influenza Hospital Surveillance Network (GIHSN)

Lily E. Cohen,<sup>1,2,9</sup> Chelsea L. Hansen,<sup>3,4,5</sup> Melissa K. Andrew,<sup>6</sup> Shelly A. McNeil,<sup>6</sup> Philippe Vanhems,<sup>7</sup> Jan Kyncl,<sup>8,9</sup> Javier Diez Domingo,<sup>10</sup> Tao Zhang,<sup>11</sup> Ghassan Dbaibo,<sup>12</sup> Victor Alberto Laguna-Torres,<sup>13</sup> Anca Draganescu,<sup>14</sup> Elsa Baumeister,<sup>15</sup> Doris Gomez,<sup>16</sup> Sonia M. Raboni,<sup>17</sup> Heloisa I. G. Giamberardino,<sup>17</sup> Marta C. Nunes,<sup>18,19</sup> Elena Burtseva,<sup>20</sup> Anna Sominina,<sup>21</sup> Snežana Medić,<sup>22,23</sup> Daouda Coulibaly,<sup>24</sup> Affi Ben Salah,<sup>25,26</sup> Nancy A. Otiemo,<sup>27</sup> Parvaiz A. Koul,<sup>28</sup> Serhat Unal,<sup>28,30</sup> Mine Durusu Tanriover,<sup>30,31</sup> Marie Mazur,<sup>3</sup> Joseph Bresee,<sup>3</sup> Cecile Viboud,<sup>3</sup> and Sandra S. Chaves<sup>32</sup>

## GIHSN featured in Science

### 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<sup>1</sup>, Cedric Mehl<sup>1\*</sup>, Sandra S. Chaves<sup>2\*</sup>

The emergence and spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has disrupted the circulation of other respiratory viruses. We used a model to explore the potential impact of the COVID-19 pandemic on the circulation of influenza A and B viruses. Our model suggests that the pandemic may have led to a reduction in population-level immunity to these viruses, which could increase the risk of future influenza epidemics. Expanded genomic and clinical surveillance are needed to understand the spread of respiratory viruses.

What can be expected once this pandemic subsides and 1975 are (likely) if there is a reduction in population-level immunity to endemic respiratory viruses could emerge 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 susceptibility of influenza virus evolution and the role of latent 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 (2). RSV is a common respiratory virus that often circulates latently and results 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 infections throughout a life span. Data from surveillance systems have recently identified an increase in circulation of RSV in both Northern and Southern hemispheres, albeit to lower magnitudes than is 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 (3). Periodic circulation of RSV, even if limited, may maintain the pool of susceptible population in the long term and prevent large outbreaks in the future (4).

For influenza viruses, the overall modeling conclusions are less robust than for RSV (5). The rapid evolution and the dynamics of host immunity associated with influenza virus infections add further complexity 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 viral), environmental and temperate 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 season, could present an opportunity for viral mutations (8) through antigenic drift (a process of gradual accumulation of mutations in the surface glycoprotein, or antigen, 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 real-world countries (11).

The pool of susceptible individuals could also change qualitatively, with children being especially vulnerable during future influenza epidemics if the rest of the population maintains cross-protection from infections with previous seasonal strains. The implementation 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 H5N1 viruses, which are often detected during surveillance in the US from exposure to wild in agricultural fairs (12). These variant strains readily affect children because of population immunity from other H2N3 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.

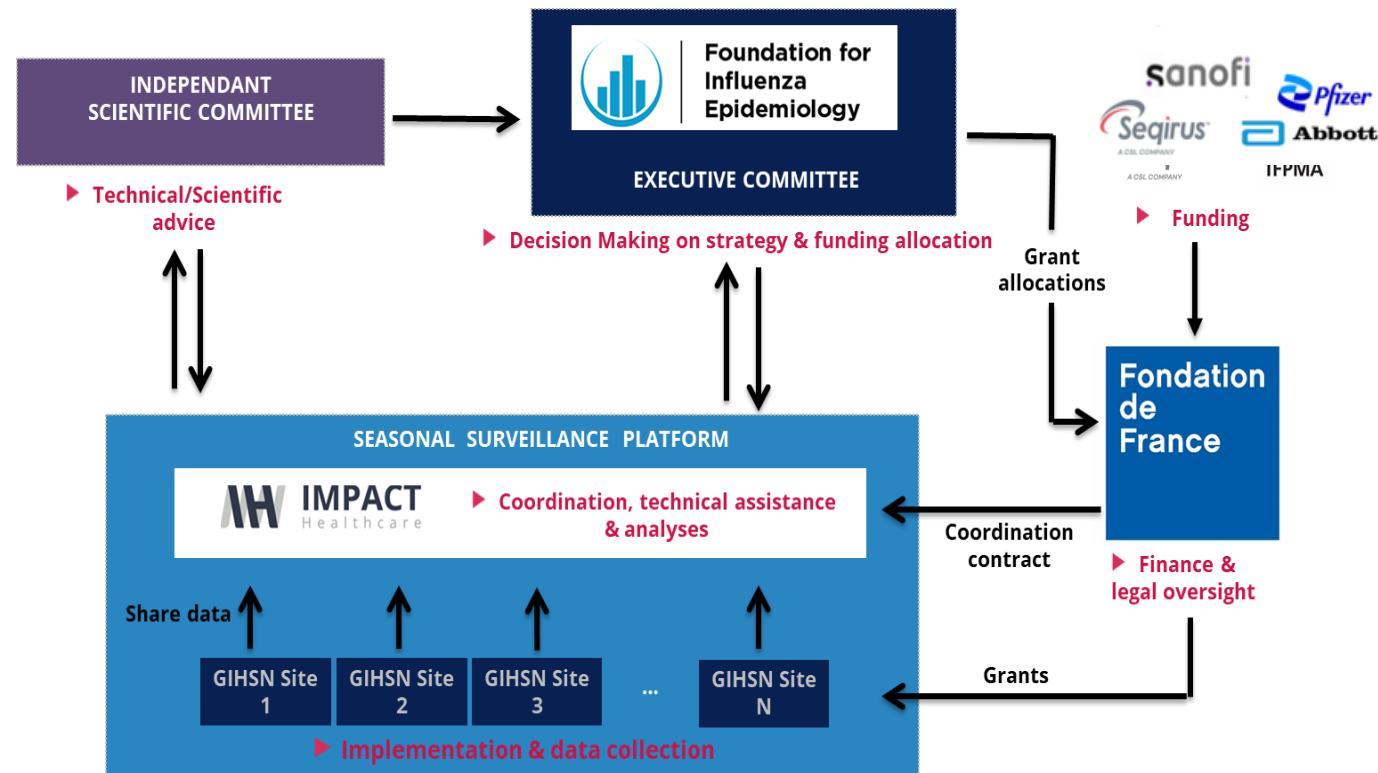
The evolution of SARS-CoV-2 and the appearance of variants threatening the effectiveness of widely available vaccines have underscored the importance and limitations of genomic surveillance systems in a globally

2023: 80+ participants from 30+ countries in WHO HQ



# Governance of the GIHSN

- Dedicated fund under the **Fondation de France** umbrella: the **Foundation for Influenza Epidemiology (FIE)**
  - This funding only represent 1/3 of the actual implementation cost
- A **transparent governance system** is already in place with an **Executive Committee** and an **Independent Scientific Committee**
- **Coordination of the network partners** and operational implementation, incl. data hosting, is supported by **Impact Healthcare** funded by the FIE





# Value of GIHSN

**Research**



**Public Health**

- An agile research platform & community (data collected, samples storage, capability)
- Generation of robust data on respiratory virus pathogens circulation, serotype/strains distribution, at risk population, drivers of disease severity (lack of hospital based clinical surveillance)
- Identification of virus sequence linked to severity/vaccine failure
- A powerfully and agile alert system



# Data and samples

- Data are owned by sites but the Foundation has access to the data stored in a consolidated and curated data-warehouse (>170,000 patients with up to 60 variables so far)
- A complete descriptive analysis is performed every year and publications on various thematics are encouraged
- The data warehouse can only be access by not-for-profit
- All research projects are vetted by the Independent Scientific Committee for scientific relevance
- Funders can only use results publicly available
- Sites are storing swabs for 1-2 year to allow for potential additional studies



# MoU with WHO

- The MoU make of the Foundation for Influenza Epidemiology (FIE) a Non state actor engaged in technical collaboration with WHO - a necessary condition to engage in official relations and exchange resources with WHO.
- It shows that the FIE/GIHSN has demonstrated strong governance, transparency, and audit processes together with measurable and impactful public health value

## Areas of collaboration already identified with WHO to shape a roadmap

### MEMORANDUM OF UNDERSTANDING

between

**the World Health Organization,  
20 avenue Appia, 1211 Geneva, Switzerland  
("WHO")**

and

**Fondation pour l'épidémiologie de la grippe, Fondation de France, 40 avenue  
Hoche, 75008 Paris, France,**

For the World Health Organization

  
Signature:

Name:

Title: **Dr Michael J. Ryan**  
Executive Director

Date: WHO Health Emergencies Programme

For the Fondation pour l'épidémiologie de la grippe

  
Signature:

Name: Dr Cédric Mahé

Title: President, Fondation pour l'épidémiologie de la grippe

Date: 16 Oct 2023

03 OCT 2023



# AREA 1: VIRUS CO-CIRCULATION AND ALERT MECHANISMS

GIHSN can describe a wide range of respiratory virus circulation at the level of hospitalized patients. It can also potentially trigger an alert by identifying unexpected cluster of cases.

	In progress	To address
Improvement of the timeliness of the reporting in the GIHSN	X	
GIHSN dashboard	X	
Sharing of data with WHO		X
Local alignment and sharing of information.		X
GIHSN country expansion	X	



## AREA 2: COMBINATION OF SEVERITY AND WGS FOR STRAIN SELECTION

	In progress	To address
Building of local capabilities/interface for WGS	X	
Develop collaboration with GISAID	X	
Sequencing for other viruses (SARS-Cov2, RSV)		X



# AREA 3: BURDEN OF DISEASE ESTIMATION AND OTHER RESEARCH ACTIVITIES

The GIHSN relies on 3 research pillars:

- a motivated and diverse researchers/clinicians' community
- a hospital/lab infrastructure able to carry strong quality research
- a rich and unique data generated every year (>170,000 patients tested so far).

This infrastructure should be leveraged to address specific research questions.

## **Example of topics:**

- Catchment area estimation for incidence estimation.
- EV-68 burden
- Comparative burden of RSV & flu post pandemic.



# AGENDA OF THE MEETING (1)

**Monday 25 November AM**

## PLENARY SESSION

9:00: Opening of the Meeting. GIHSN Strategy & Perspectives - Cedric Mahé, Foundation for Influenza Epidemiology + Q/A *45'*

9:45: GIHSN Data report 2023-24: Presentation & Discussion - Catherine Commaille-Chapus, Impact Healthcare - *25' + 20'*

10:30 COFFEE BREAK *30'*

11:00: **Panel 1**: Site experience in the GIHSN - Moderated by Laurence Torcel-Pagnon, Foundation for Influenza Epidemiology - *75'*

- Around the room introduction from recurrent sites (*2' each*)
- Introduction of recent sites 2023-2024: Uganda, New Zealand, Poland (1 slide - *3' each*)
- Newcomers 2024-25 (remotely or video - *2' each*)

12:30: LUNCH BREAK



# AGENDA OF THE MEETING (2)

## Monday 25 November PM

14:00: GISAID role in WGS activities (history of GISAID scale up, latest developments in GISAID analytics ...) - Peter Bogner, GISAID - 20'

### WORKSHOP 1: WGS

14:20: Introduction by Nicola Lewis, Crick WHO CC (*remotely*) - 15'

14:35: Breakout groups (split the attendance in 3 pre-defined groups - 45'), then sharing in Plenary (45')

*Moderators of groups*: Bruno Lina (France NIC), John McCauley (Crick WHO CC), Dimitriy Pereyaslov (WHO/GIP)

- Specimen selection for WGS
- Which options for sequencing: Locally / In Lyon (GIHSN platform) / With WHO CC
- Considerations on shipment (to be optimized)
- Upload of results on GISAID (GIHSN tag ...)





# AGENDA OF THE MEETING (3)

## PLENARY SESSION

15:20: Sharing in Plenary - 45'

16:05 COFFEE BREAK 25'

16:30: **Panel 2**: Research projects leveraging the GIHSN platform - Moderated by Marta Nunes (CERP) & Sandra Chaves (Foundation for Influenza Epidemiology) - 60'

- Specific influenza activity from South Africa - Vicky Baillie, University of the Witwatersrand, Johannesburg (7' + 3')
- Respiratory syncytial virus in pediatric patients with severe acute respiratory infections in Senegal - Ndongo Dia, Institut Pasteur of Dakar, Dakar (7' + 3')
- Pediatric Influenza 2024: Clinical and Laboratory Aspects - Sonia M Raboni, Pequeno Príncipe Hospital and Federal University of Parana, Brazil (7' + 3')
- Association of Influenza Viral Genetic Information with Severity Markers in Hospitalized Patients - Aung Pone Myint, CERP, Hospices Civils de Lyon and Université Claude Bernard Lyon 1 (7' + 3')
- EV-D68 surveillance: protocol overview and proposed collaboration with the GIHSN - Miranda Delahoy, US Centers for Disease Control and Prevention (7' + 3')

17:30: Closing Day 1

## KIOSKS

17:45 - 18:15: Kiosks on operational topics

- Screening strategy/Sampling frame (Sandra Chaves)
- Data entry (Catherine Commaille)
- WGS operating procedures (Bruno Lina)
- EV-68 surveillance (Miranda Delahoy)



# AGENDA OF THE MEETING (4)

**Tuesday 26 November - AM**

## PLENARY SESSION

9:00: Opening by Wenqing Zhang, WHO/GIP - 20'

9:20: *Keynote* - Vision of Respiratory Surveillance in the Post-pandemic era - Maria Zambon, UKHSA - *Presentation followed by Q/A 30'+15'*

10:05: WHO integrated sentinel surveillance standards and guidance - Stefano Tempia (*tbc*), WHO (remotely) - 15'

10:20: COFFEE BREAK 20'

10:40: GIHSN Dashboard - Introduction & Live presentation + Discussion - Laurence Torcel-Pagnon - 15'+ 10'



# AGENDA OF THE MEETING (5)

## WORKSHOP 2: Improving data collection, quality and reporting timeliness

11:05: Breakout groups (split the attendance in 3 pre-defined groups - 45'), then sharing in Plenary (45')

*Moderators of groups* : Marta Nunes (CERP), Sandra Chaves (FIE), Melissa Rolfes (WHO/GIP, *tbc*), Laurence Torcel-Pagnon (FIE), Catherine Commaille-Chapus (Impact Healthcare)

- Screening and sampling frame strategy
- Data flow and quality
- Timeliness of reporting
- Core set of variables to be reported weekly

## PLENARY SESSION

11:50: Sharing in Plenary - 45'

12:35: Closing of the Meeting & Next Steps - Cedric Mahe & Wenqing Zhang - 10'

12:45: LUNCH BREAK





Global Influenza  
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THANK YOU !



Foundation for  
Influenza  
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GIHSN 12TH ANNUAL MEETING, 25-26 NOVEMBER 2024

## GIHSN DATA REPORT 2023-24 (TO DATE)

Catherine COMMAILLE-CHAPUS, GIHSN Coordination & Data Management



Foundation for  
Influenza  
Epidemiology

Sous l'égide de

Fondation  
de  
France



# 20 SITES PARTICIPATED IN THE GIHSN IN 2023-24



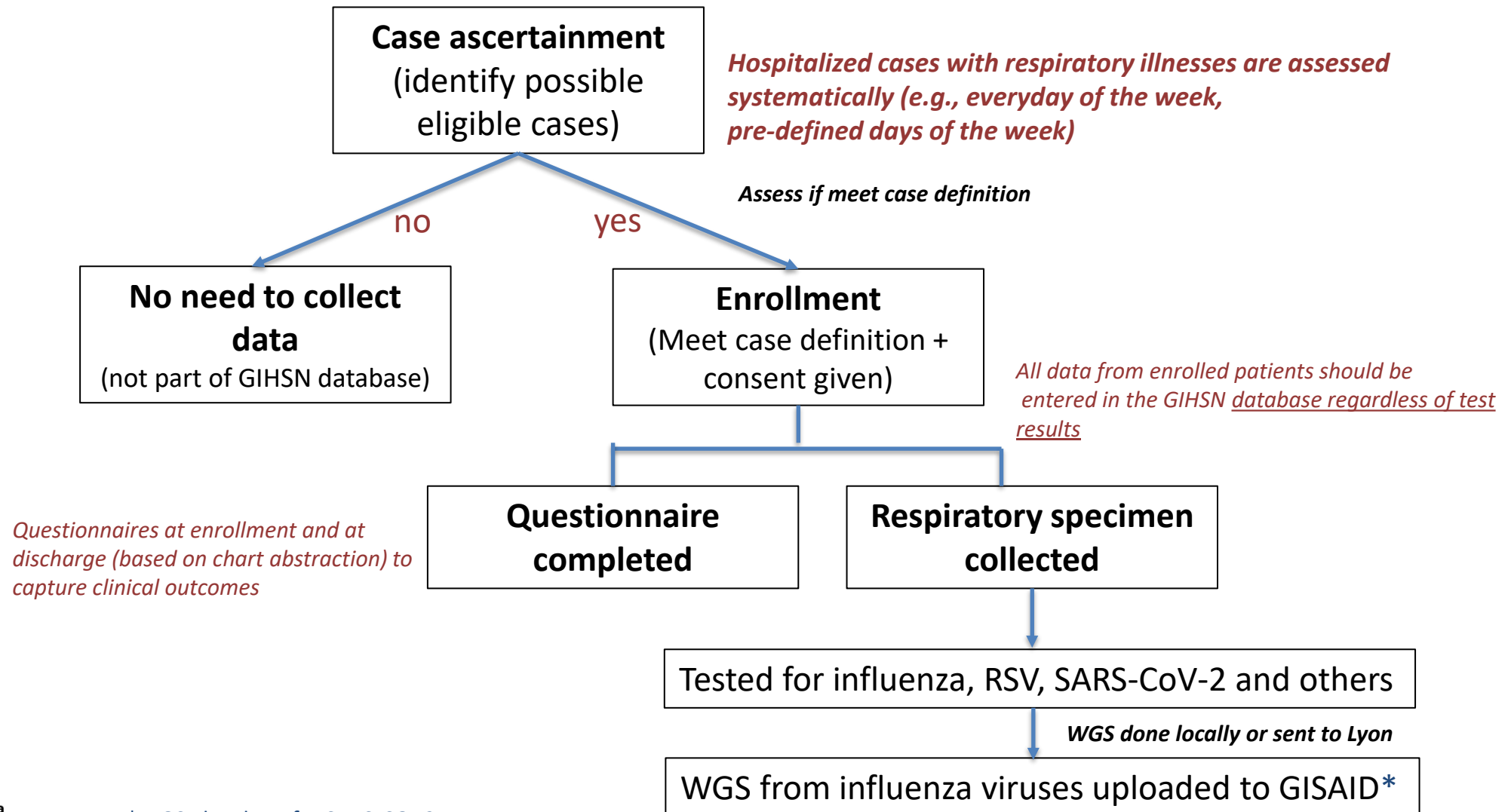
● GIHSN sites (2023-24)  
\* No data shared for 2023-24

ⓧ Number of hospitals per site  
From which x are peds hospitals

● Hospitals location

★ No fund allocated

# PROCESS FOR IDENTIFICATION OF CASES AND DATA COLLECTION - GIHSN



\*WGS also done for SARS-COV2

# VIRUSES TESTED BY SITES 2023-24

(BASED ON DATA SHARED IN THE GIHSN THIS SEASON – AS OF NOV 14TH)

		Testing in 2023-24 include :													
Country	Site/Institution	Influenza	SARS-CoV-2	RSV	HCoV	HMPV	AdV	HBoV	HPIV	RhV	EVs	MERS-CoV	Picornavirus	SARS-CoV	ORV
<b>Africa</b>															
Ivory Coast	Institut National d'Hygiène Publique (INHP), Abidjan	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Kenya	Kenya Medical Research Institute (KEMRI), Nairobi	█	█	█											
Senegal	Institut Pasteur of Dakar (IPD), Dakar	█	█	█	█	█	█	█	█	█	█		█		
South Africa	University of the Witwatersrand, Johannesburg	█	█	█		█	█		█	█	█				
Uganda	Makerere University Walter Reed Project, Kampala	█	█	█	█	█	█	█	█	█	█	█			
<b>Asia/Pacific</b>															
New Zealand	Institute of Environmental Science and Research, Wallaceville	█	█	█		█	█		█	█	█				
Pakistan	National institute of health Islamabad Pakistan	█	█	█	█	█	█	█	█	█	█	█	█	█	█
<b>Middle East</b>															
Lebanon	American University of Beirut, Beirut	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Turkiye	Turkish Society of Internal Medicine, Ankara	█	█	█											

# VIRUSES TESTED BY SITES 2023-24

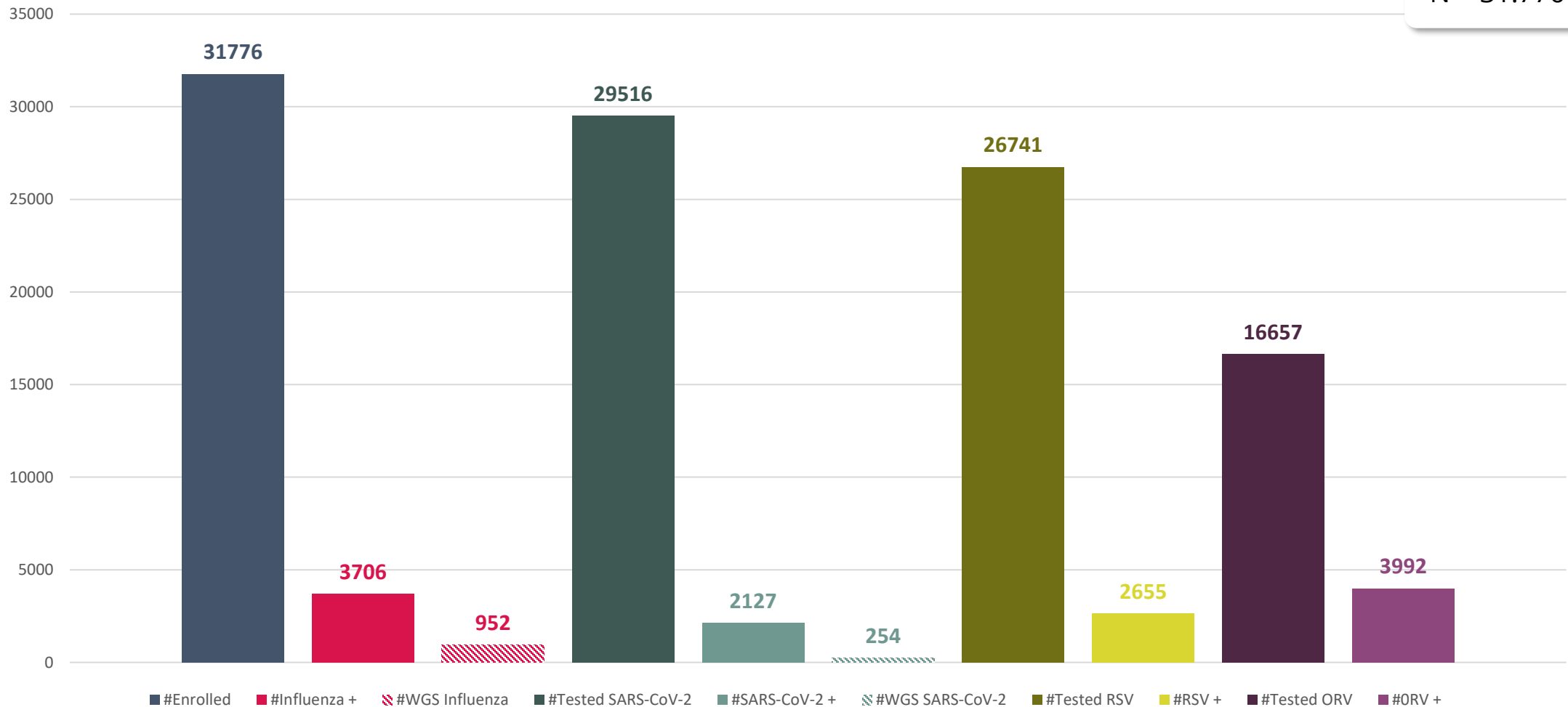
(BASED ON DATA SHARED IN THE GIHSN THIS SEASON – AS OF NOV 14TH)

2/2

		Testing in 2023-24 include :													
Country	Site/Institution	Influenza	SARS-CoV-2	RSV	HCoV	HMPV	AdV	HBoV	HPIV	RhV	EVs	MERS-CoV	Picornavirus	SARS-CoV	ORV
<b>Eurasia</b>															
Poland	The National Institute of Tuberculosis and Lung Diseases, Warsaw	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Romania	National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Russia - Moscow	FSBI "N.F. Gamaleya NRCEM" Ministry of Health, Moscow	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Spain - Valencia	FISABIO, Valencia	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Ukraine	SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine, Kyiv	█	█	█	█	█	█	█	█	█	█	█	█	█	█
<b>North America</b>															
Canada	The CIRN Serious Outcomes Surveillance (SOS) Network, Halifax	█	█	█	█	█	█	█	█	█	█	█	█	█	█
USA	Icahn School of Medicine at Mount Sinai, NYC	█	█	█	█	█	█	█	█	█	█	█	█	█	█
<b>South America</b>															
Brazil	Hospital Pequeno Principe, Curitiba	█	█	█	█	█	█	█	█	█	█	█	█	█	█
Peru	Instituto de Medicina Tropical, Lima	█	█	█	█	█	█	█	█	█	█	█	█	█	█

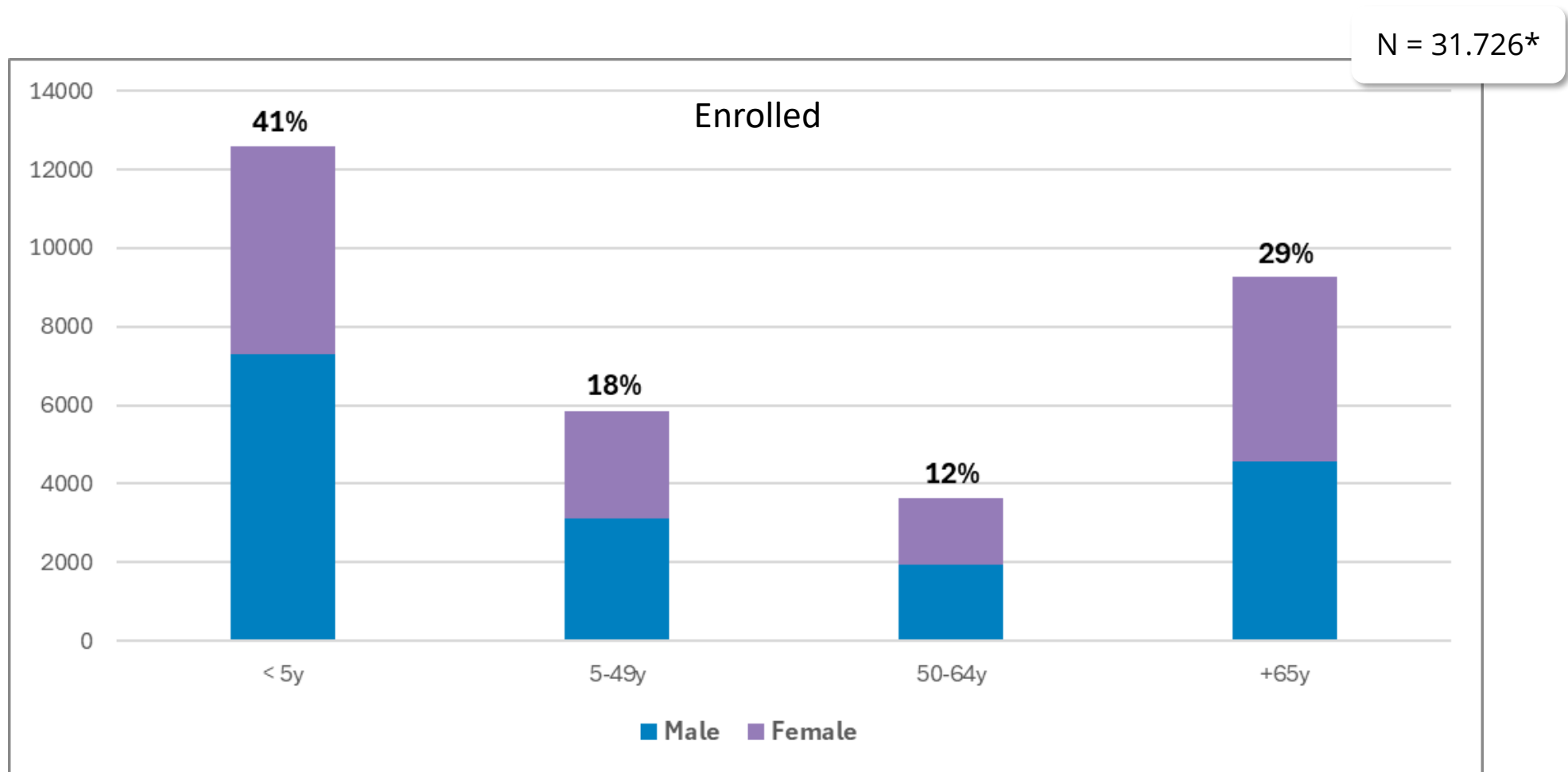
# OVERALL NB OF PATIENTS ENROLLED AND POSITIVE CASES OF INFLUENZA, SARS-COV2, RSV AND ORV (2023-24) (#) (AS OF NOVEMBER 14TH, 2024)

N = 31.776



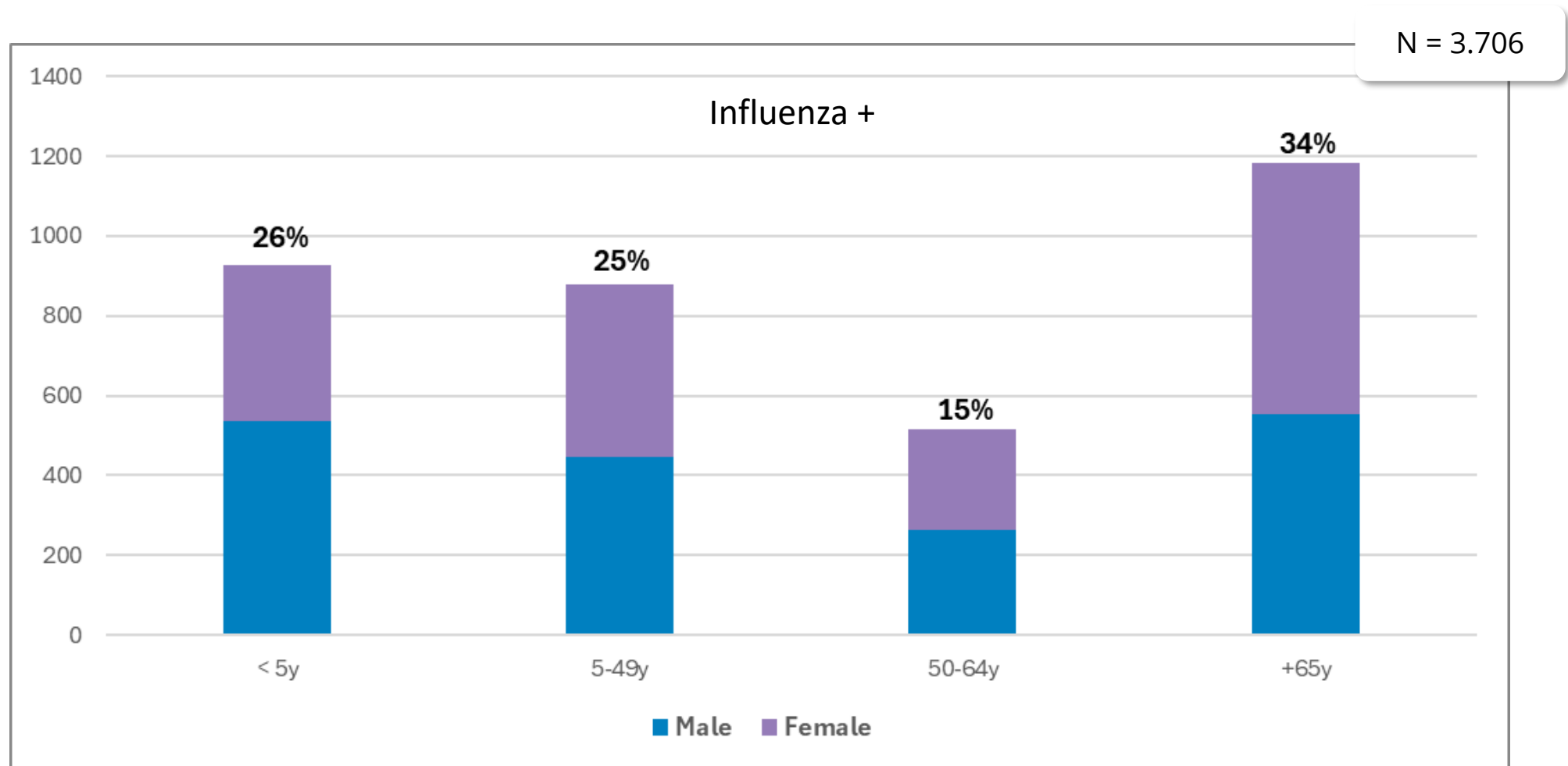


# DISTRIBUTION OF ENROLLED PATIENTS BY AGE GROUP AND SEX – ALL SITES (2023-34) (#) (AS OF NOVEMBER 14TH, 2024)

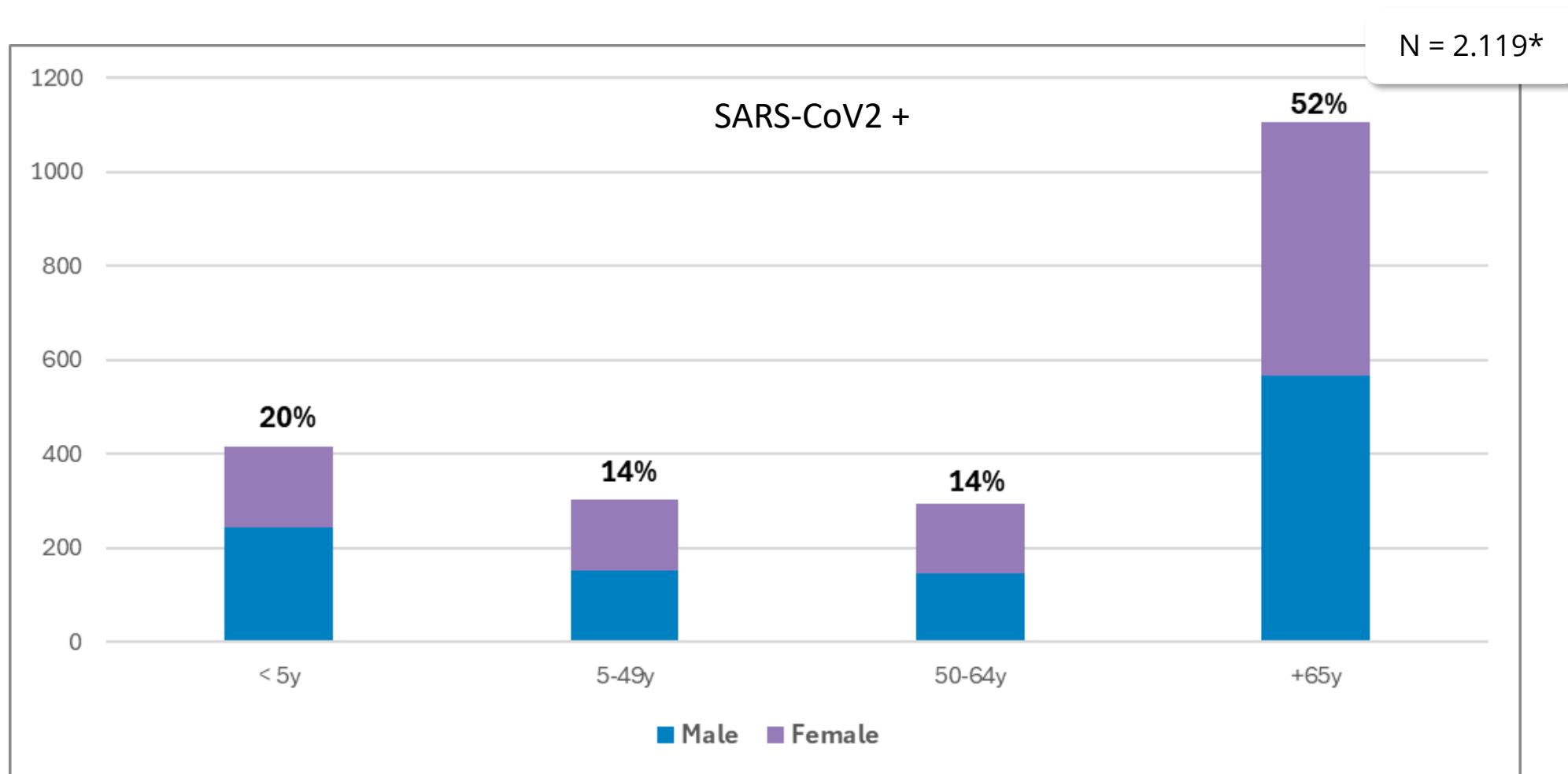


\*50 patients have no age recorded (missing data)

# DISTRIBUTION OF LAB CONFIRMED INFLUENZA CASES BY AGE GROUP AND SEX – ALL SITES (2023-34) (#) (AS OF NOVEMBER 14TH, 2024)

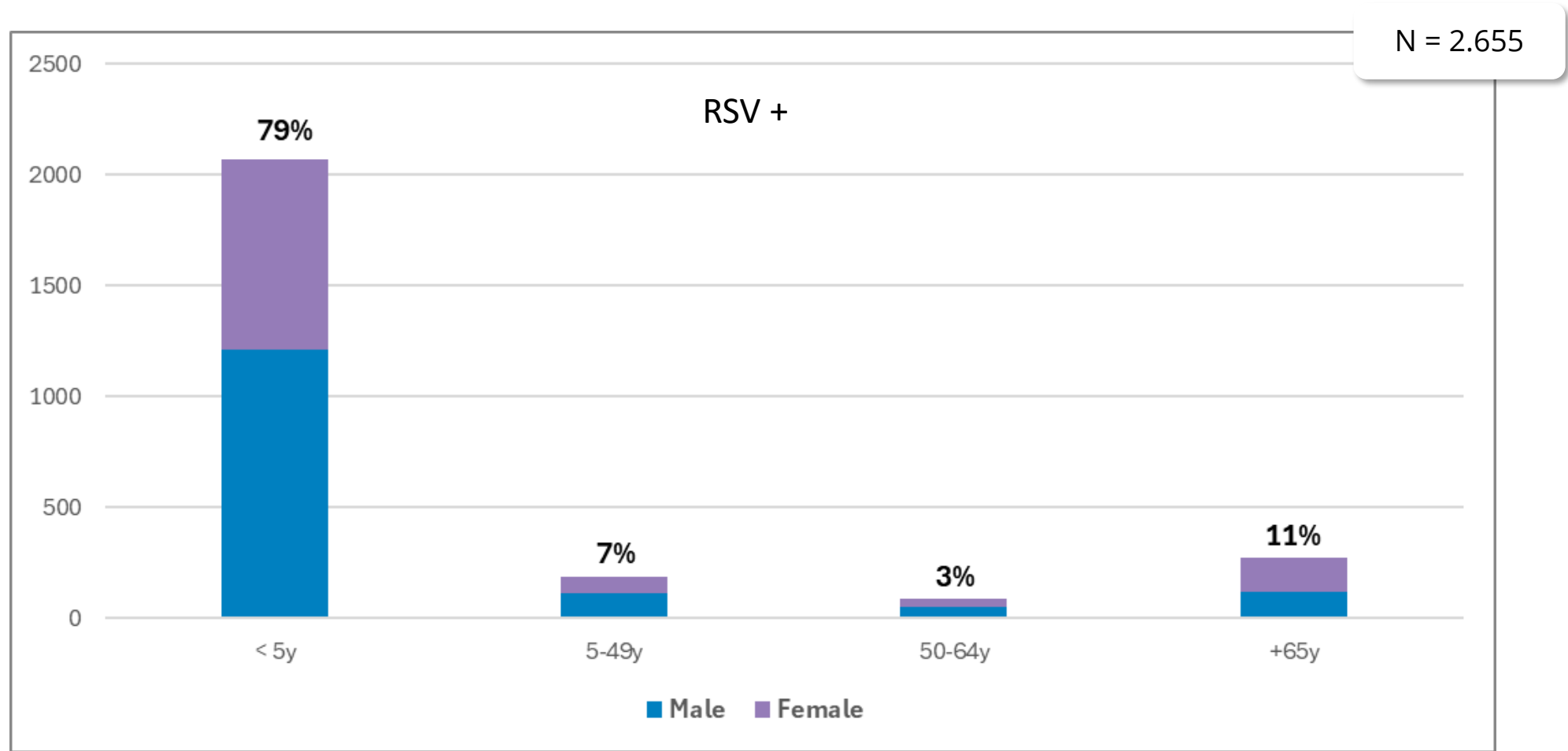


# DISTRIBUTION OF LAB CONFIRMED SARS-COV-2 CASES BY AGE GROUP AND SEX – ALL SITES (2023-34) (#) (AS OF NOVEMBER 14TH, 2024)

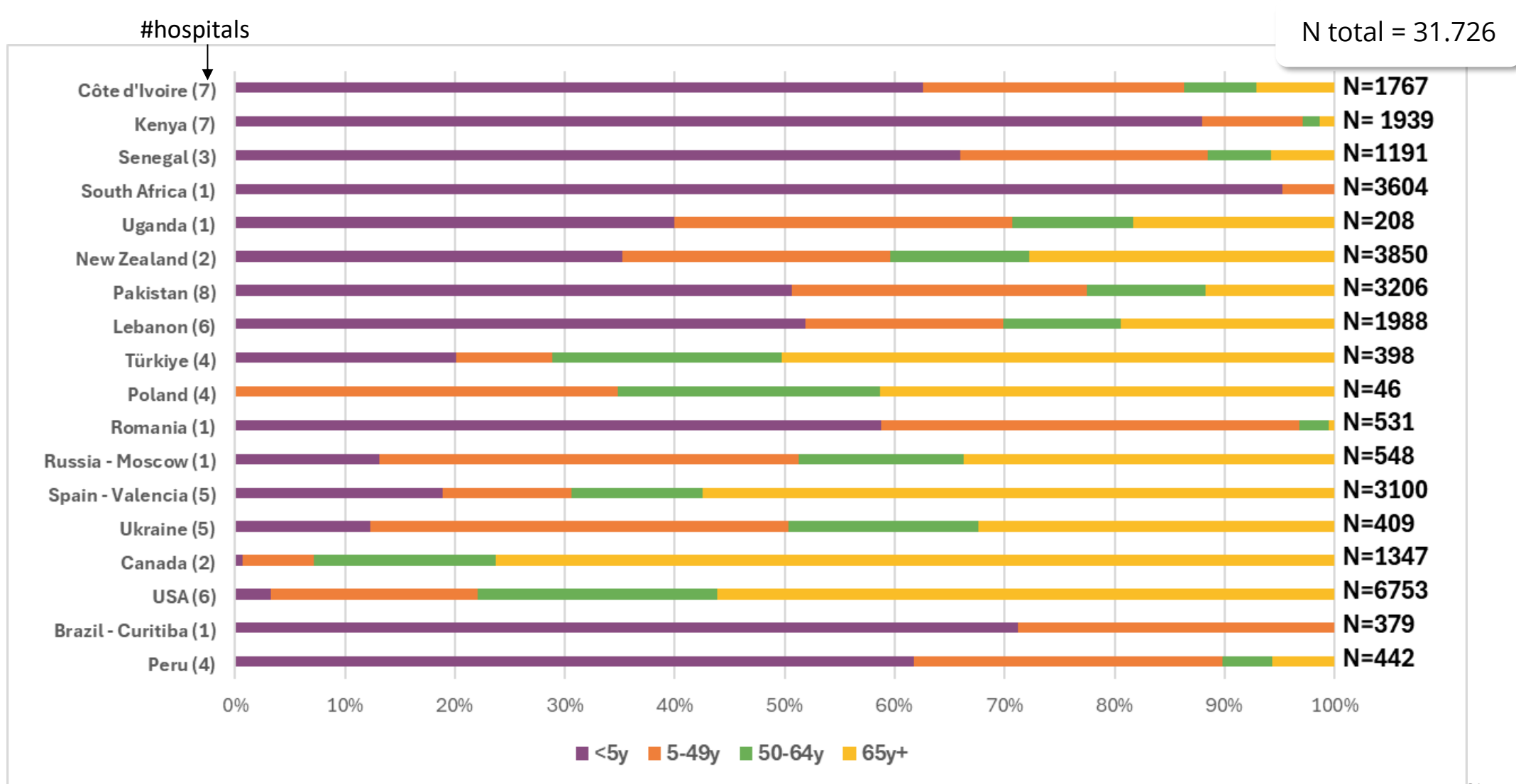


\*8 patients have no age recorded (missing data)

# DISTRIBUTION OF OF LAB CONFIRMED RSV CASES BY AGE GROUP AND SEX – ALL SITES (2023-34) (#) (AS OF NOVEMBER 14TH, 2024)

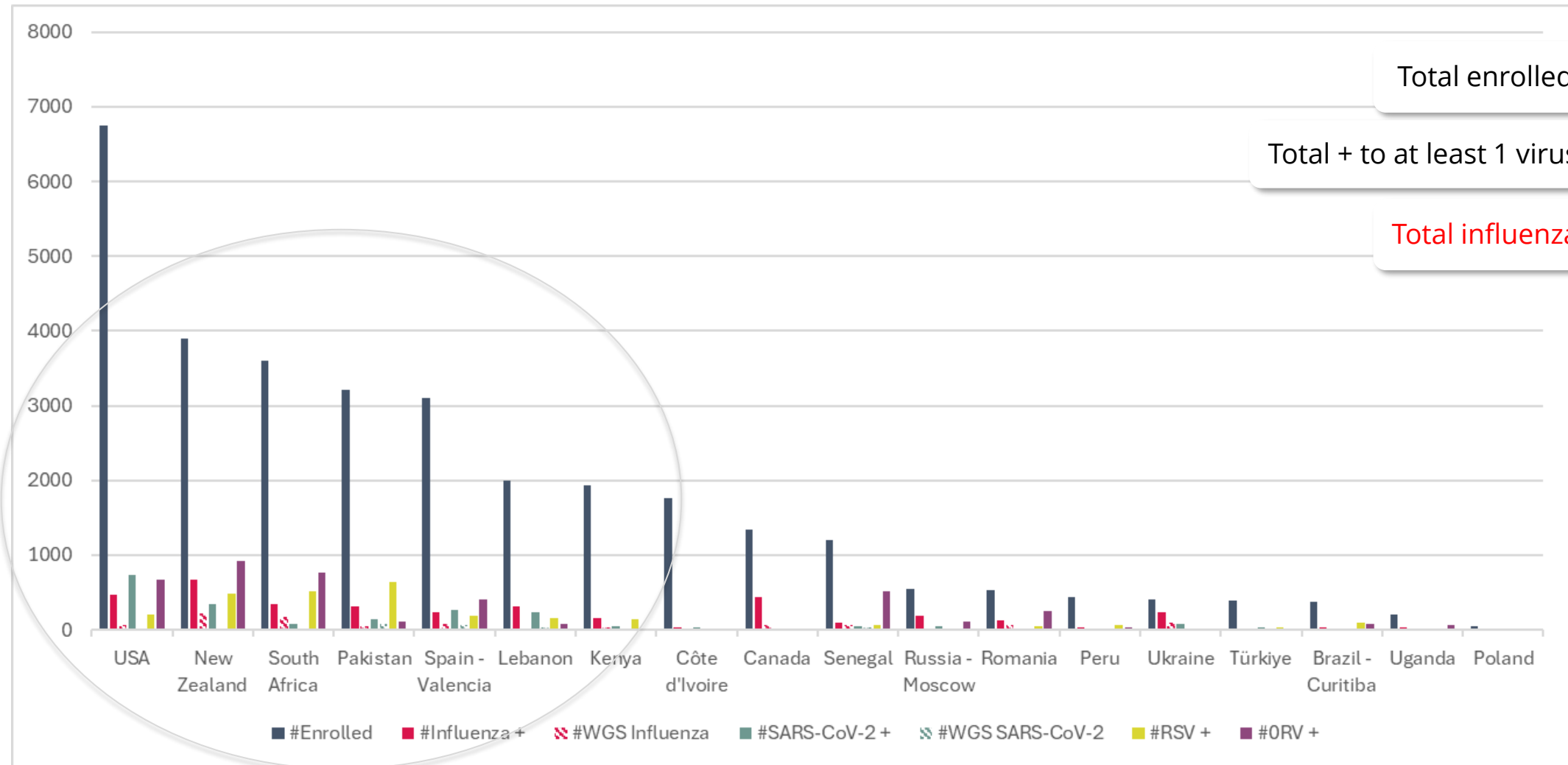


# DISTRIBUTION OF ENROLLED PATIENTS BY AGE GROUP – BY SITE (2023-34) (#) (AS OF NOVEMBER 14TH, 2024)



# DISTRIBUTION OF PATIENTS BY SITE (2023-24) (#)

## (AS OF NOVEMBER 14TH, 2024)



Total enrolled = 31.776

Total + to at least 1 virus = 11.778

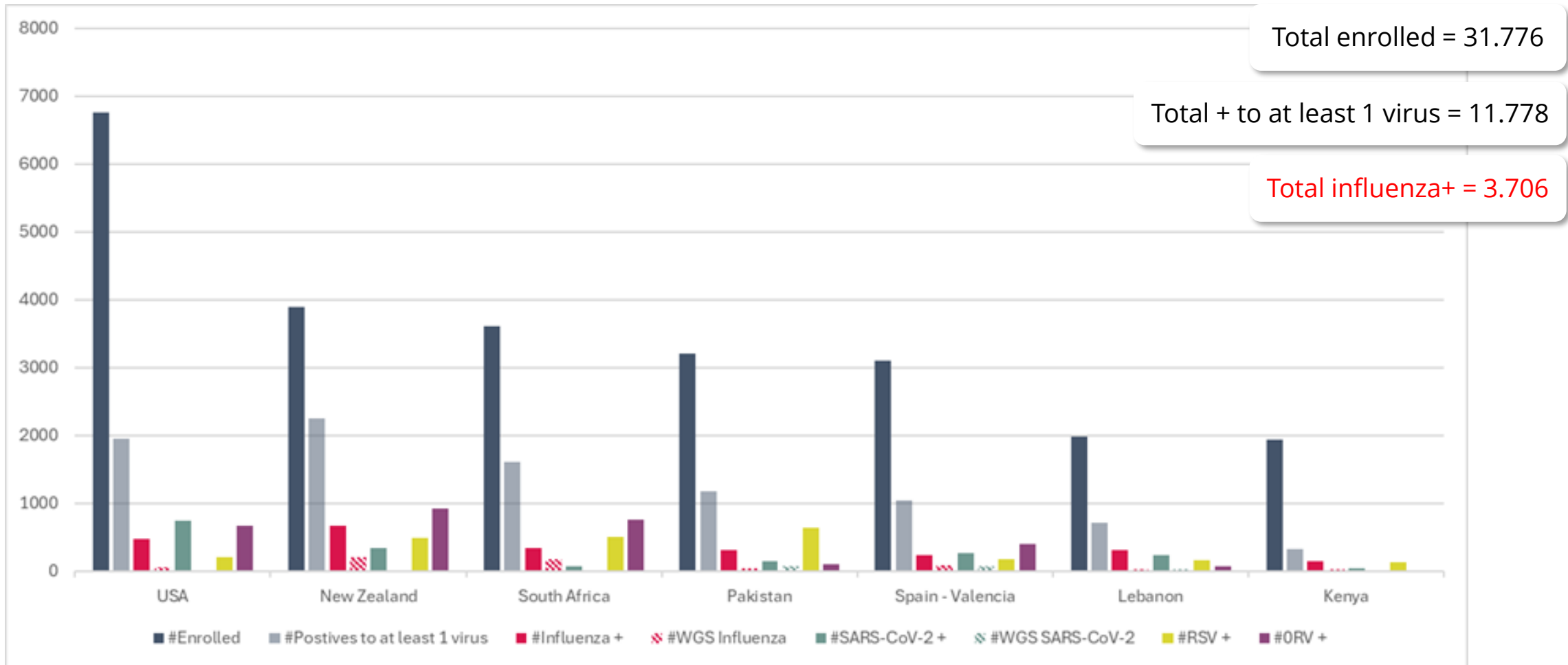
Total influenza+ = 3.706





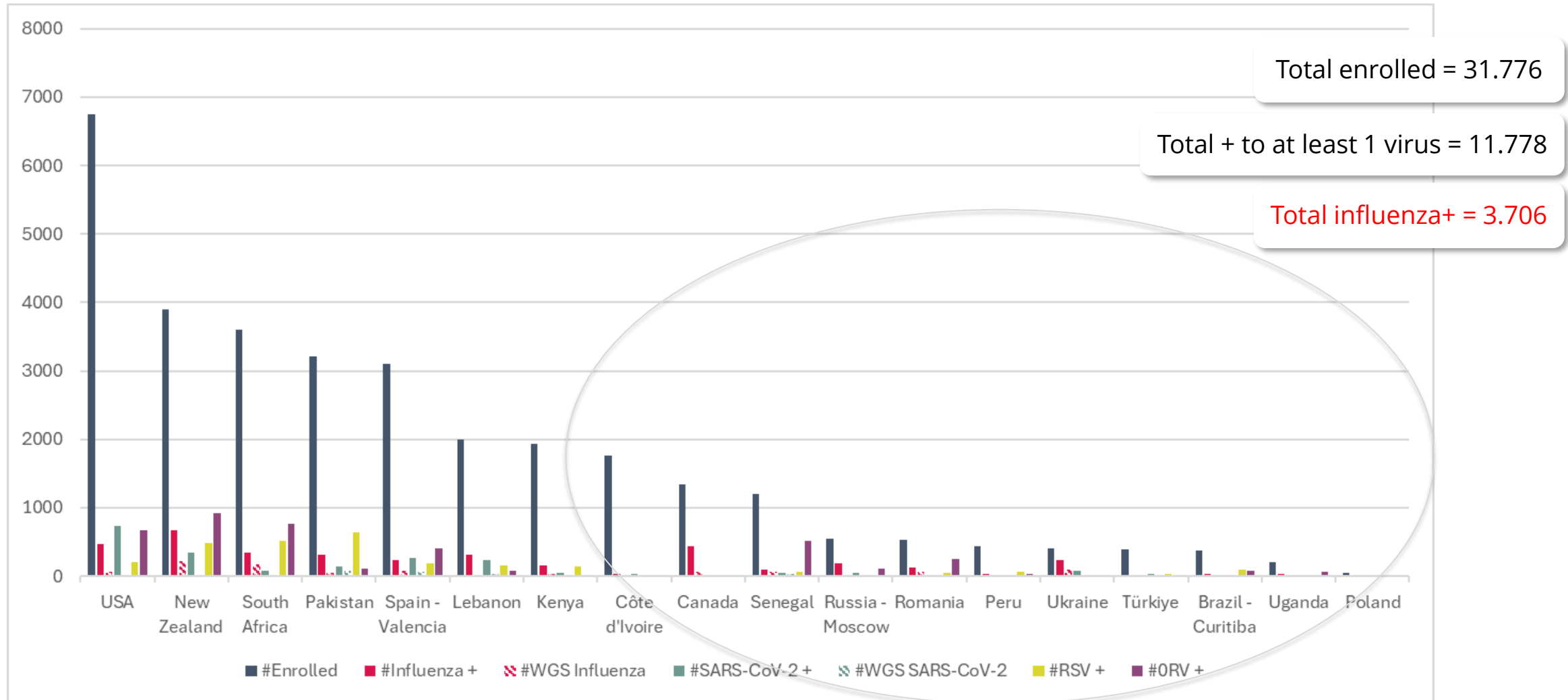
# DISTRIBUTION OF PATIENTS BY SITE (2023-24) (#)

## (AS OF NOVEMBER 14TH, 2024)



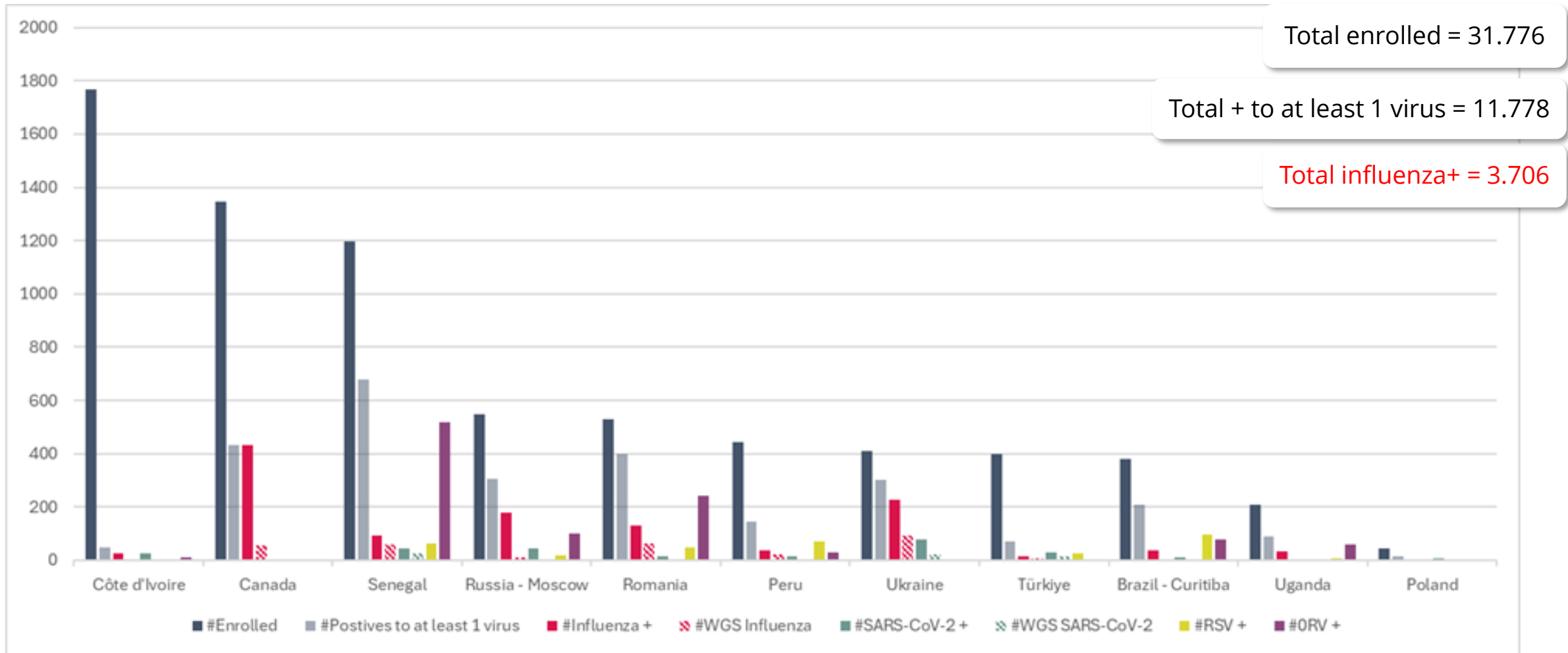
# DISTRIBUTION OF PATIENTS BY SITE (2023-24) (#)

## (AS OF NOVEMBER 14TH, 2024)



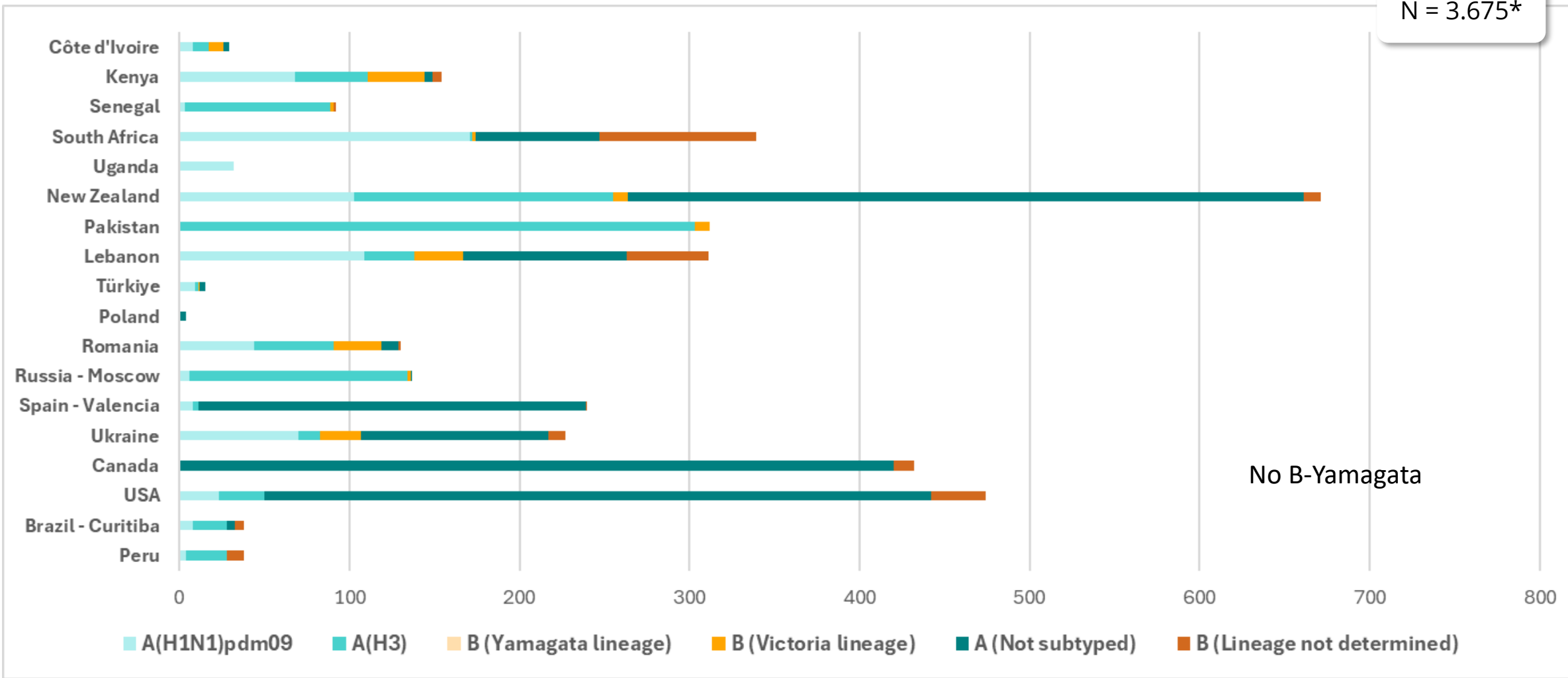
# DISTRIBUTION OF PATIENTS BY SITE (2023-24) (#)

## (AS OF NOVEMBER 14TH, 2024)



# DISTRIBUTION OF LAB CONFIRMED INFLUENZA CASES BY VIRUS SUBTYPE AND LINEAGE (2023-24) (#) (AS OF NOVEMBER 14TH, 2024)

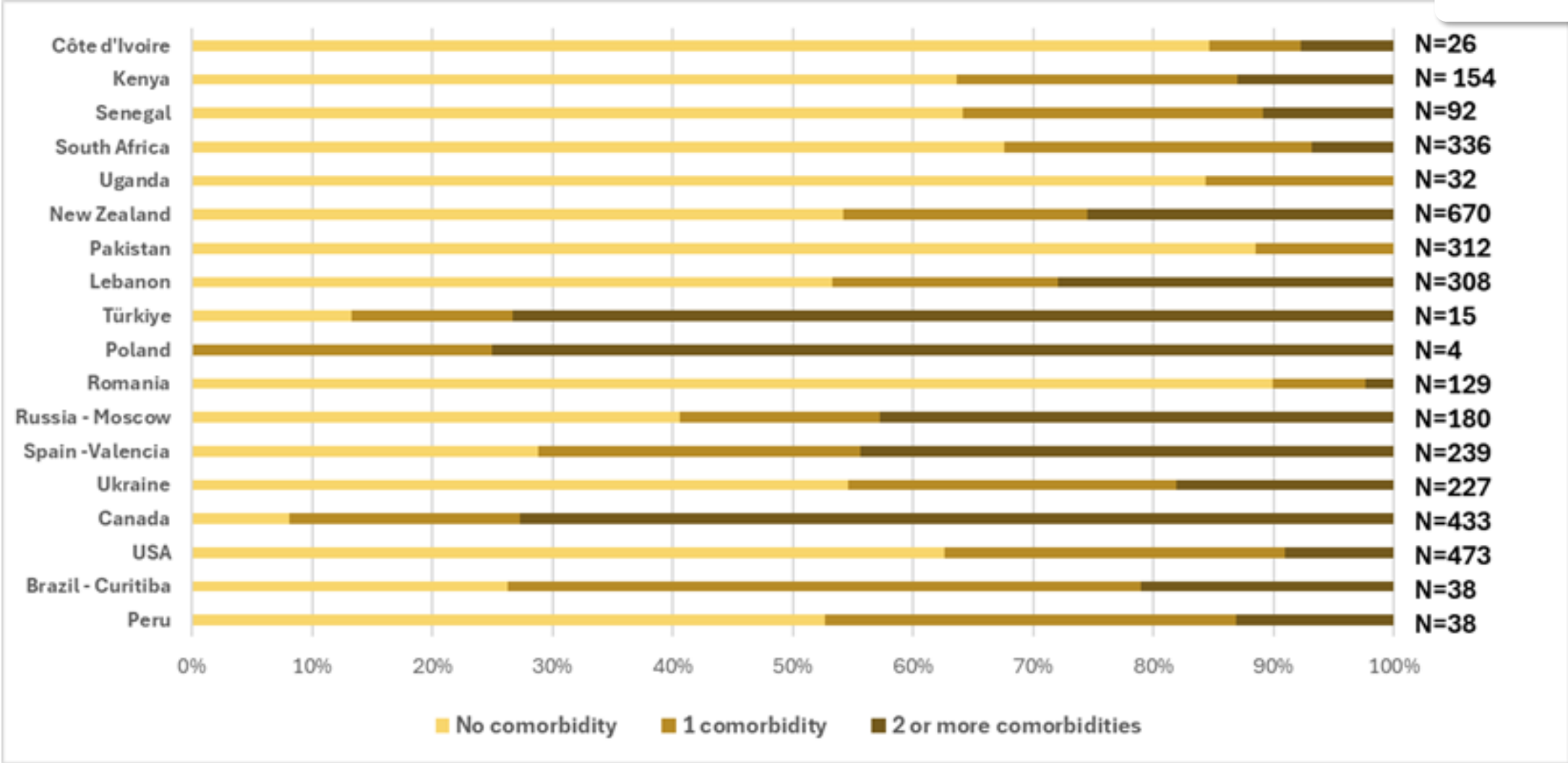
N = 3,675\*



\*44 patients have no strain recorded (pending data)

# PRESENCE OF COMORBIDITIES AMONG LAB CONFIRMED INFLUENZA CASES - BY SITE (2023-24) (%) (AS OF NOVEMBER 14TH, 2024)

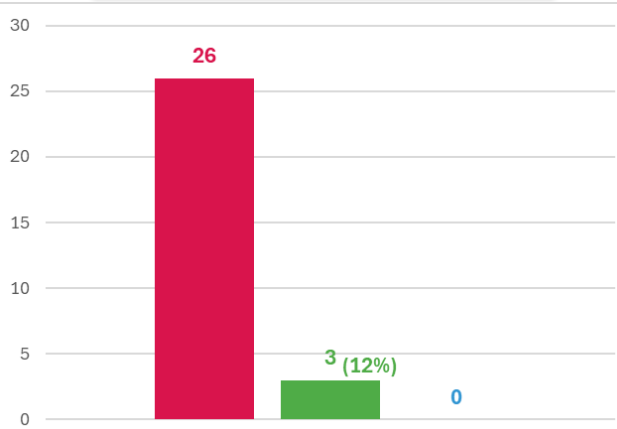
N = 3.706



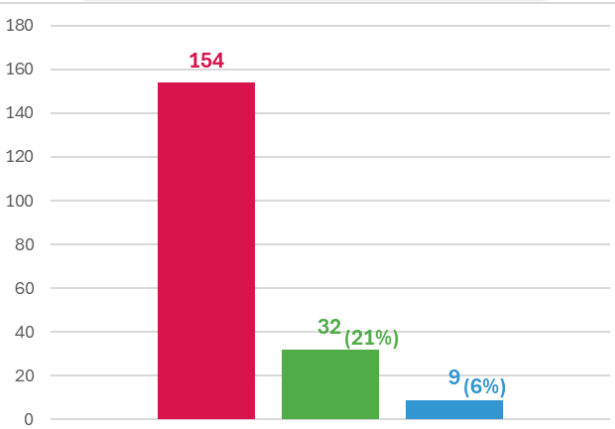
# ICU ADMISSIONS AND DEATHS AMONG LAB CONFIRMED INFLUENZA CASES – BY SITE (2023-24) (#) (AS OF NOVEMBER 14TH, 2024)

## AFRICA

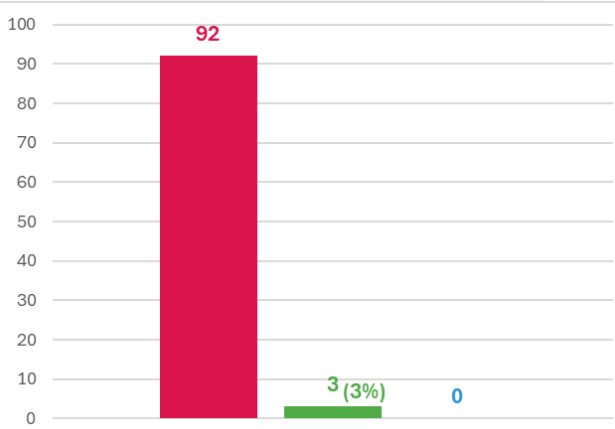
### Côte d'Ivoire



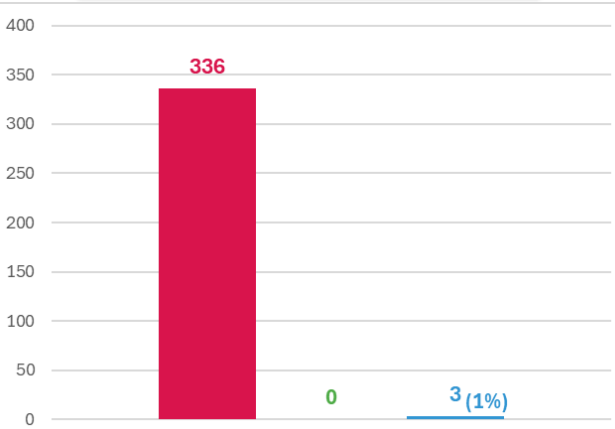
### Kenya



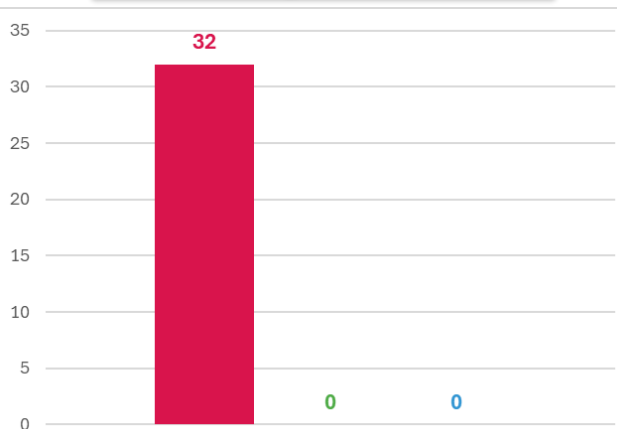
### Senegal



### South Africa



### Uganda



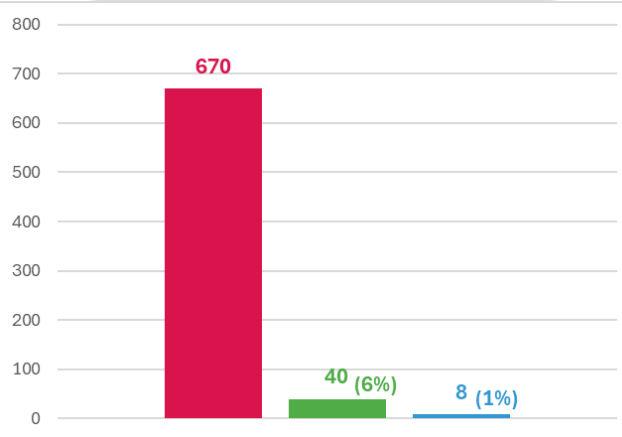
#Influenza+ #ICU admissions #Deaths



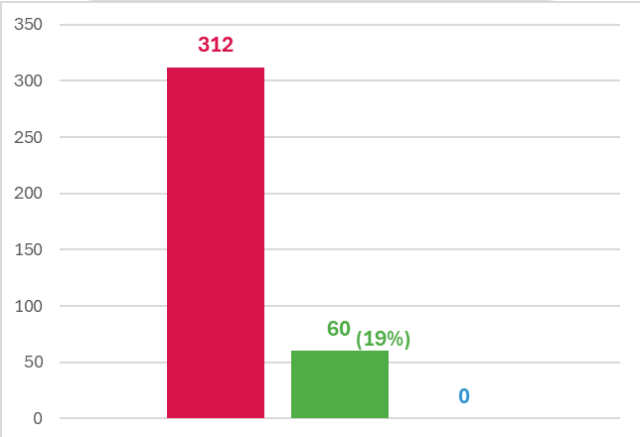
# ICU ADMISSIONS AND DEATHS AMONG LAB CONFIRMED INFLUENZA CASES – BY SITE (2023-24) (#) (AS OF NOVEMBER 14TH, 2024)

## ASIA/PACIFIC

### New Zealand

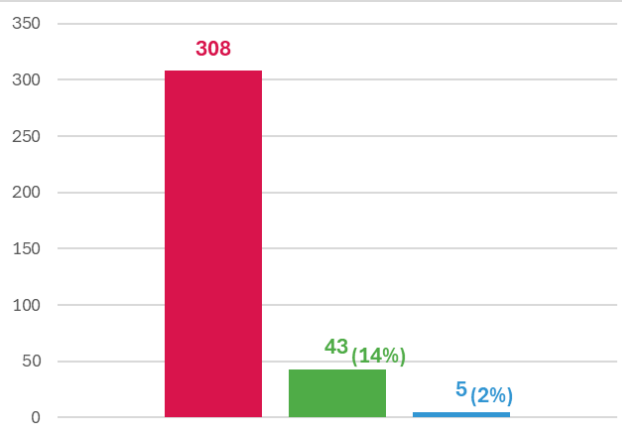


### Pakistan

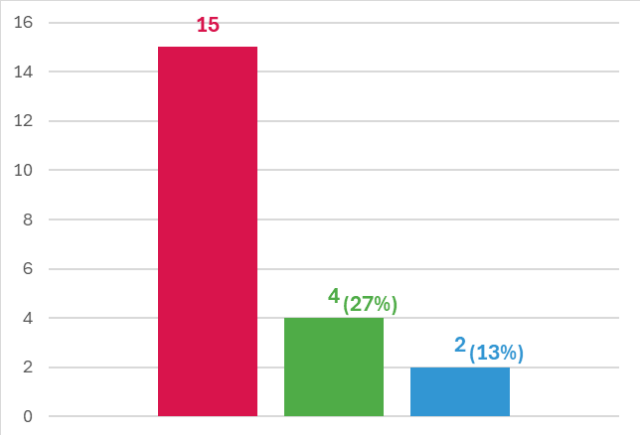


## MIDDLE EAST

### Lebanon



### Türkiye



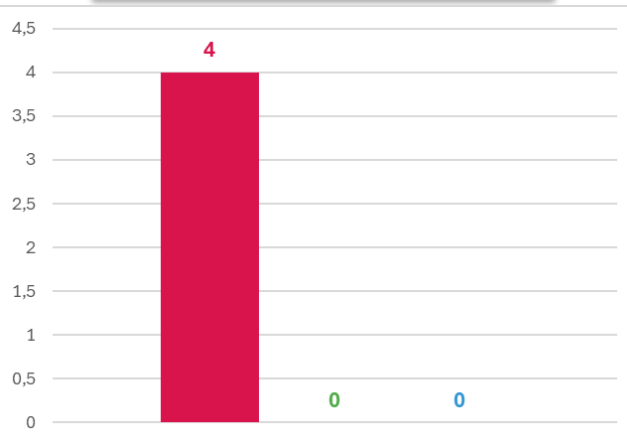
#Influenza+ #ICU admissions #Deaths

# ICU ADMISSIONS AND DEATHS AMONG LAB CONFIRMED INFLUENZA CASES – BY SITE (2023-24) (#)

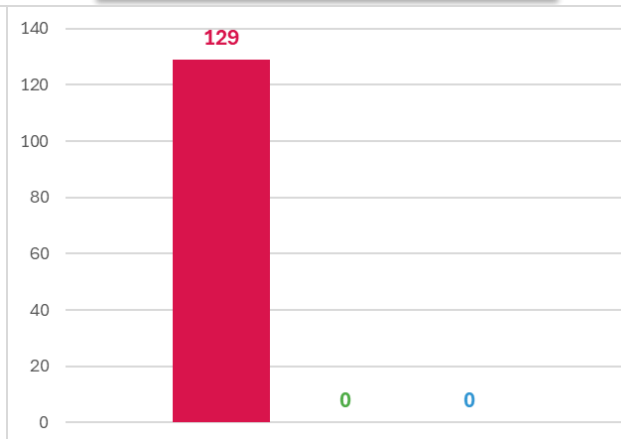
## (AS OF NOVEMBER 14TH, 2024)

### EURASIA

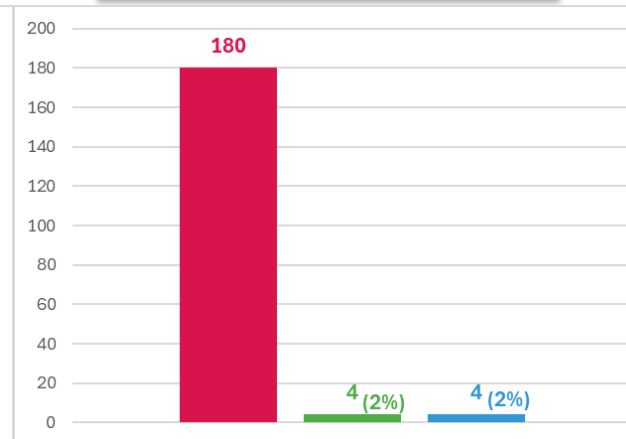
#### Poland



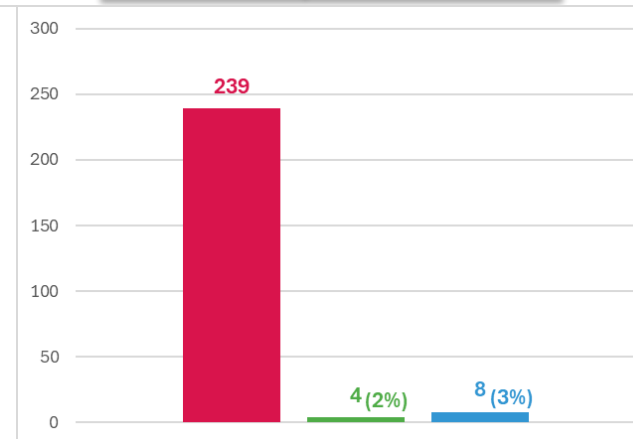
#### Romania



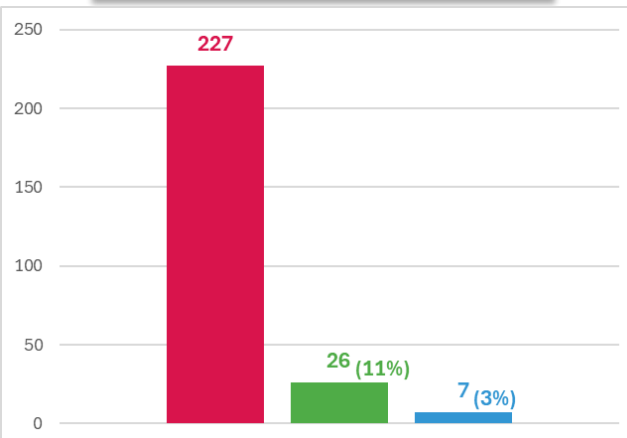
#### Russia - Moscow



#### Spain



#### Ukraine

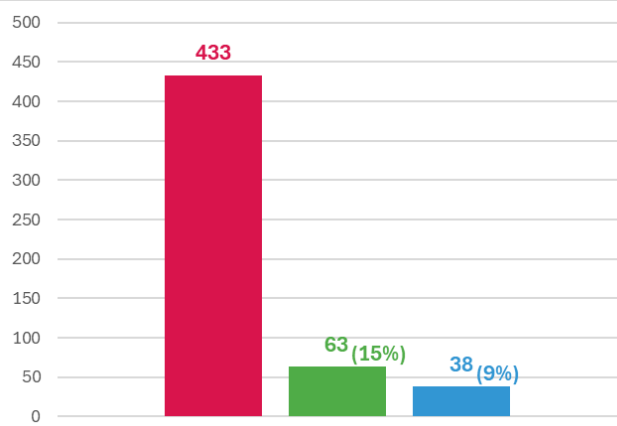


■ #Influenza+ ■ #ICU admissions ■ #Deaths

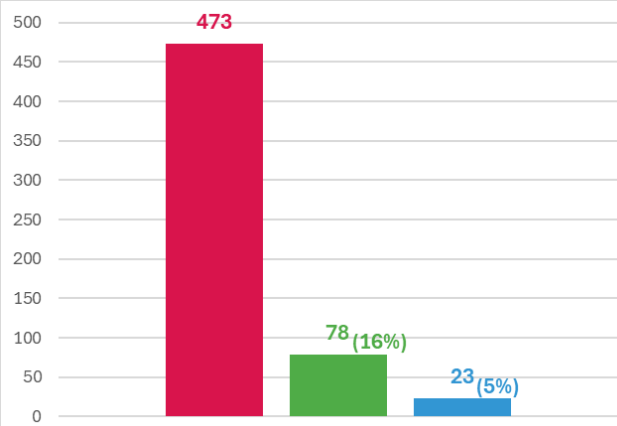
# ICU ADMISSIONS AND DEATHS AMONG LAB CONFIRMED INFLUENZA CASES – BY SITE (2023-24) (#) (AS OF NOVEMBER 14TH, 2024)

## AMERICAS

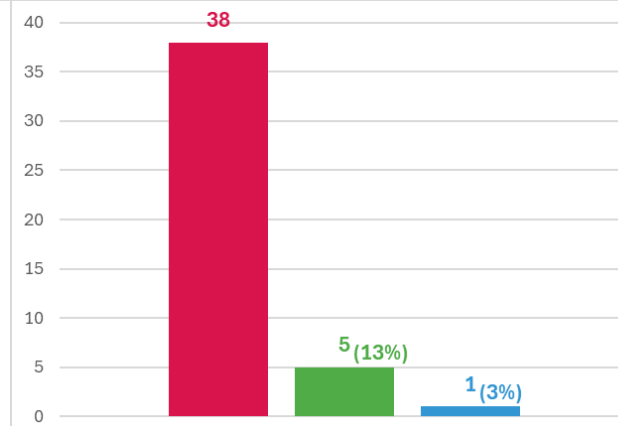
### Canada



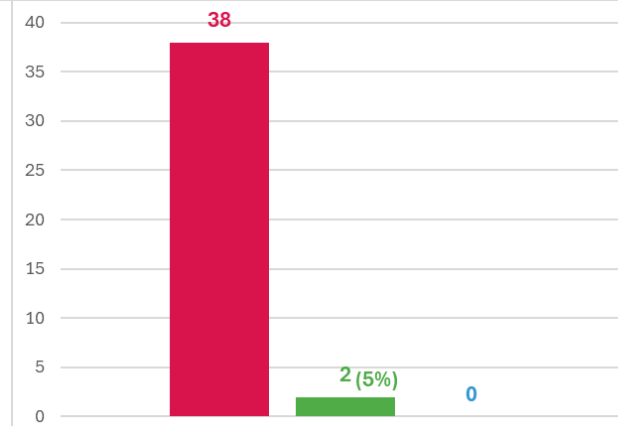
### USA



### Brazil



### Peru



#Influenza+ #ICU admissions #Deaths



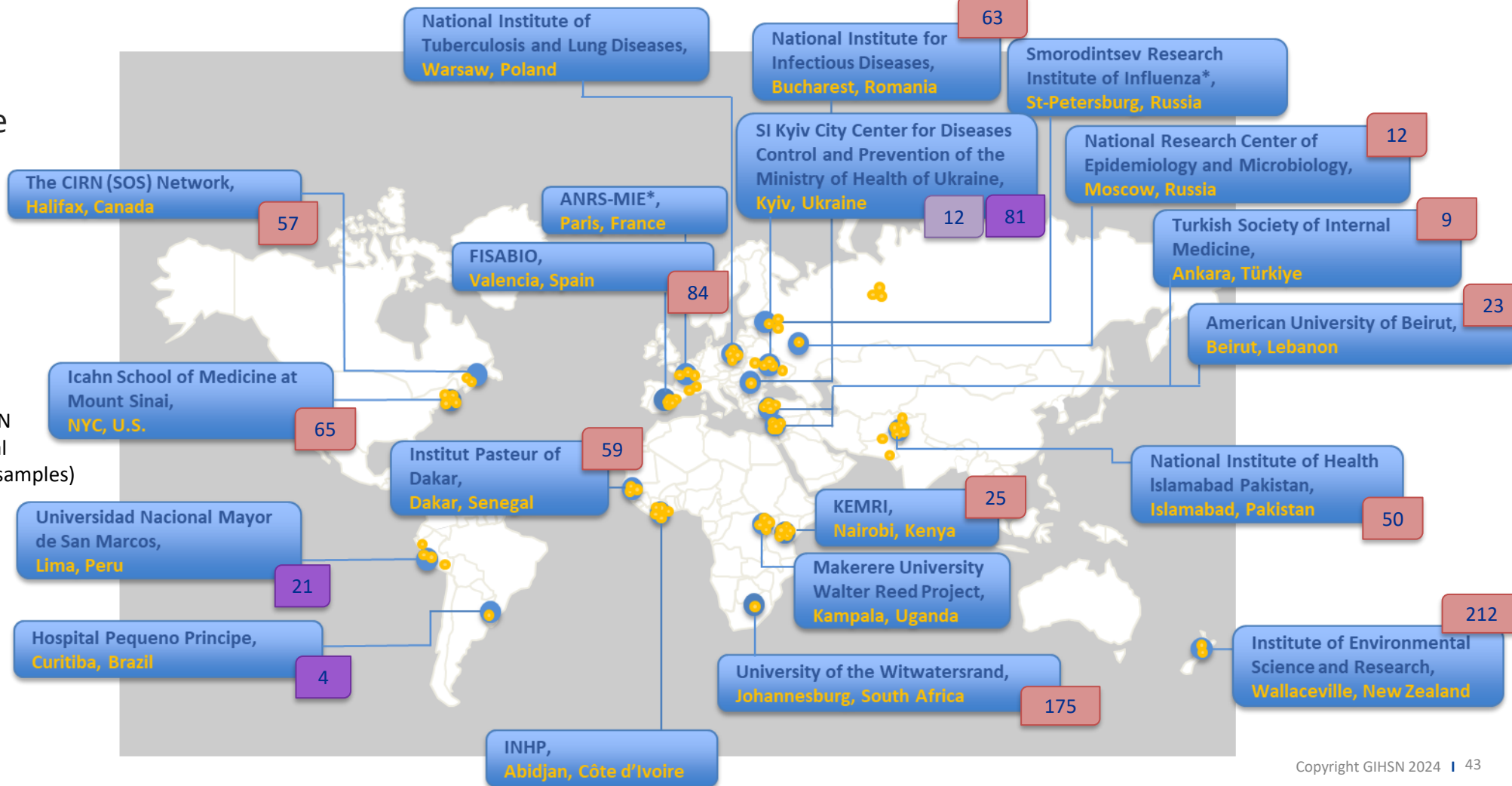
# OVERVIEW OF INFLUENZA VIRUSES SEQUENCED (2023-24) (#)

## (AS OF NOVEMBER 14TH, 2024 IN THE GIHSN DATABASE)

**952 influenza positive samples were detected and fully sequenced** (+ 83 additional WGS received since Nov 14<sup>th</sup>), either locally by sites or through in Lyon NIC (GIHSN sequencing platform)

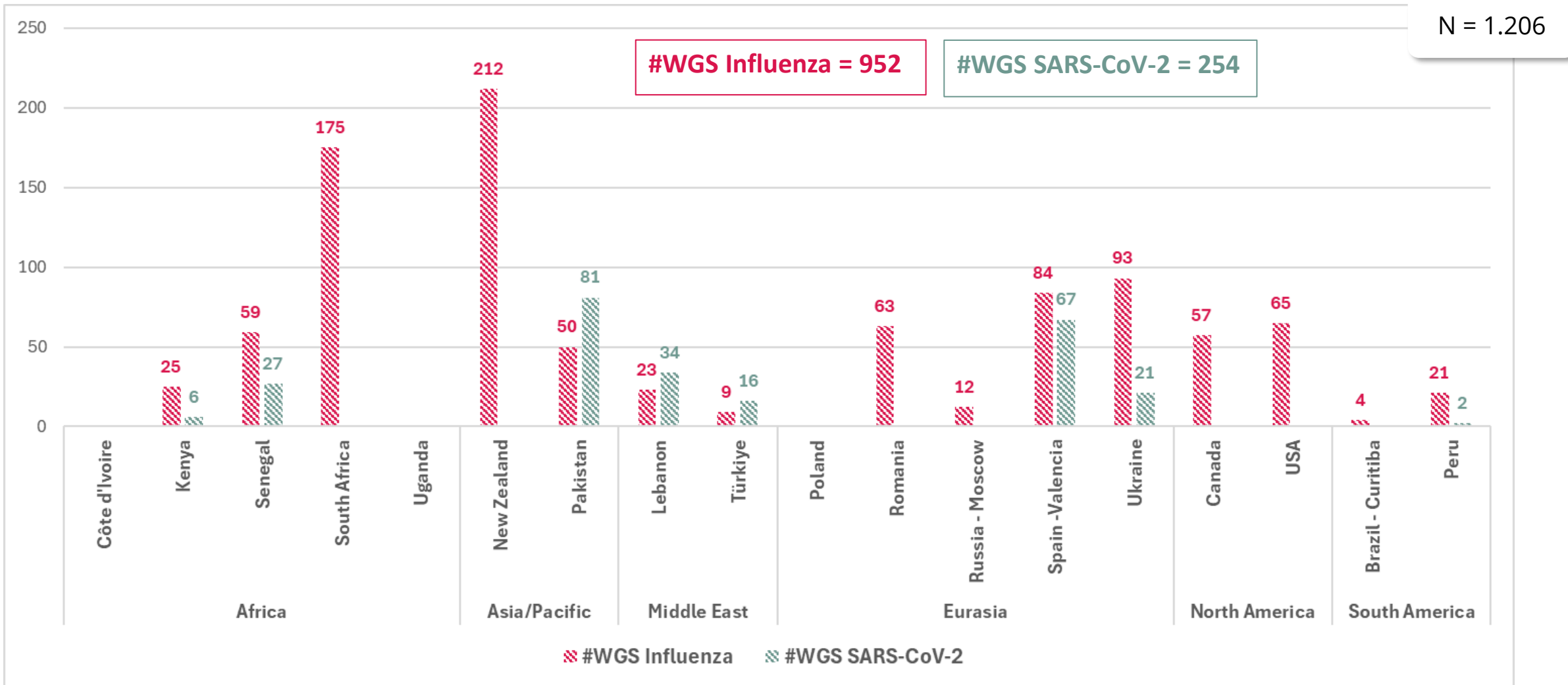
Results were shared with WHO in preparation of the Vaccine Composition Meetings of Feb and Sep 2024.

- Sequencing done locally (total 834 samples)
- Sequencing done through the GIHSN sequencing platform at the National Influenza center in Lyon (total 106 samples)
- Sequencing done through WHO CC (total 12 samples)



# WGS BY SITE (2023-24) (#)

(AS OF NOVEMBER 14TH, 2024 IN THE GIHSN DATABASE)



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*\*Data collection is still ongoing, 129 WGS were added in the GIHSN database since November 14th: Spain (+29 influenza /+46 SARS-CoV-2), USA (+45 influenza), Pakistan (+9 influenza)*

# GIHSN reports provided to the WHO prior to the 2 VCM in February and September 2024



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## GIHSN report of activity prior to the WHO Consultation on the Composition of Influenza Virus Vaccines for use in the 2024-2025 Northern Hemisphere Influenza Season.

Report prepared the 13<sup>th</sup> of September 2024

### 1 - Description of the network

GIHSN is collecting clinical and virological information from hospitalized cases through a network of sites (20) located in different regions of the world (figure 1). This combined clinical and virological surveillance allows the identification of viruses responsible for severe influenza. This severity is assessed by the oxygen requirement of cases registered by the sites. In this report, viruses detected and sequenced from cases requiring oxygen supplementation are identified in the phylogenetic trees provided, to determine if specific lineages or clades are associated with more frequent severe presentation. It has been noted in the GIHSN report of the 2023 surveillance for the southern hemisphere VCM that O2 requirement seemed to be more frequently reported in the A(H3N2) 3C.2a1b.2a.3a HA lineage. This was not confirmed in the 2023-2024 Northern Hemisphere report.

For the SH 2024 surveillance in GIHSN, influenza activity was mainly due to Influenza A viruses in most countries, with co-circulation of A/H1N1 and A/H3N2 in different relative proportions.

Regarding the Influenza B viruses, as for the NH 2023-2024 surveillance, it has been reported a very limited number of detections of B/Victoria lineage viruses, and no B/Yamagata viruses have been detected by the network. This is the 3<sup>rd</sup> year of GIHSN surveillance with no detection of B/Yamagata viruses. Due to the very limited data available on influenza B viruses, no analysis regarding severity can be done at this stage.

This report is colliding the available sequencing data from 12 sites collected on patients admitted in hospital between February 1<sup>st</sup>, 2024 and August 31<sup>st</sup>, 2024: Brazil (4), Kenya (25), Pakistan (50), Peru (21), Romania (63), Russia Moscow (12), Senegal (15), Spain (84), South Africa (175), Türkiye (9), Ukraine (80), USA (65). All 603 sequences, from hospitalized cases only, have been uploaded in the GISAID database with a GIHSN tag.



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Sequencing results indicated that 30% of these viruses belonged to 6B.1A.5a.2a.1 clade close to reference strains A/Victoria/4897/2022 and A/Wisconsin/67/2022, while 70% belonged to 6B.1A.5a.2a clade (Fig. 2). The diversity of origin of these clade 6 B.1A.5a.2a viruses was larger, as compared to the clade 6B.1A.5a.2a1 viruses.

Among 5a.2a clade, all viruses but one belonged to C1 subclade, which can be further differentiated based on HA1 amino acid substitutions into different haplotypes including: C.1:197T; C.1:137S; C.1:120A,169Q; C.1:47I,96T,120A; C.1: 38D,120A,169Q. One virus belonged to C.1.7 subclade.

All viruses from clade 5a.2a.1 belonged to C.1.1.1 subclade. Clade 5a.2a.1 viruses were closer to A/Victoria/4897/2022 reference strain than A/Wisconsin/67/2022, and were characterized by HA1: T216A substitution. Additional HA1 substitutions in some viruses included: R45K, S85P and R113K.

The frequency of report of Oxygen requirement does not seem to be more frequent in cases with specific sub clades of H1N1 viruses (Fig. 2).

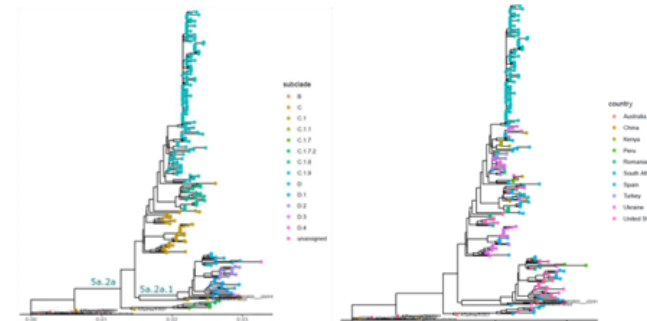


Fig 2a

Fig 2b

Fig 2: Phylogenetic tree of the A(H1N1pdm09) viruses analyzed between February 1st, 2024 and August 31st, 2024. The phylogeny has been inferred using a Neighbor Joining approach (Seaview). Visualization was displayed using ggtree in R.

Fig 2a provide the phylogenetic tree with clade and sub clade distribution;

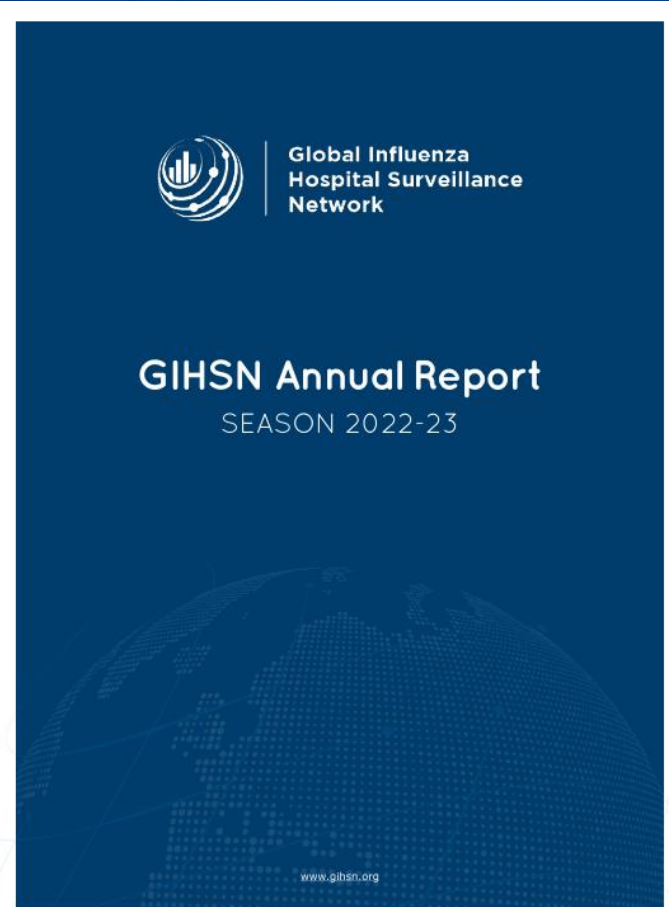
Fig 2b provide the geographic origin of the viruses sequenced by the laboratories of GIHSN, with vaccine reference strains displayed in black.





# ALL RESULTS WILL BE PRESENTED IN THE GIHSN ANNUAL REPORT 2023-24

Proposed cut-off date for 2023-24: mid/end January 2025



[Annual Report 2022-2023 - \(gihsn.org\)](https://gihsn.org)



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THANK YOU!

Q&A

# COFFEE BREAK





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GIHSN 12TH ANNUAL MEETING, 24-26 NOVEMBER 2024

## PANEL 1: SITE EXPERIENCE IN THE GIHSN

*Moderator:* Laurence TORCEL-PAGNON, Foundation for Influenza Epidemiology



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Epidemiology

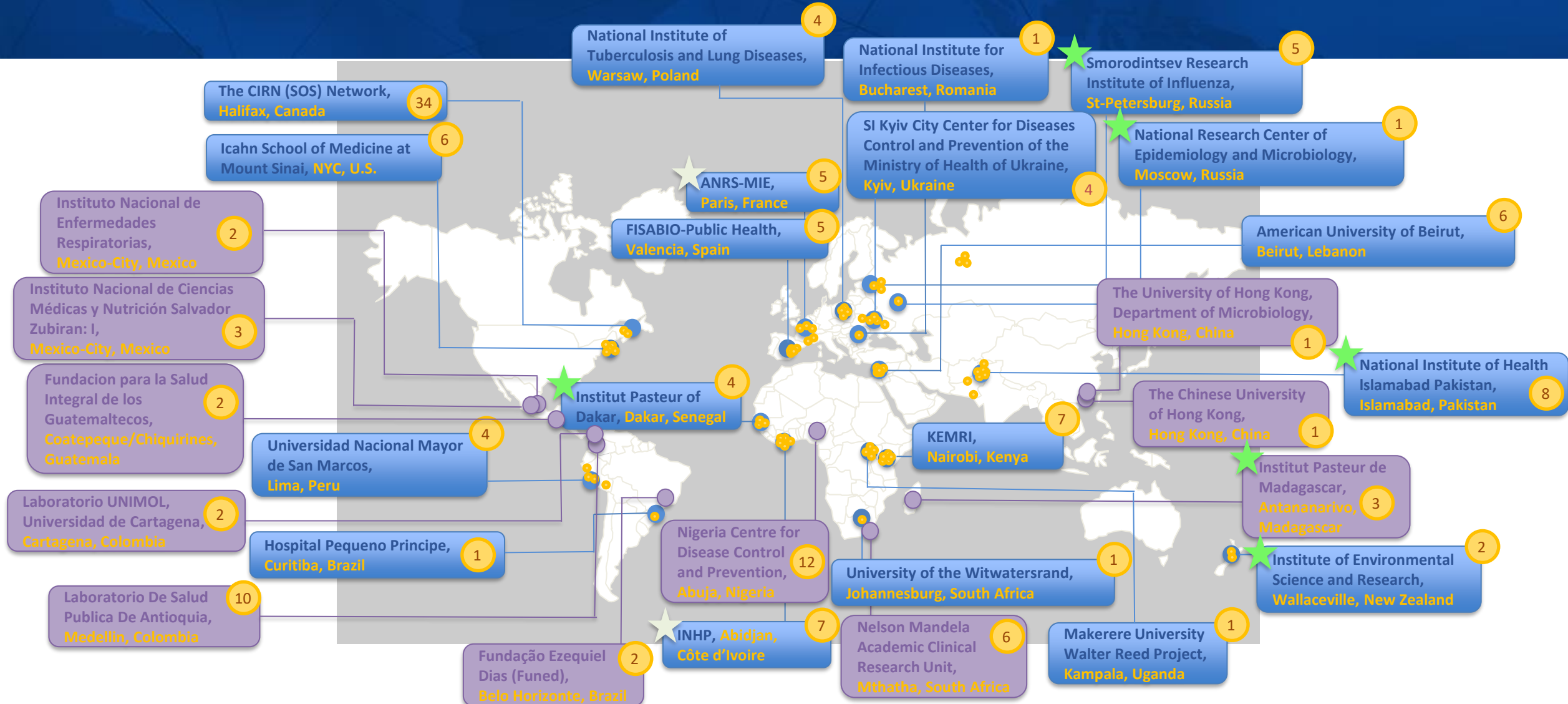
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de  
France

Coordination

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# GIHSN SITES 2024-25 (30)



- Sites already in GIHSN 2023-24
- (x) Number of hospitals per site
- Hospital location
- New sites (2024-25)
- ★ National Influenza Center (NIC)
- ★ Close collaboration with NIC

- ❖ **Around the room introduction from recurrent sites (2' each)**
- ❖ Introduction of recent sites 2023-2024: Uganda, New Zealand, Poland (1 slide - 3' each)
- ❖ Presentation of newcomers 2024-2025 (remotely or video – 2' each)



- ❖ Around the room introduction from recurrent sites (*2' each*)
- ❖ **Introduction of recent sites 2023-2024: Uganda, New Zealand, Poland (*1 slide - 3' each*)**
- ❖ Presentation of newcomers 2024-2025 (remotely or video – *2' each*)





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**GIHSN ANNUAL MEETING, 25 NOVEMBER 2024**

**SITE: UGANDA: MAKERERE UNIVERSITY WALTER REED PROGRAM**

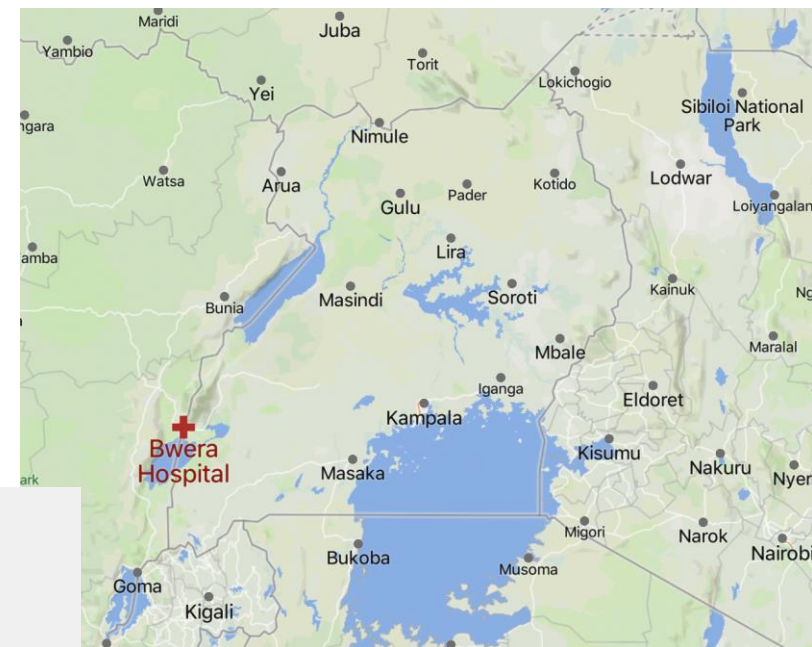
PI/Speaker: Prof Denis K. Byarugaba

# UGANDA

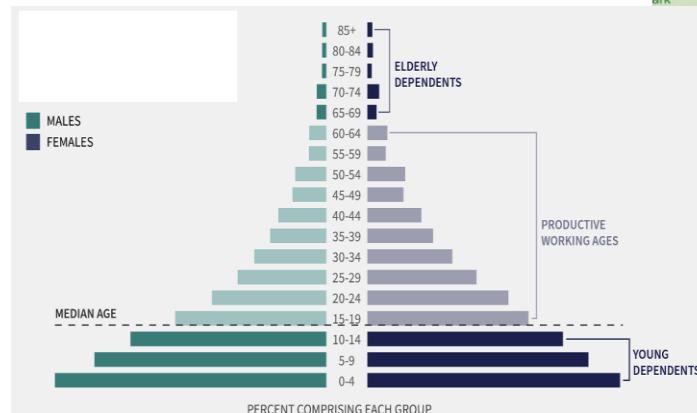


## Site description

- **Coordinating site: Makerere University Walter Reed Program (MUWRP)**
  - Established in 2002 as a non-for-profit Organization guaranteed by Makerere University and The Henry M. Jackson Foundation
  - Engaged in Infectious Disease Surveillance, Vaccine Research (HIV, Ebola etc) and Health care support through PEPFAR
- **Participating hospital: BWERA HOSPITAL**
  - *A public tertiary district hospital owned by the Uganda Ministry of Health.*
  - *Serves Kasese District with patients of all age groups, including from Democratic Republic of the Congo.*
  - *Bed capacity is 100, (may admit up to 300).*
  - *Has a population of about 800,000 inhabitants with a largely young population as shown*



Hospital location





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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

**SITE: NEW ZEALAND**

PI: Prof. Sue Huang

# NEW ZEALAND

## SARI and non-SARI Hospital surveillance, Auckland, NZ

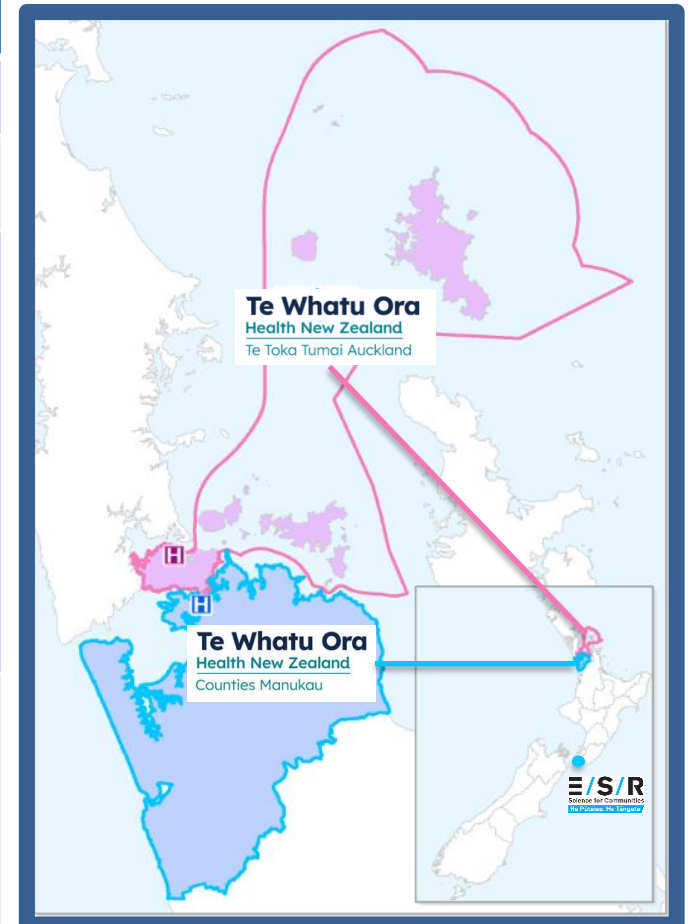
- Coordinating site: ESR, Wallaceville, Upper Hutt, New Zealand

Participating hospitals:	Te Whatu Ora Te Toka Tumai Auckland	Te Whatu Ora Counties Manukau
<b>Setting</b>	Urban	Urban
<b>Capacity</b>	Auckland City Hospital      1000 beds Starship Kids Hospital      219 beds	Middlemore Hospital      860 beds Kidz First Children’s Hospital      82 beds
<b>Services</b>	<p>Secondary-level (hospital and specialist) care Specialist tertiary services (organ transplants (heart, lung, and liver), acute major airway obstruction transferred for laser or stent placement, massive haemoptysis surgery, hepatic surgery, specialist paediatric services, epilepsy surgery, deep brain stimulation, high-risk obstetrics, intensive care)</p> <p>Affiliated University: Faculty of Medical and Health Sciences, University of Auckland</p>	<p>Secondary-level (hospital and specialist) care Specialist tertiary services (orthopaedics and plastic surgery, burns, spinal injury rehabilitation, renal dialysis, neonatal intensive care) Paediatric inpatient surgical care</p>
<b>Population</b>	<p>Estimated 493,000<sup>1</sup></p> <p>8% Maori, 11% Pasifika, 34% Asian, 47% European/Other<sup>2</sup></p> <p>Second highest life expectancy in New Zealand at 83.4 years<sup>2</sup></p>	<p>Estimated 567,000<sup>1</sup></p> <p>16% Maori, 22% Pasifika, 30% Asian, 31% European/Other<sup>3</sup></p> <p>37% of the population, and almost 1 in 2 of the 132,000 children living within Counties Manukau, live in areas of high socioeconomic deprivation<sup>3</sup></p>

<sup>1</sup>2018 census

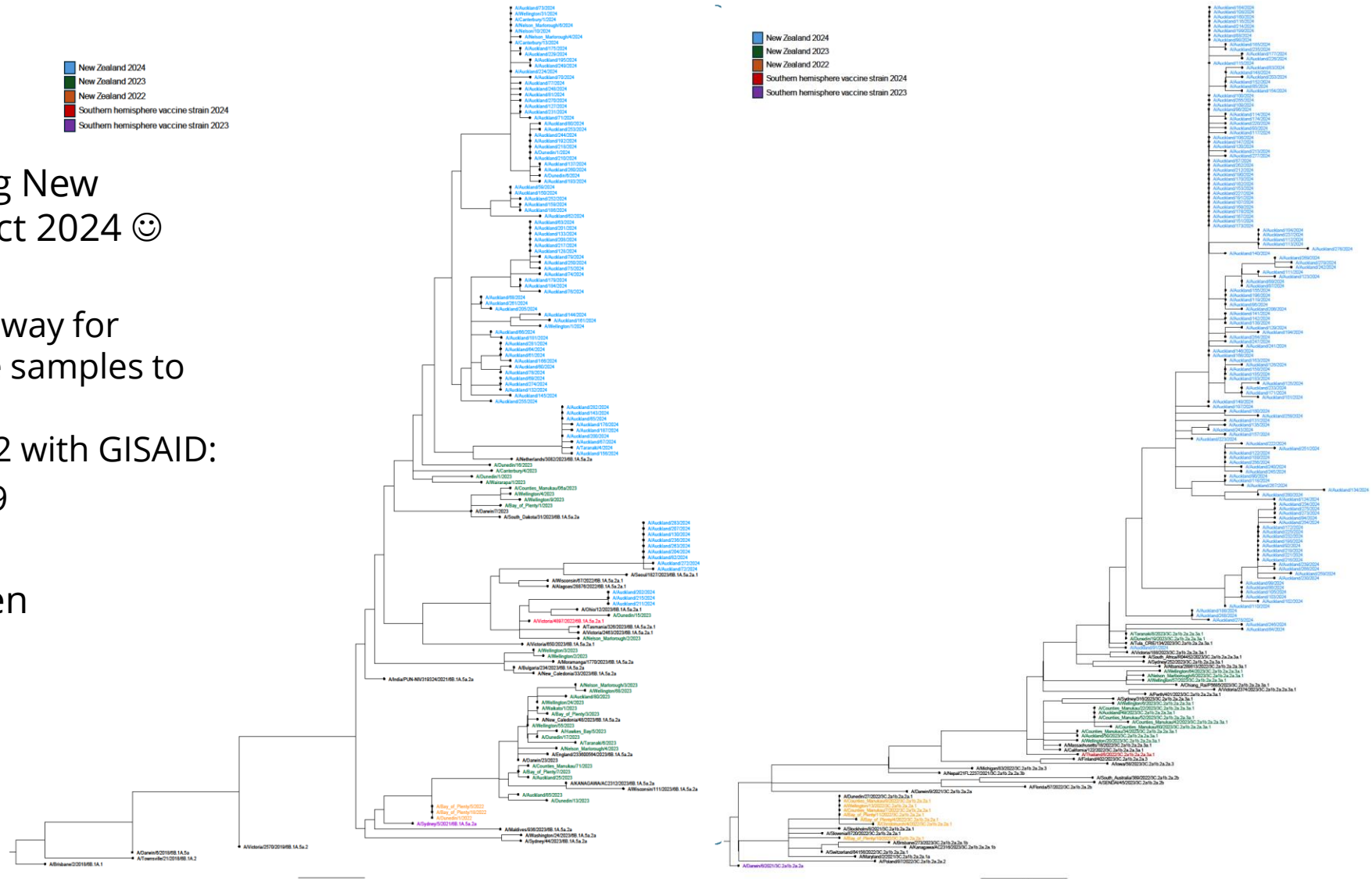
<sup>2</sup>ADHB-Annual-Report-202021

<sup>3</sup>Annual-Report-2021-22-Counties-Manukau





# MAIN TAKE-HOME MESSAGE FROM FIRST YEAR OF PARTICIPATION IN GIHSN



3C.2a1b.2a.2a.1  
3C.2a1b.2a.2a.3  
3C.2a1b.2a.2a.2b  
3C.2a1b.2a.2a.1

- THANK YOU for including New Zealand in Nov 2023 – Oct 2024 😊
- WGS
  - Established referral pathway for hospital SARI-flu positive samples to ESR for WGS
  - Conducted WGS with 222 with GISAID:
    - 80 A(H1N1)pdm09
    - 142 A(H3N2)
- Severity markers – oxygen requirements:
  - Update in CRF





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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

**POLAND - NATIONAL INSTITUTE OF TUBERCULOSIS AND LUNG DISEASES, WARSAW**

PI: Prof. Joanna Chorostowska-Wynimko

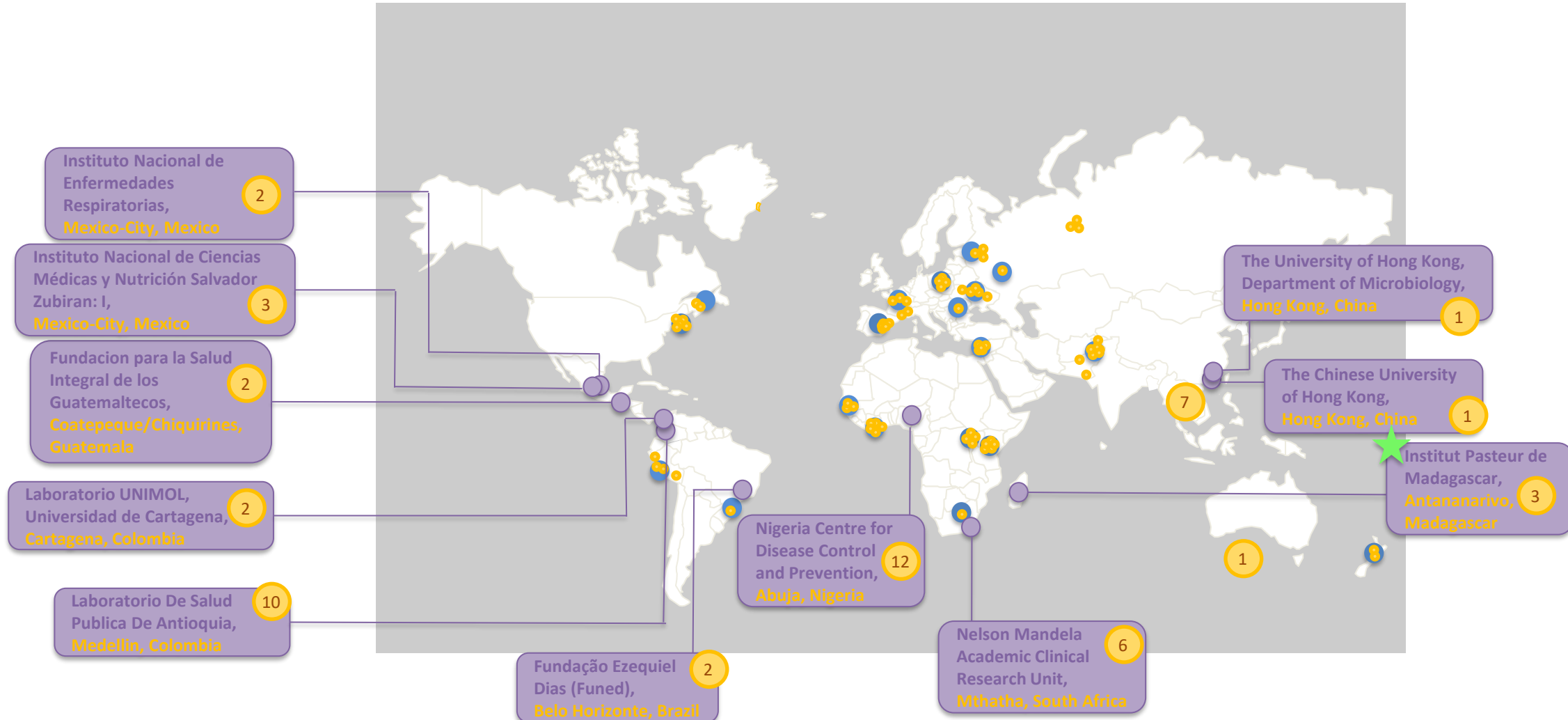
## Site description

- **Coordinating site: The National Institute of Tuberculosis and Lung Diseases (NITLD)**
  - NITLD has had the active internal surveillance program since 2010 with on-site laboratory (based in the Department of Genetics and Clinical Immunology) providing the rapid molecular diagnostic for influenza, RSV, SARS-CoV-2 (since 2020) and other respiratory viral pathogens (parainfluenza (1, 2, 3, 4), human metapneumovirus, human rhinovirus, adenovirus).
- **3 participating hospitals are Urban hospitals - Population: Adults & Elderly**
  - National Institute of Tuberculosis and Lung Diseases (2,5 million catchment area / 300 beds)
  - University Clinical Hospital - Central Veteran Hospital (800 000 catchment area / 630 beds)
  - Kuyavian-Pomeranian Pulmonology Center (330 000 catchment area / 176 beds)
- **Site case ascertainment:** Hospital logs and electronic boards used to check on respiratory illness
- **Case definition:** Patients of any age will be included in the study if they present with up to seven days of community onset influenza like-illness and fulfill the ECDC modified case definition for influenza like-illness (ILI) in last 7 days.
- **Difficulties in engaging hospitals 2 & 3 in this first year with the GIHSN.**



- ❖ Around the room introduction from recurrent sites (*2' each*)
- ❖ Introduction of recent sites 2023-2024: Uganda, New Zealand, Poland (*1 slide - 3' each*)
- ❖ **Presentation of newcomers 2024-2025 (*remotely or video - 2' each*)**

# NEWCOMERS 2024-25 (11)



- Sites already in GIHSN 2023-24
- New sites (2024-25)
- x Number of hospitals per site
- ★ National Influenza Center (NIC)
- ★ Close collaboration with NIC
- Hospital location

# NEWCOMERS 2024-25 (11)

## ASIA

Institution	PI
The University of Hong Kong, Department of Microbiology, Hong Kong, China	Kelvin TO
The Chinese University of Hong Kong, Hong Kong, China	Christopher LAI KOON CHI



## AFRICA

Institution	PI
Institut Pasteur de Madagascar, Antananarivo, Madagascar	Vincent LACOSTE Norosoa RAZANAJATOVO
Nigeria Centre for Disease Control and Prevention, Abuja, Nigeria	Sikiru Olanrewaju BADARU
Nelson Mandela Academic Clinical Research Unit, Mthatha, South Africa	T. APALATA

# NEWCOMERS 2024-25 (11)

## LATAM

Institution	PI
Fundação Ezequiel Dias (Funed), Belo Horizonte, Brazil	Talita Émile RIBEIRO ADELINO
Laboratorio UNIMOL, Universidad de Cartagena, Cartagena, Colombia	Doris GOMEZ CAMARGO
Laboratorio De Salud Publica De Antioquia, Medellin, Colombia	Idabely BETANCUR ORTIZ
Fundacion para la Salud Integral de los Guatemaltecos, Coatepeque/Chiquirines, Guatemala	Daniel OLSON
Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubiran: I, Mexico-City, Mexico	Guillermo M. RUIZ-PALACIOS
Instituto Nacional de Enfermedades Respiratorias, Mexico-City, Mexico	Joel Armando VAZQUEZ-PEREZ





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