



**Global Influenza
Hospital Surveillance
Network**

GIHSN Annual Report

SEASON 2022-23

www.gihsn.org



**Foundation for
Influenza
Epidemiology**

**Fondation
de
France**

IMPACT
Healthcare

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Foreword

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As I write these lines, a large group of international experts or decision makers are conducting the latest round of negotiations of the world's first pandemic treaty - a noble attempt to deal with the next pandemic quicker, better, and more equitably than happened with Covid-19. But, as of today (end of the 9th Intergovernmental Negotiating Body), countries do not seem to be close to a deal notably on the Pathogen Access and Benefit Sharing part.

Trust is a pre-requisite for such a treaty. Trust can be enabled by co-construction. A pragmatic approach with a progressive scale up of few joint initiatives as a proof of concept is probably the way to go.

The Covid-19 pandemic has further exposed weaknesses in disease surveillance and highlighted the importance of strategic and targeted investments for optimal response. Ensuring laboratories and clinics are connected and have good geographic representativeness is essential if we are to understand the public health relevance of the circulating pathogens.

The Foundation for Influenza Epidemiology (FIE) offers the opportunity to join forces and to contribute to a more comprehensive respiratory virus surveillance system by scaling up the existing Global Influenza Hospital Surveillance Network (GIHSN). Collaboration with such an agile surveillance framework, can enhance response, potentially being more effective in capturing the epidemiologic characteristics of an emerging virus, and identifying risk groups to be prioritized for interventions. The GIHSN offers critical capabilities in support of future needs and incentives to engage industry, leveraging both catalytic funding and in-kind contributions. Improving surveillance by a mosaic of complementary and communicating networks working together is probably the more inclusive, cheaper, and agile approach.

GIHSN, more than a research or public health platform, could become the proof of concept that we can all work together and build the mutual trust needed between private sector, multilaterals, member states and civil society. The Memorandum of Understanding signed with the World Health Organization (WHO) in October 2023 is a first promising step in this direction.

”



Dr Cedric Mahe

President, Foundation for Influenza Epidemiology



Abbreviations and definitions

APDC (Abbott Pandemic Defense Coalition): a global industry-led scientific and public health partnership dedicated to the early detection of, and rapid response to, future pandemic threats.

eCRF: electronic Case Report Form.

FIE: Foundation for Influenza Epidemiology.

FluNet: an online tool used for virological surveillance of influenza. FluNet is operated by GISRS (see below) <https://www.who.int/tools/fluNet>

GDPR (General Data Protection regulation): the Regulation in European law on data protection and privacy.

GIHSN (Global Influenza Hospital Surveillance Network): a global network of clinical centers/hospitals, connected with laboratories, established in 2012 to generate clinical and virological data on severe influenza. The GIHSN is operated by a dedicated fund, the Foundation for Influenza Epidemiology, under the auspices of Fondation de France. <https://www.gihsn.org/>

GISAID (Global Initiative on Sharing Avian Influenza Data): a global science initiative established in 2008 that provides open access to genomic data of influenza viruses and the coronavirus responsible for the COVID-19 pandemic. <https://gisaid.org/>

GISRS (Global Influenza Surveillance and Response System): a global network of laboratories which was established in 1952 to conduct global influenza surveillance. GISRS is coordinated by WHO and endorsed by national governments. GISRS operates FluNet, an online tool used for virological surveillance of influenza. <https://www.who.int/initiatives/global-influenza-surveillance-and-response-system>

ICU: Intensive Care Unit.

ICD: International Classification of Diseases.

ISC: Independent Scientific Committee.

IVI (International Vaccine Institute): a nonprofit international organization established in 1997 as an initiative of the United Nations Development Program (UNDP). IVI is dedicated to vaccines and vaccination for global health. <https://www.ivi.int/>

NICs: National Influenza Centers are national institutions designated by national Ministries of Health which collect virus specimens in their country and ship representative clinical specimens and isolated viruses to WHO Collaborating Centers for advanced antigenic and genetic analysis. The results form the basis for WHO recommendations on the composition of seasonal influenza vaccine each year. Several NICs participate in the GIHSN.

R&D: Research and Development.

RSV: Respiratory syncytial virus.

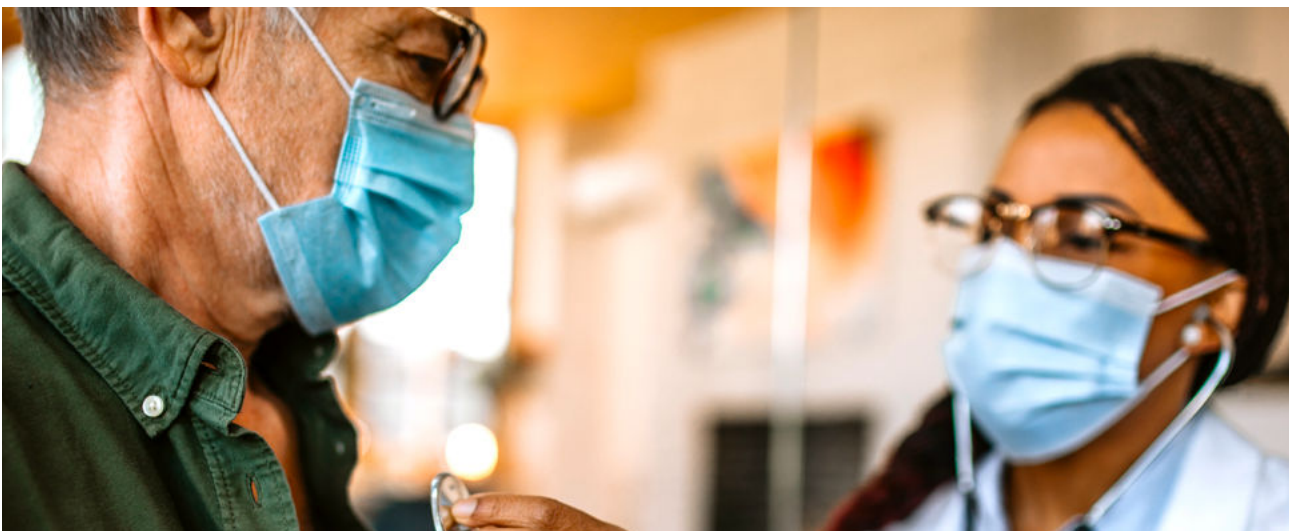
RT-PCR: Reverse Transcription - Polymerase Chain Reaction.

SARI: Severe Acute Respiratory Infection.

SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2.

WGS: Whole Genome Sequencing.

WHO: World Health Organization.



PART I.

The Global Influenza Hospital Surveillance Network (GIHSN)

The Global Influenza Hospital Surveillance Network is a platform that collects standardized data from hospitalized patients with severe acute respiratory illnesses across countries, including low-, middle-, and high-income countries from both hemispheres. The GIHSN has evolved over the last 11 years to focus on linking

epidemiologic and clinical data with WGS information to facilitate exploring viral phenotypes as they relate to severity or vaccine-breakthrough cases. This information is shared with local public health authorities, the World Health Organization (WHO) and the scientific community at large.

Objectives of the GIHSN

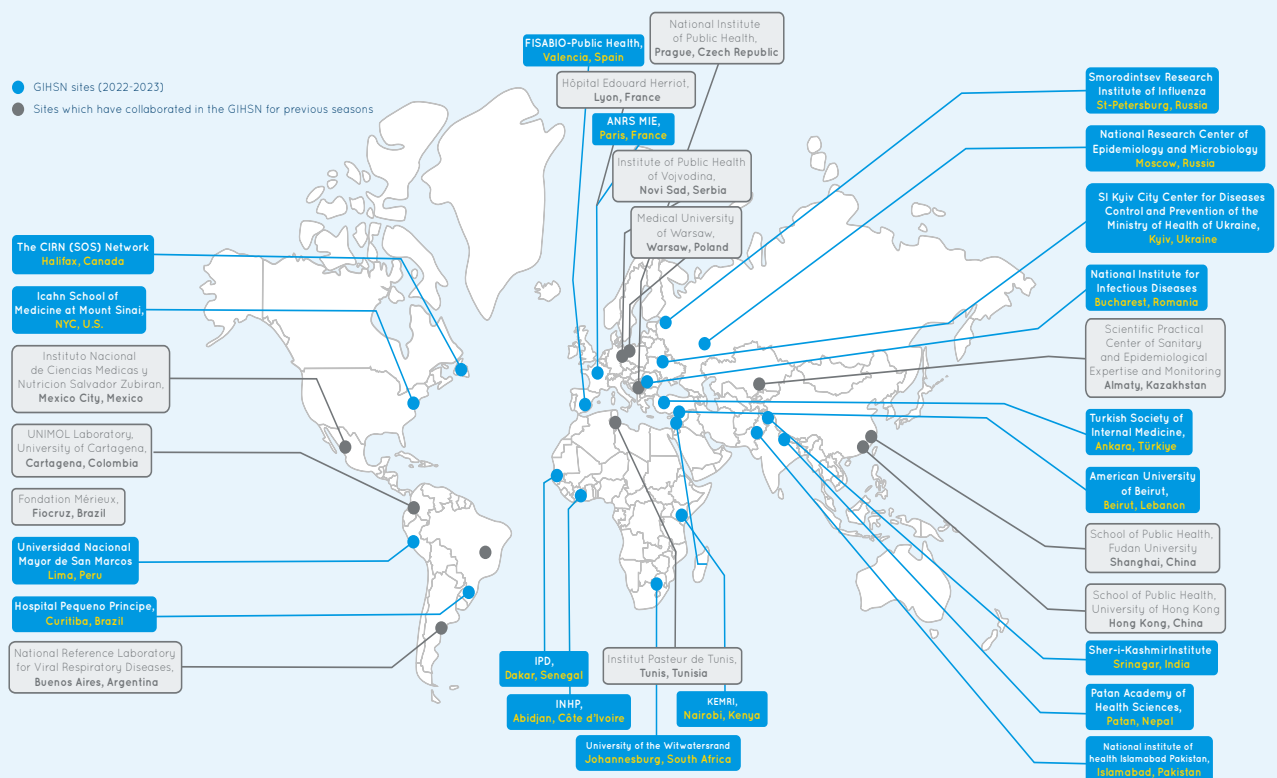
1. Generate strong epidemiological and medical evidence on hospitalized patients with respiratory virus infection to better understand virus circulation, related severity, and risk factors.
2. Support vaccine strain selection improvement through timely sharing of clinical and laboratory data (including whole genome sequencing data) from patients hospitalized with influenza from both northern and southern hemispheres.
3. Contribute as an alert system in case of emerging of novel influenza viruses and other pandemic-prone respiratory viruses that may trigger the need for public health response and/or R&D initiatives.

1. A community of experienced investigators worldwide

The GIHSN started its activity in 2012-2013 and has been collecting data over the seasons. It has contributed to global surveillance of influenza and other respiratory viruses for 11 years now, with over 100 hospitals involved in 27 countries worldwide.

Figure 1 shows the geographic distribution of sites which have collaborated in the GIHSN over the seasons (2012-2013 to 2022-2023).

Figure 1 : Geographic distribution of sites which contributed data in the GIHSN over the seasons (2012-2013 to 2022-2023)



Length of contribution in the GIHSN vary from one site to another: some sites have been participating in the GIHSN for several years, even from the first season; others have been recently involved, some were new in 2022-2023.

See list of sites/institutions which contributed over the years on the GIHSN website¹.

All GIHSN investigating sites are not-for-profit institutions, with experience in hospital-based surveillance for influenza and other respiratory viruses. Some of them are involved in the national surveillance in their country; some are National Influenza Centres (NICs).

Data is collected at hospital level, with one to several hospitals being included in the surveillance.

All sites have an excellent connection between a hospital surveillance platform and a virology laboratory in their country, allowing for influenza testing by RT-PCR² and subsequent sequencing (subtype/lineage) of the positive specimens. Sites connected to national influenza centers have subtype and lineage results available within seven days from receiving the samples.

All sites must have the capacity to submit WGS at a minimum consensus data of the HA and NA³ segments to the GISAID EpiFlu™ database. If a site has no capacity to generate WGS, the site is offered the possibility to ship its specimens to the GIHSN sequencing platform at the National Influenza Centre in Lyon, France.

2. A common protocol

All GIHSN sites use a common protocol⁴: demographic and clinical information are collected from patients admitted with respiratory illnesses. Respiratory specimens are collected to test for influenza and other respiratory viruses, including SARS-CoV-2 and RSV.

RT-PCR tests and whole genome sequencing are performed to provide virological information.

Key features of the GIHSN protocol:

- Screening and inclusion of hospitalized patients with respiratory illness meeting protocol case definition year-round (November, 1st 2022, to October, 31st, 2023).
- 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 (within first 72 hours) and sent for testing at the local and/or reference laboratory or National Influenza Centre.
- All specimens are tested by RT-PCR for influenza. When possible (e.g. available multiplex PCR), specimens are also tested for SARS-CoV-2, RSV and other respiratory viruses.
- Respiratory samples (swabs) from all swabbed patients are stored (-20C or -70C) for a minimum of one year. This can facilitate retrospective investigations on pathogen discovery, or evaluation of new diagnostic tools.
- WGS -see GIHSN WGS lab guidelines⁵- is done for a minimum of 50 to 100 influenza viruses per season. If the number of influenza positive cases is low, sites are encouraged to complete WGS of SARS-COV-2.
- WGS data are uploaded to GISAID by site in a reasonable timeframe, so that results are available for the bi-annual WHO Vaccine Composition Meetings.
- Link between WGS data uploaded in GISAID and clinical data in GIHSN is enabled through the reporting of the GISAID sample number into the clinical questionnaire.

3. A global database of more than 170,000 SARI hospitalized patients

During the past 11 years, a total of **169,471 patients** hospitalized with respiratory illness have been enrolled, including laboratory-confirmation of **27,698 Influenza cases** and **44,841 patients with other respiratory viruses**. The annual positivity

rate for influenza has ranged from **29% in 2019** to **2% in 2020-2021** (COVID-19 pandemic period), 7% in 2021-2022 and **10% in 2022-2023**.

1 [Contributing sites \(gihsn.org\)](https://gihsn.org)

2 RT-PCR = Reverse Transcription - Polymerase Chain Reaction.

3 HA = Hemagglutinin NA = Neuraminidase

4 The GIHSN protocol is available here: <https://gihsn.org/protocol-and-questionnaires/>

5 [WGS - Lab guidelines \(gihsn.org\)](https://gihsn.org)

4. Sharing of results and analyses

A Global Annual Meeting of the GIHSN is organised once a year in October, with all site investigators and stakeholders of the network, to share results of the year-round surveillance and discuss protocol and analyses.

In 2023, the GIHSN held its 11th Annual Meeting at the WHO Headquarters in Geneva. Over 90 scientists, clinicians and public health experts from 25+ countries gathered for 2 days and discussed lessons learned and how to strengthen collaborations across GIHSN and GISRS networks to enhance global respiratory pathogen surveillance and pandemic preparedness.

Seasonal results are shared publicly on the GIHSN website⁶.

In 11 years, the network has contributed to more than 20 published manuscripts⁷ and numerous local and international meetings and conferences.



⁶ [Results 2022-2023 \(gihsn.org\)](https://gihsn.org/Results-2022-2023)

⁷ [Scientific papers \(gihsn.org\)](https://gihsn.org/Scientific-papers)



PART II.

GIHSN 2022-2023 season

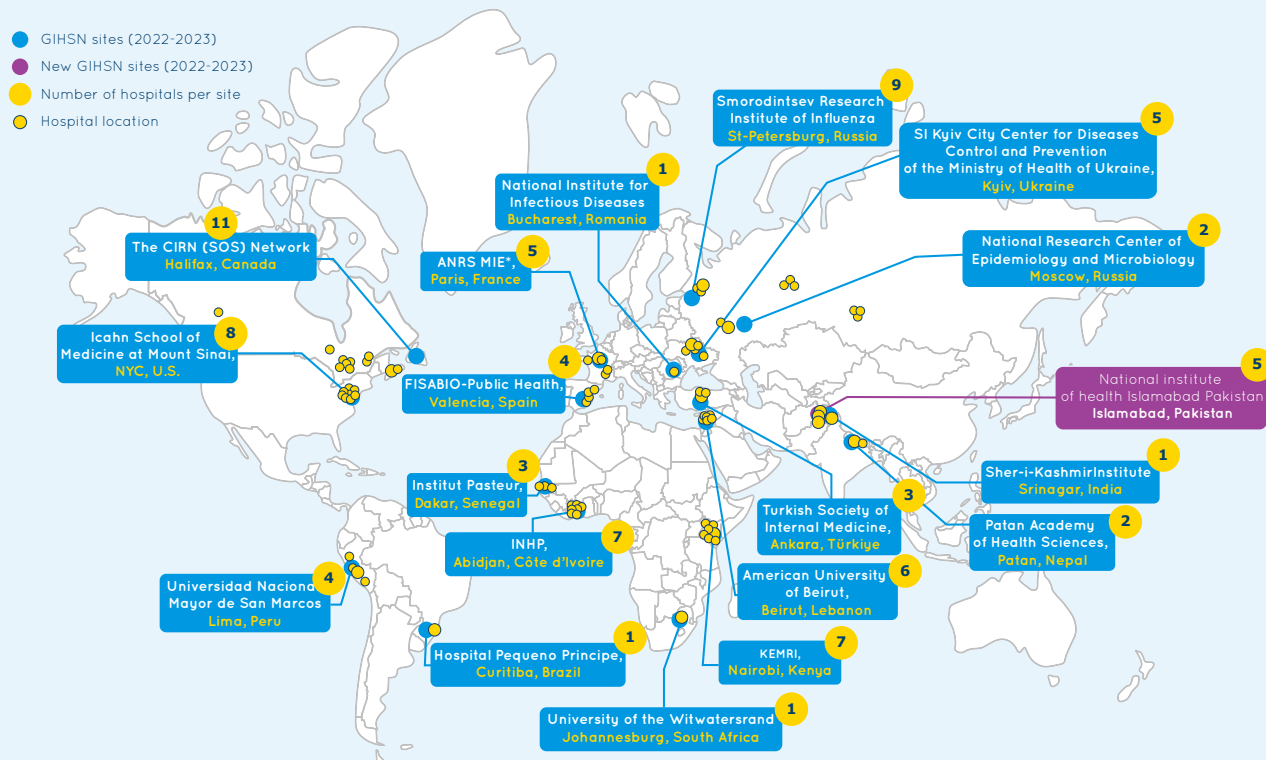
1. Participating sites

In the 2022-2023 season, the GIHSN sentinel platform included **83 hospitals** from **19 countries**, doing surveillance from November 2022 through October the following year. The network included **33,897 hospitalized patients**, of which **3,285 were tested positive for influenza**. Of these, **888 were sequenced (whole genome sequencing)**, either at local laboratories (52%), or by the National Influenza Center (NIC) in Lyon which provides support to the GIHSN sites. All data generated through whole genome sequencing are uploaded into the GISAID platform, with a unique identifier that links the virological data to the clinical data.

Beyond influenza, 7,635 respiratory viruses were detected by the network (respectively 2 864 SARS-CoV-2, 2 040 RSV and 2 731 patients with other respiratory viruses). In addition, 621 SARS-CoV-2 whole genome sequencing results were uploaded on GISAID, contributing to COVID-19 pandemic surveillance.

Figure 2 presents the sites which contributed data in the GIHSN in the 2022-2023 season (data closed end of February 2024).

Figure 2 : Geographic distribution of sites which contributed data in the GIHSN in the 2022-2023 season



*France: due to a change in the institution promoting the surveillance, discussion on data sharing agreement is still ongoing; data is expected to be shared shortly but could not be included in the present report.

**Ukraine: there was a change in the institution.

Surveillance population and settings by site can vary significantly from one site to another, depending notably on the number and type of hospitals involved, site case finding approach, laboratory and WGS capacities, site experience in influenza surveillance and within the GIHSN. These specificities by site must be carefully considered when analysing the data. Characteristics and features of each site are collected in a dedicated form and consolidated in a table, which is available on the GIHSN website⁸.

Range of viruses tested beyond influenza can also vary from one site to another. Although influenza virus surveillance is a key priority for the GIHSN, the network indeed encourages sites to include other respiratory viruses as part of their surveillance, if laboratory capacity exists locally. In 2022-23, almost all sites tested and shared data on SARS-CoV-2. 15 sites also shared data on RSV. Other respiratory viruses were also tested, including human coronaviruses, metapneumovirus, adenovirus, bocavirus, parainfluenza viruses, rhinovirus. Viruses tested by sites are presented in **Table 1** below.

⁸ Contributing sites (gihsn.org)

Table 1 : Virus tested by sites (2022-2023)

Based on data reported by sites over the 2022-2023 season (cut-off data: end of February 2024)

Country	Site/Institution	Influenza	SARS-CoV2	RSV*	HCoV*	HMPV*	AdV*	HBoV*	HPIV*	RhV*	ORV*
Africa											
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										
Asia/Pacific											
India	Sher-i-Kashmir Institute, Srinagar										
Nepal	Patan Academy of Health Sciences										
Pakistan	National institute of health Islamabad Pakistan										
Middle East											
Türkiye	Turkish Society of Internal Medicine, Ankara										
Lebanon	American University of Beirut, Beirut										
Eurasia											
Russia - St Petersburg	Smorodintsev Research Institute of Influenza, St Petersburg, Russia										
Russia - Moscow	FSBI "N.F. Gamaleya NRCEM" Ministry of Health, Moscow										
Ukraine	SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine, Kyiv										
Spain	FISABIO, Valencia										
Romania	National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest										
France	ANRS MIE, Paris										
North America											
Canada	The CIRN Serious Outcomes Surveillance (SOS) Network, Halifax										
USA	Icahn School of Medicine at Mount Sinai, NYC										
South America											
Brazil	Hospital Pequeno Principe, Curitiba										
Peru	Instituto de Medicina Tropical, Lima										

*RSV: Respiratory Syncytial Virus; HCoV: Human Coronaviruses; HMPV: Metapneumovirus; AdV: Adenovirus; HBoV: Bocavirus; HPIV: Parainfluenza viruses; RhV: Rhinovirus; ORV : Other Respiratory Viruses.

2. Data report

Based on data reported by sites over the 2022-2023 season (cut-off data: end of February 2024)

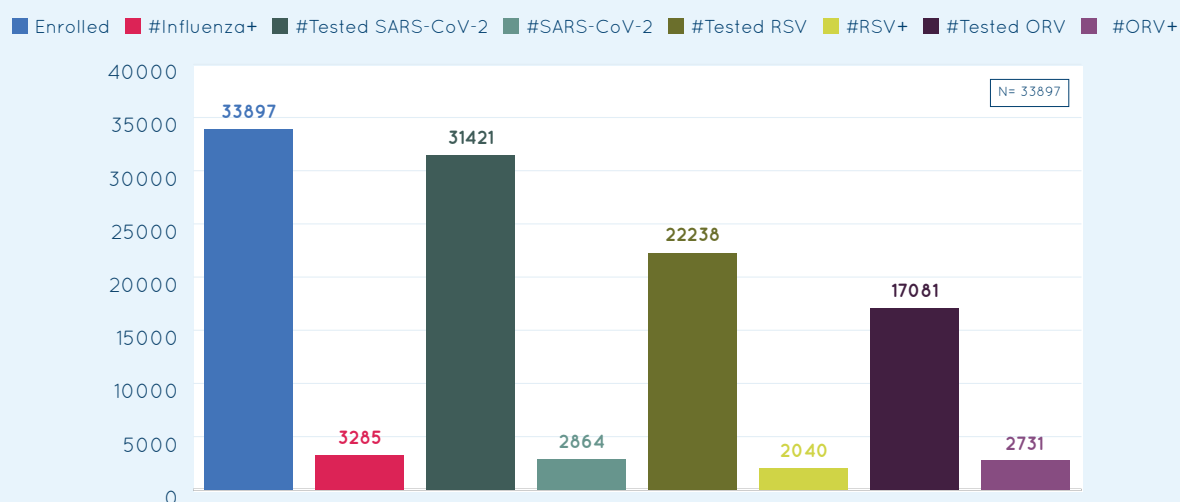
2.a. Overview of the GIHSN 2022-2023 SARI cases

Overall, **33 897 patients were enrolled in the 2022-2023 season**. All 33 897 cases were documented following the GIHSN questionnaire⁹.

As per the GIHSN protocol, all patients enrolled are to be tested by RT-PCR for influenza¹⁰. In all, **3 285 influenza positives were detected during the 2022-2023 season**.

When possible (e.g., available multiplex PCR), specimens collected were also tested for SARS-CoV-2, RSV and other respiratory viruses (see **Figure 3**).

Figure 3 : Overall number of patients enrolled and positive cases for influenza, SARS-CoV2, RSV and other respiratory viruses (2022-2023)

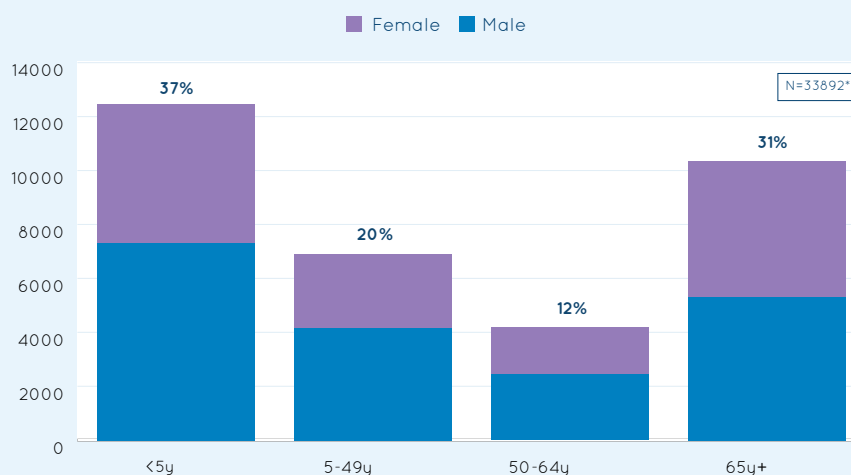


*ORV: Other Respiratory Viruses

2.b. Patient distribution by age group

The GIHSN patients enrolled during the season comprise 37% of children <5 years old, as shown on **Figure 4**. The paediatric population mainly comes from the following sites: Kenya, Côte d'Ivoire, Senegal, South Africa, Lebanon, Russia-St Petersburg, Romania, Brazil and Peru (see **Figure 5**). Some of these sites enrol patients in paediatric hospitals.

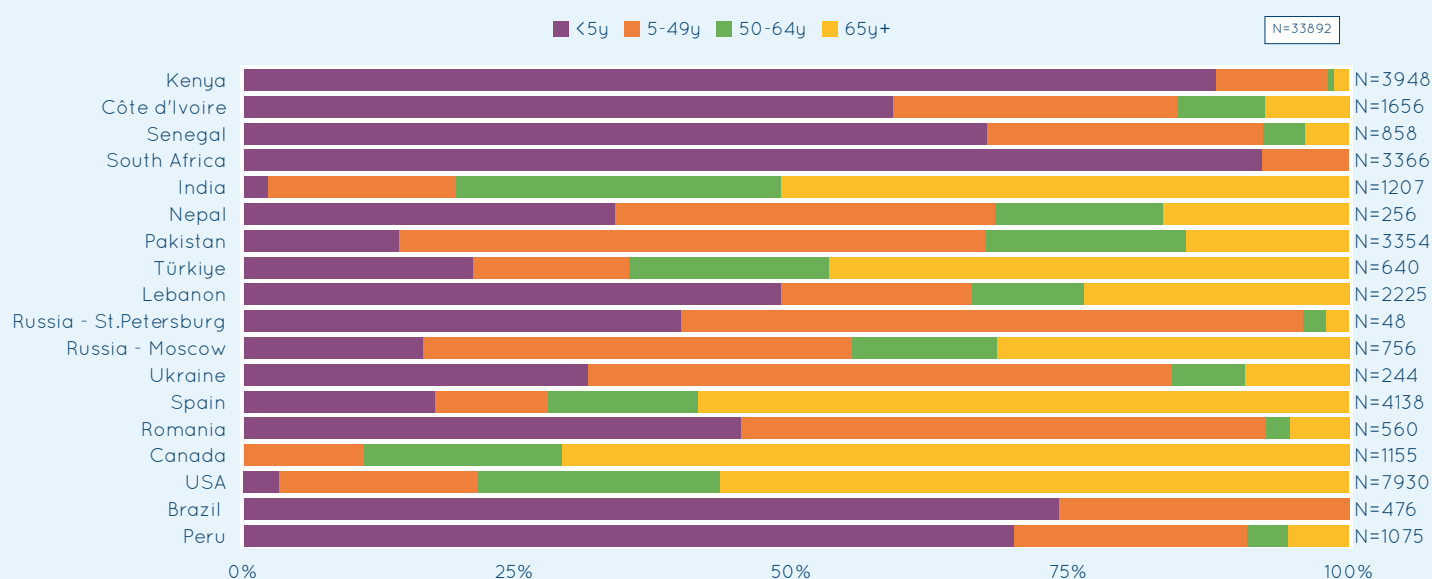
Figure 4 : Distribution of enrolled patients by age group and sex - All sites (2022-2023)



*5 patients with missing data at cut-of date (end of February 2024)

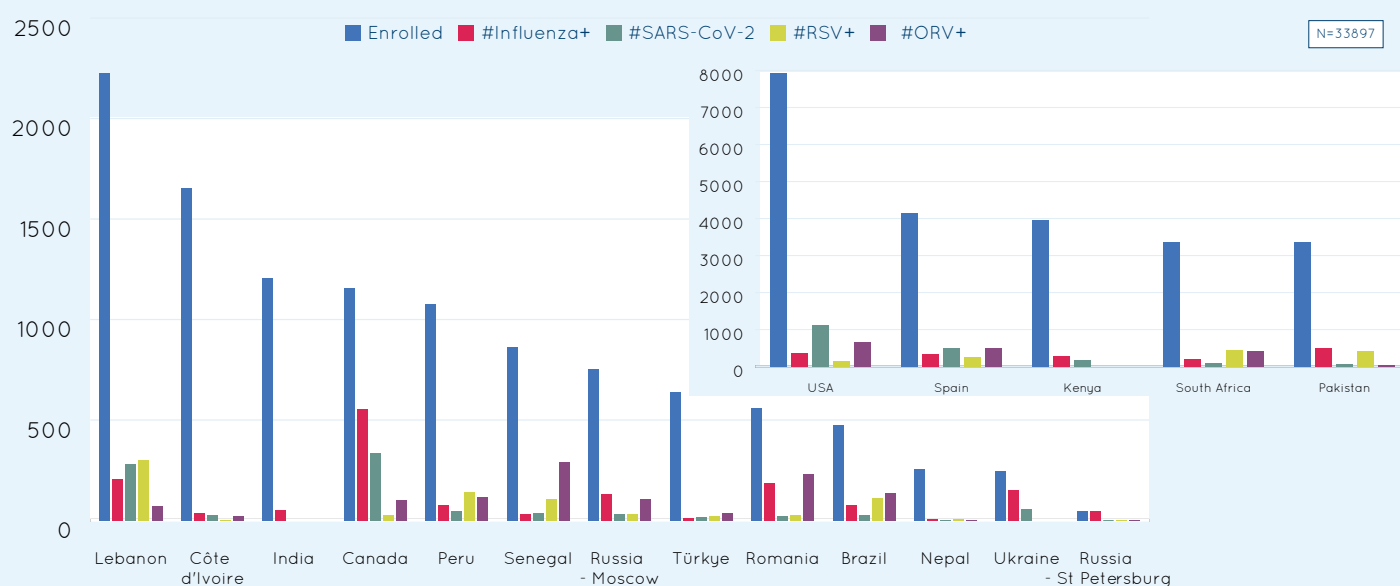
9 [Protocol and questionnaires \(gihsn.org\)](https://gihsn.org)

10 In rare known circumstances, systematic testing was not possible because of unavailability of reagents.

Figure 5 : Distribution of enrolled patients by age group - By site (2022-2023)

2.c. Patient distribution by site (2022-2023)

Figure 6 shows the distribution of enrolled patients by site, and, for each site, the distribution of viruses detected. Detailed count of patients by site is provided in [Annex](#).

Figure 6 : Distribution of patients by site: number of enrolled patients and number of viruses detected by site (2022-2023)

3. Results overview: Influenza

3.a. Positivity

The influenza positivity rates vary substantially by site.

Figure 7 shows, for each site, the number of enrolled patients, of which how many were tested positive to influenza, and, among these, how many influenza viruses were sequenced.

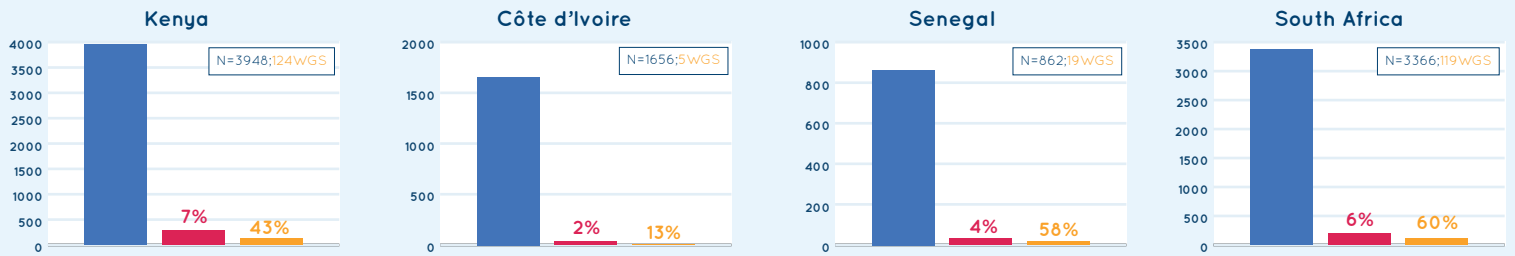
Positivity rate is derived from the number of laboratory-confirmed patients with influenza among all patients enrolled. Percentage of whole genome sequencing derived from the total number of influenza patients.

During the 2022-23 season, 15 sites provided influenza Whole Genome Sequencing results.

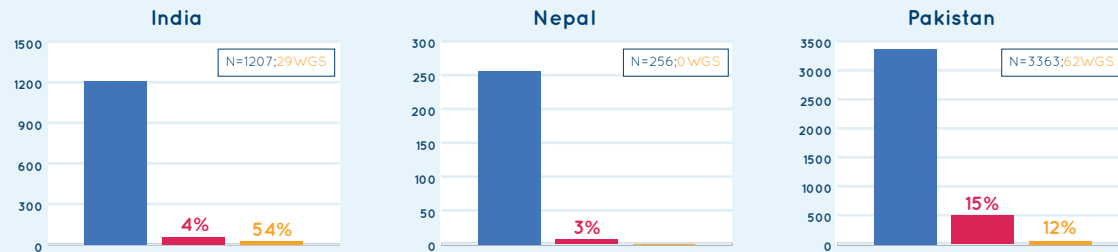
Figure 7 : Number of enrolled patients, influenza positivity rate and percentage of influenza viruses with whole genome sequencing data available - By site (2022-2023)

■ Enrolled ■ #Influenza+ ■ #WGS Influenza

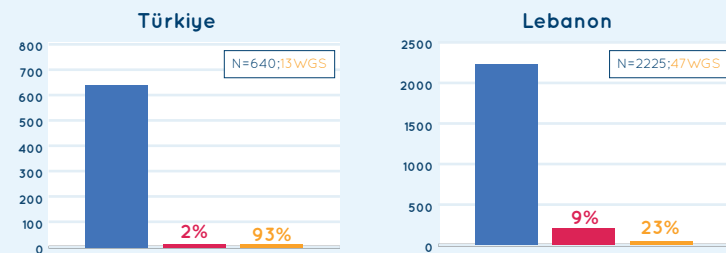
AFRICA



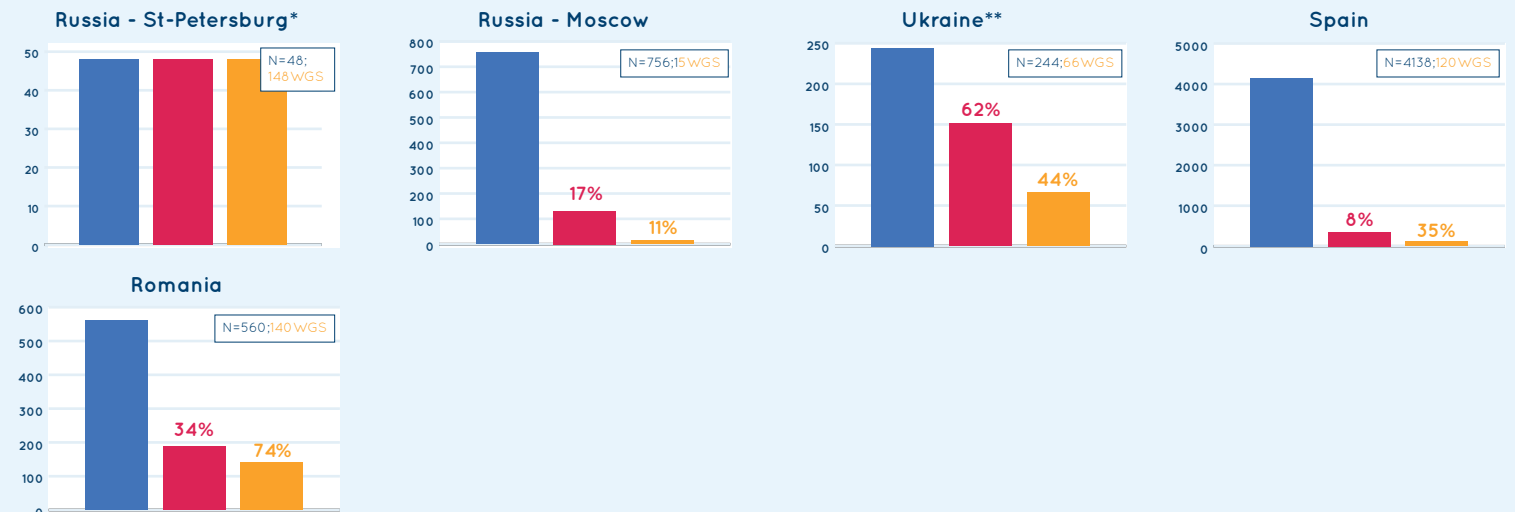
ASIA



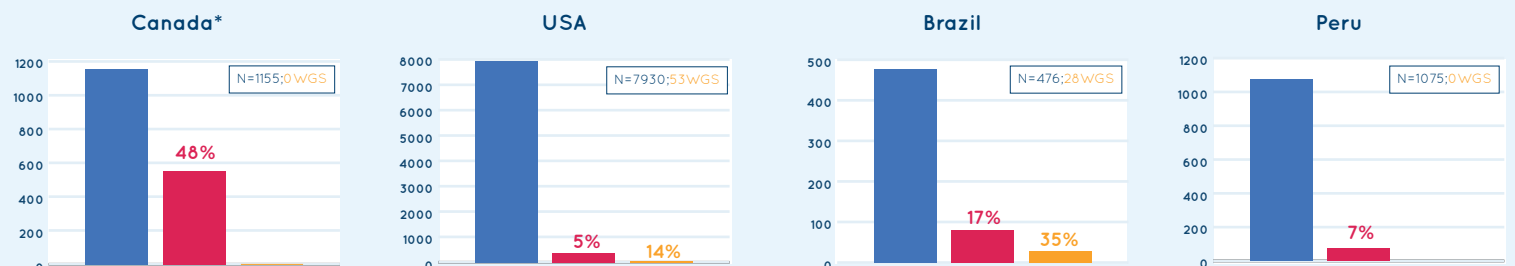
MIDDLE EAST



EURASIA



AMERICAS



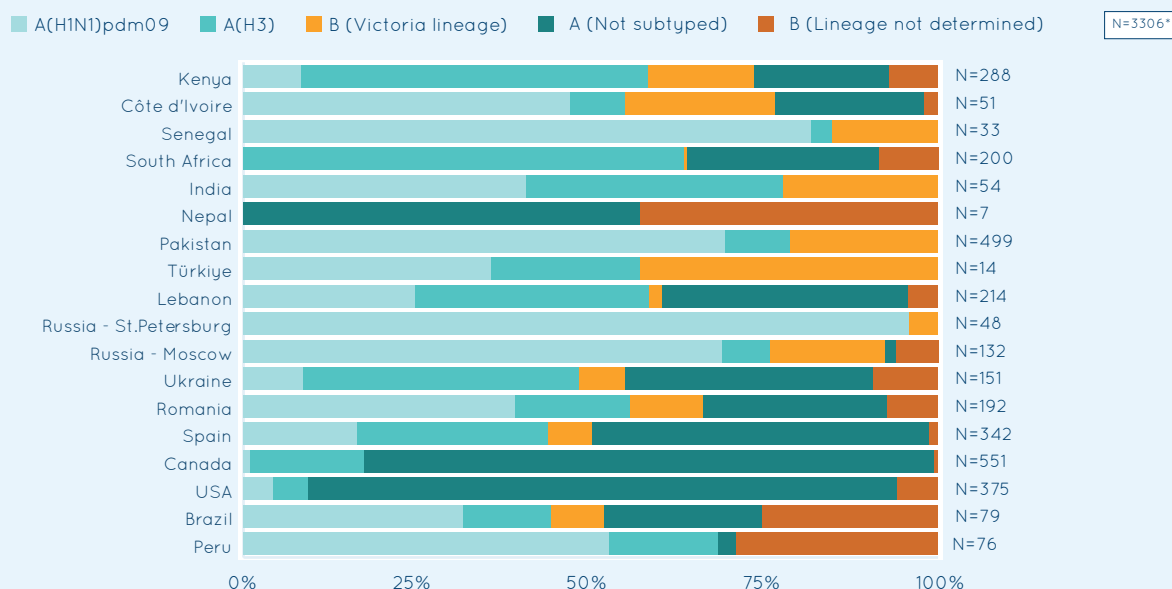
*Positivity rate should be interpreted cautiously as there were heterogeneity in the way some sites applied the screening and enrollment guidance from the protocol.

**Ukraine relies on physician's driven testing and focus on periods where influenza is circulating, which may justify high number of positive influenza cases. Efforts to harmonize sampling frame with the rest of the network is under discussion

3.b. Virus distribution

Most of the influenza viruses were influenza type A viruses, with some rare influenza B viruses. No influenza B Yamagata was detected (Figure 8).

Figure 8 : Distribution of laboratory-confirmed influenza cases by influenza virus subtype and lineage - By site (2022-2023)

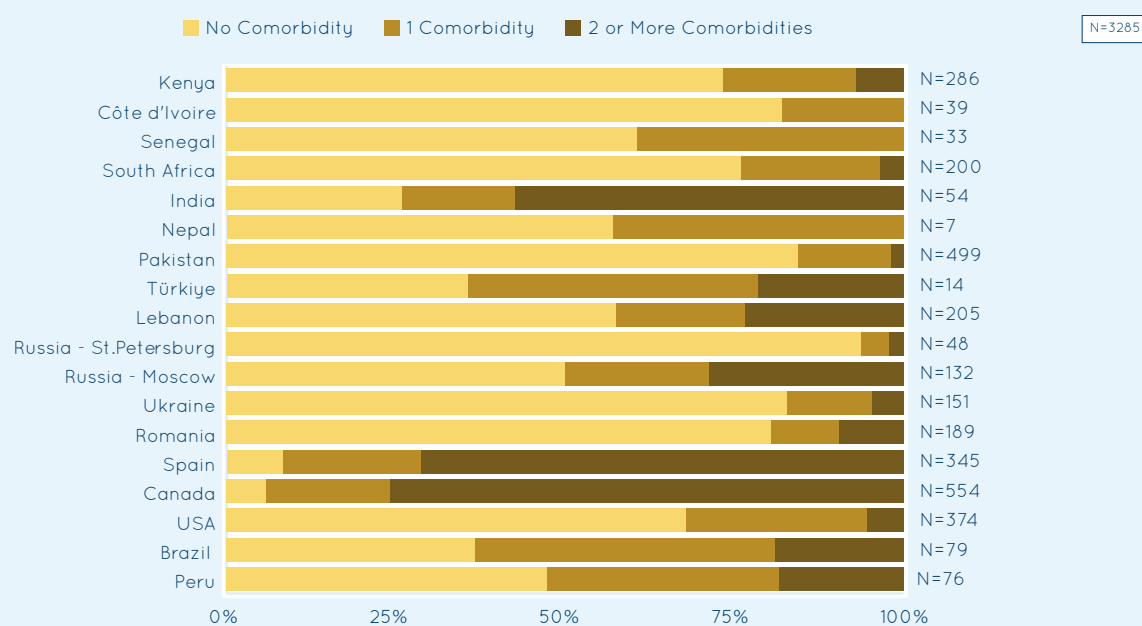


*This includes co-infections.

3.c. Comorbidities

Figure 9 shows the number of comorbidities (none / 1 / 2 or more) among laboratory-confirmed influenza cases, by site. Comorbidities are listed and captured in the clinical questionnaire¹¹.

Figure 9 : Presence of comorbidities among laboratory-confirmed influenza cases - By site (2022-2023)



11 [Protocol and questionnaires \(gihsn.org\)](https://gihsn.org/protocol-and-questionnaires)

3.d. Severity

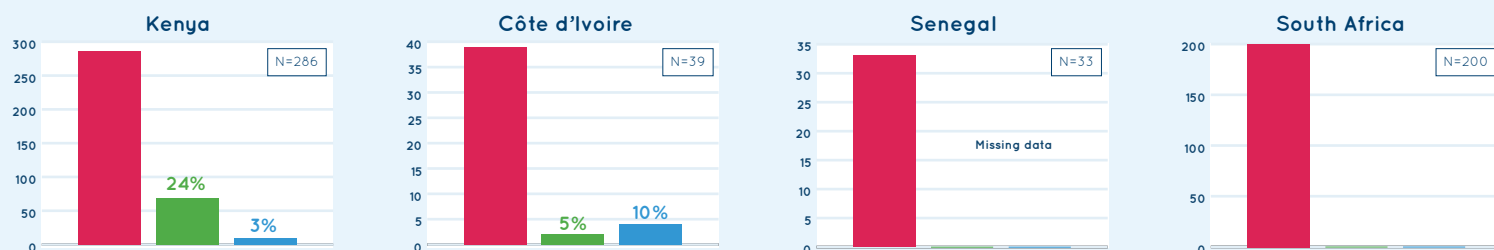
Severity is captured at admission (e.g., lethargy, oxygen saturation, need for supplement oxygen), during admission (e.g., ICU, mechanical ventilation) and at patient discharge/death. **Figure 10** shows ICU admissions and deaths among laboratory-confirmed influenza cases, in each participating site.

The percentages on top of the bars represent the number of ICU admissions by total patients with influenza. Deaths represent total deaths by the total number of influenza cases (it is not a subset of those admitted to the ICU).

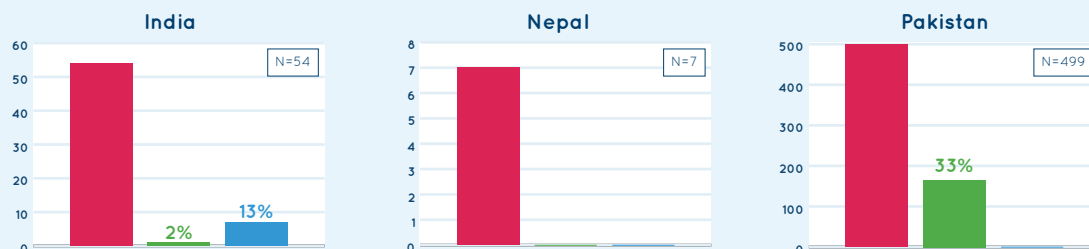
Figure 10 : Intensive care unit (ICU) admissions and deaths among laboratory-confirmed influenza cases - By site (2022-2023)

#Influenza+ #ICU admissions #Deaths

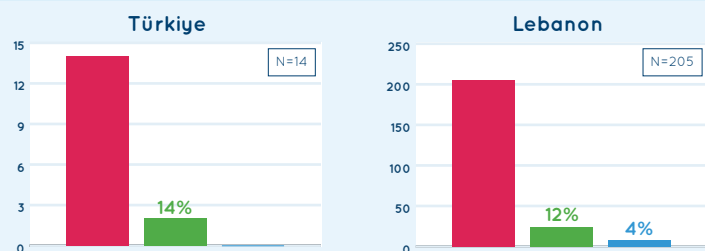
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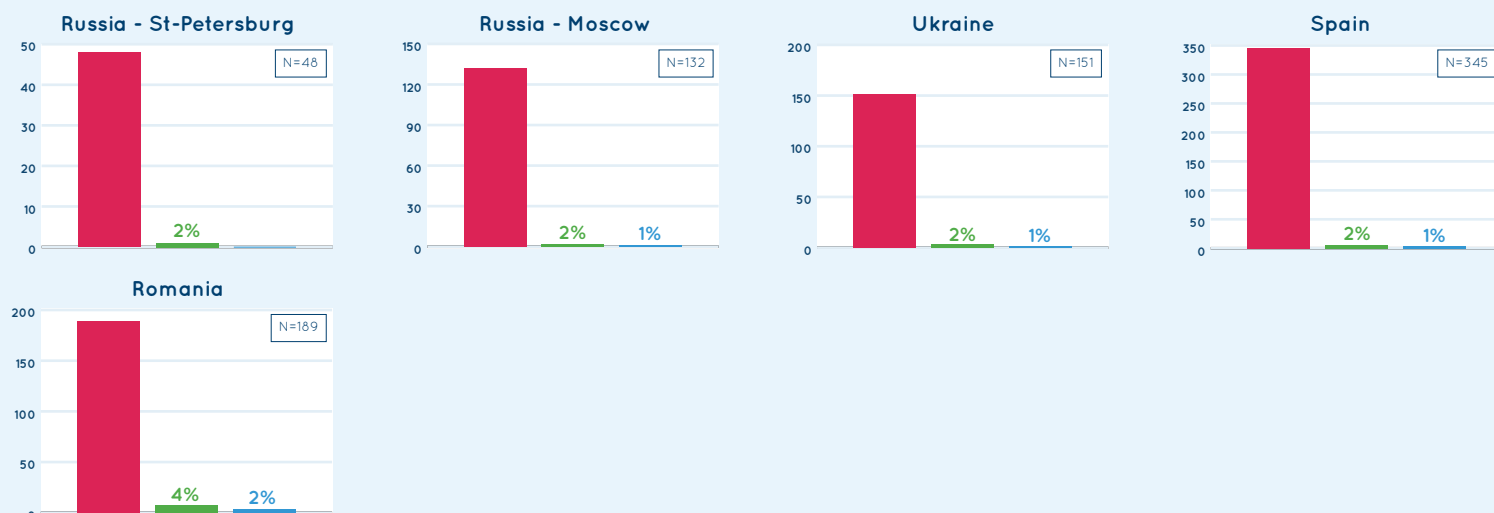
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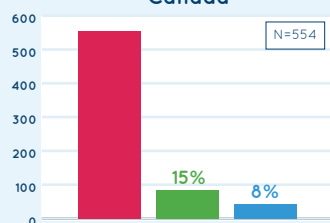


EURASIA

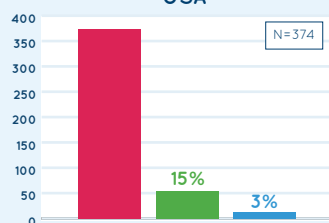


AMERICAS

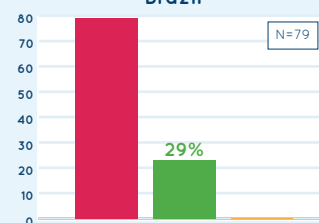
Canada



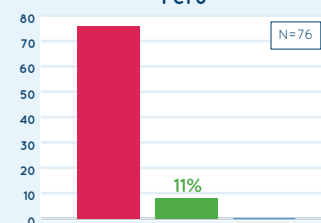
USA



Brazil



Peru



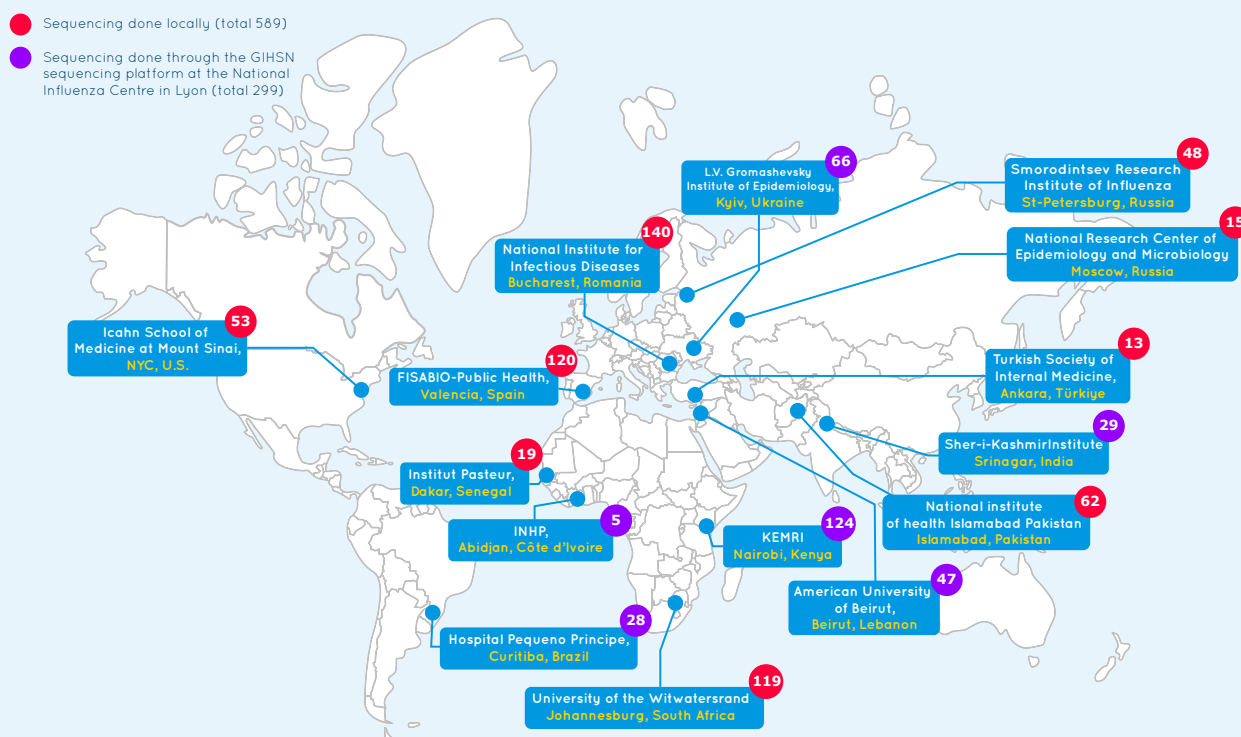
4. Sequencing Analysis of Influenza viruses

4.a. Overview of influenza viruses sequenced

For the 2022-2023 surveillance in GIHSN, influenza activity returned to levels typical of pre-COVID-19 pandemic years. During this period, influenza A(H1N1)pdm09, A(H3N2) and influenza B viruses circulated.

In total, **888 influenza positive samples were fully sequenced**, either locally by sites, or through the GIHSN sequencing platform at the National Influenza Centre in Lyon, France (**Figure 11**).

Figure 11 : Geographic distribution of influenza WGS (2022-2023)



Influenza A viruses predominated in most countries, with co-circulation of A(H1N1)pdm09 and A(H3N2) in different relative proportions. Regarding the Influenza B viruses, it has been reported a more limited number of detections of B/Victoria lineage viruses, and no B/Yamagata viruses have been detected by the network. This is the 2nd season of GIHSN surveillance with no detection of B/Yamagata viruses.

All sequences have been uploaded in the GISAID database¹².

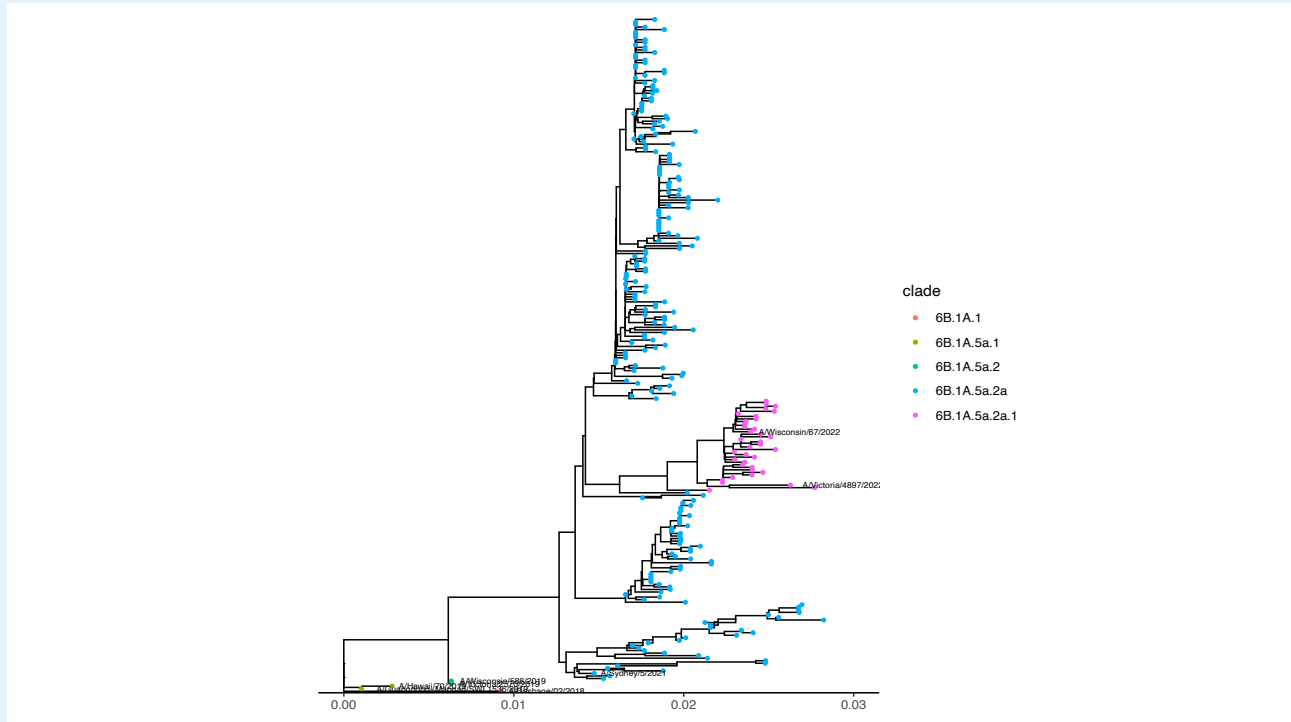
4.b. Description of the influenza A H1N1pdm09 viruses

The majority of the H1N1pdm09 viruses analyzed in the GIHSN network (87%) belonged to the 6B.1A.5a.2a clade and a minority (13%) to 6B.1A.5a.2a.1 clade close to reference strains A/Victoria/4897/2022 and A/Wisconsin/67/2022 (Fig. 1), as for most of the recent viruses reported by the global WHO surveillance. Large genetic diversity was observed in clade 6B.1A.5a.2a with 3 major subclades.

12 GISAID – gisaid.org

Figure 12 : Phylogenetic tree of the A(H1N1pdm09) viruses sampled within the GIHSN network between 1st of November 2022 and 31st of October 2023 (1)

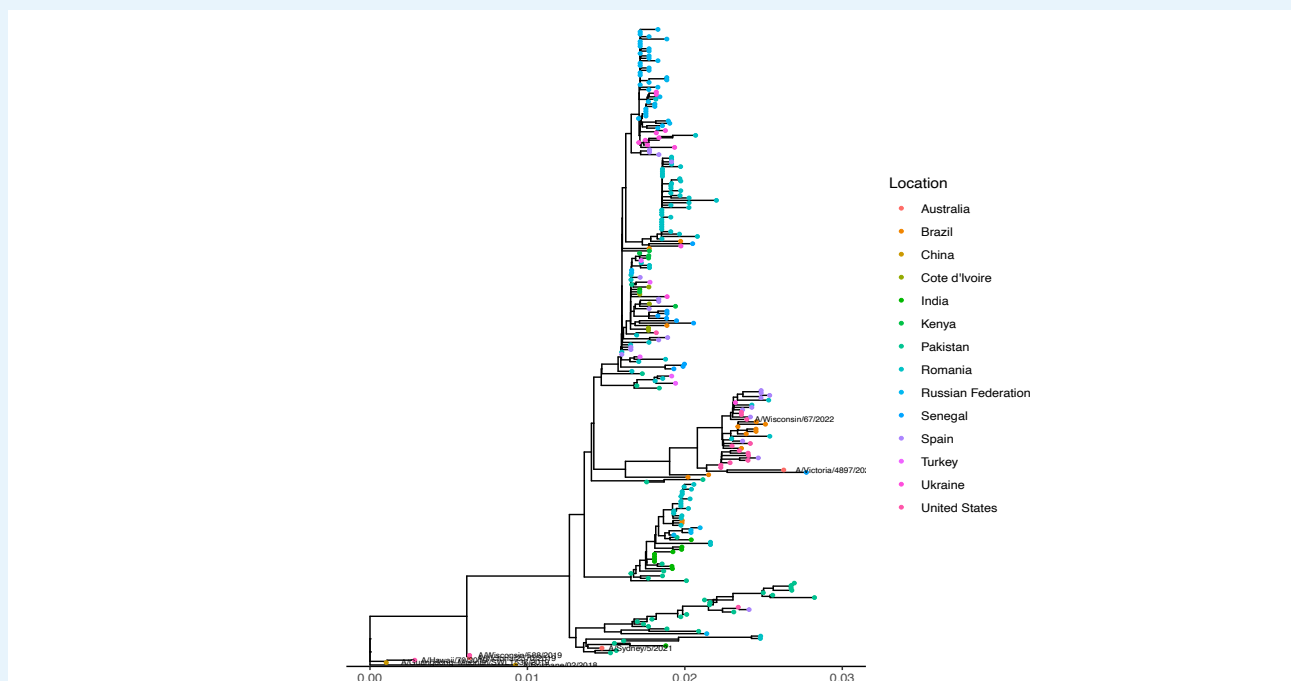
Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to clades assignment.



Viruses within clades 6B.1A.5a.2a.1 and subclades of 6B.1A.5a.2a co-circulated with regional differences in proportionality (**Figure 13**).

Figure 13 : Phylogenetic tree of the A(H1N1pdm09) viruses sampled within the GIHSN network between 1st of November 2022 and 31st of October 2023 (2)

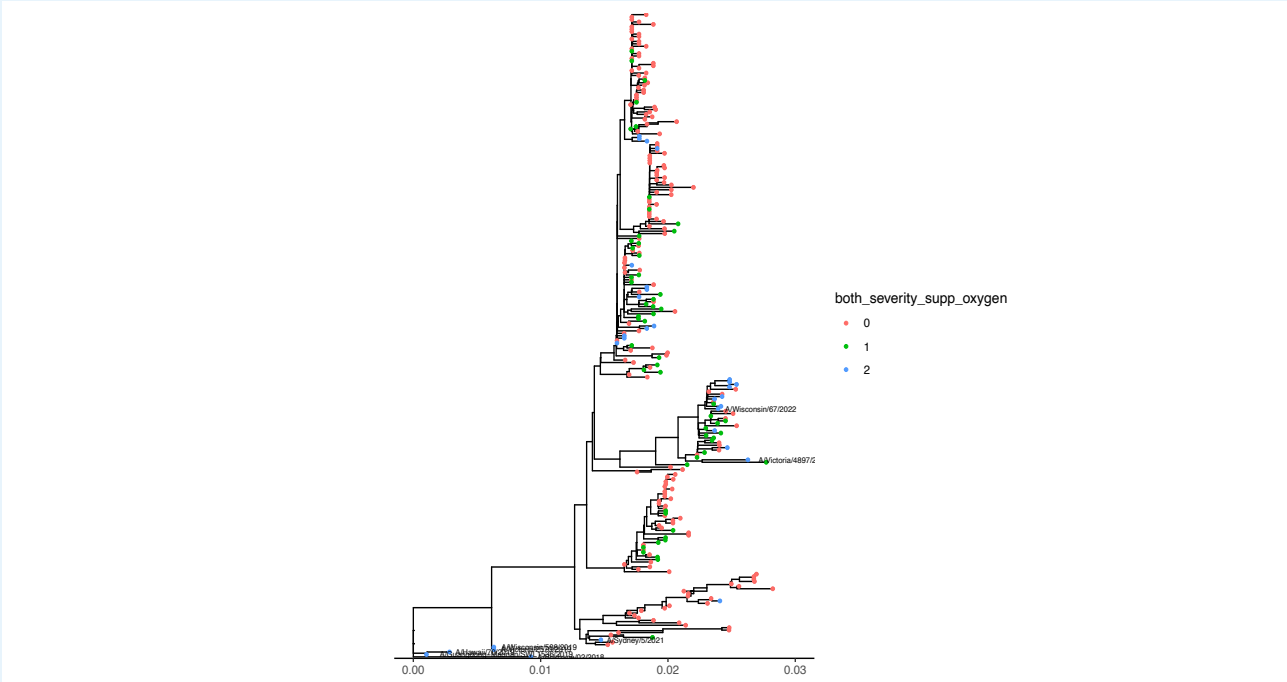
Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to samples location.



No specific clade could be associated with oxygen supplementation (**Figure 14**).

Figure 14 : Phylogenetic tree of the A(H1N1pdm09) viruses sampled within the GIHSN network between 1st of November 2022 and 31rd of October 2023 (3)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to oxygen requirement (0 = no / 1 = yes / 2 = unknown).

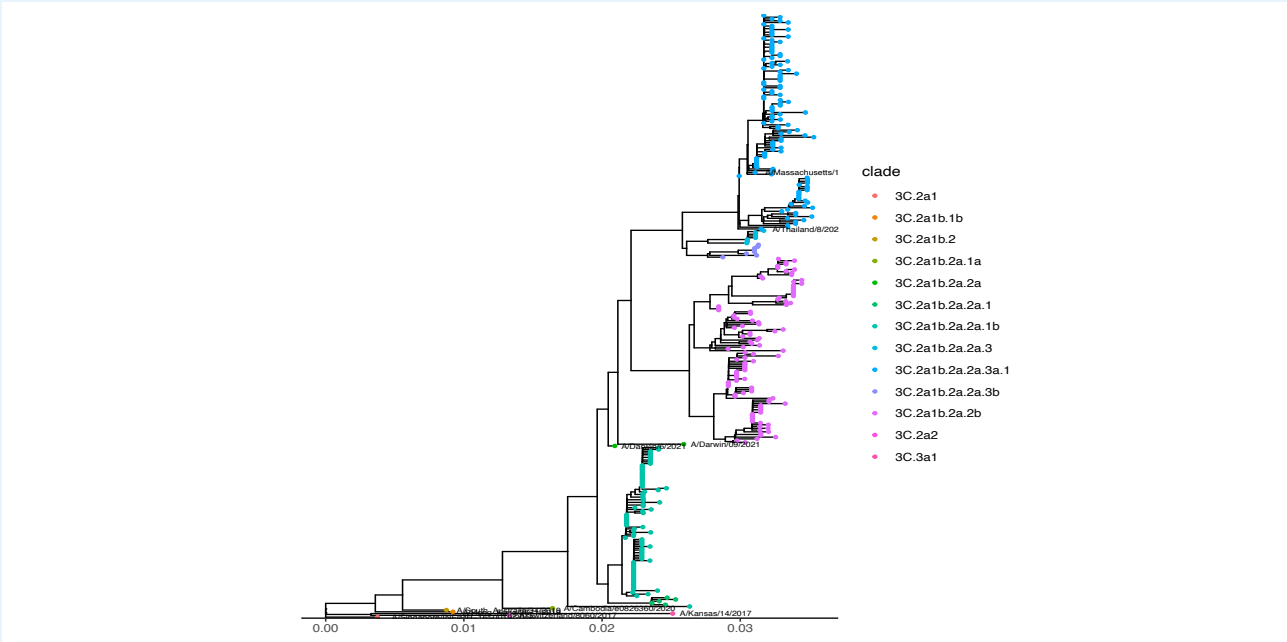


4.c. Description of the influenza A H3N2 viruses

All the A(H3N2) viruses sequenced by the GIHSN belonged to the 3C.2a1b.2a.2 clade, as observed with the vast majority of viruses circulating worldwide in 2022-2023 within the WHO network (**Figure 15**).

Figure 15 : Phylogenetic tree of the A(H3N2) viruses sampled within the GIHSN network between 1st of November 2022 and 31rd of October 2023 (1)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to clades assignation.



Clade 3C.2a1b.2a.2 diversified in different subclades with 3 main subclades representing the GIHSN diversity : 3C.2a1b.2a.2a.1b (26% of the A(H3N2) sequences), 3C.2a1b.2a.2b (32% of the sequences), and 3C.2a1b.2a.2a.3a.1 (A/Massachusetts/18/2022 –like, 36% of the sequences).

Subclade 3C.2a1b.2a.2b circulated globally, while 3C.2a1b.2a.2a.1b and 3C.2a1b.2a.2a.3a.1 viruses showed regional preferences (**Figure 16**).

No specific clade could be associated with oxygen supplementation (**Figure 17**).

Figure 16 : Phylogenetic tree of the A(H3N2) viruses sampled within the GIHSN network between 1st of November 2022 and 31st of October 2023 (2)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to samples location.

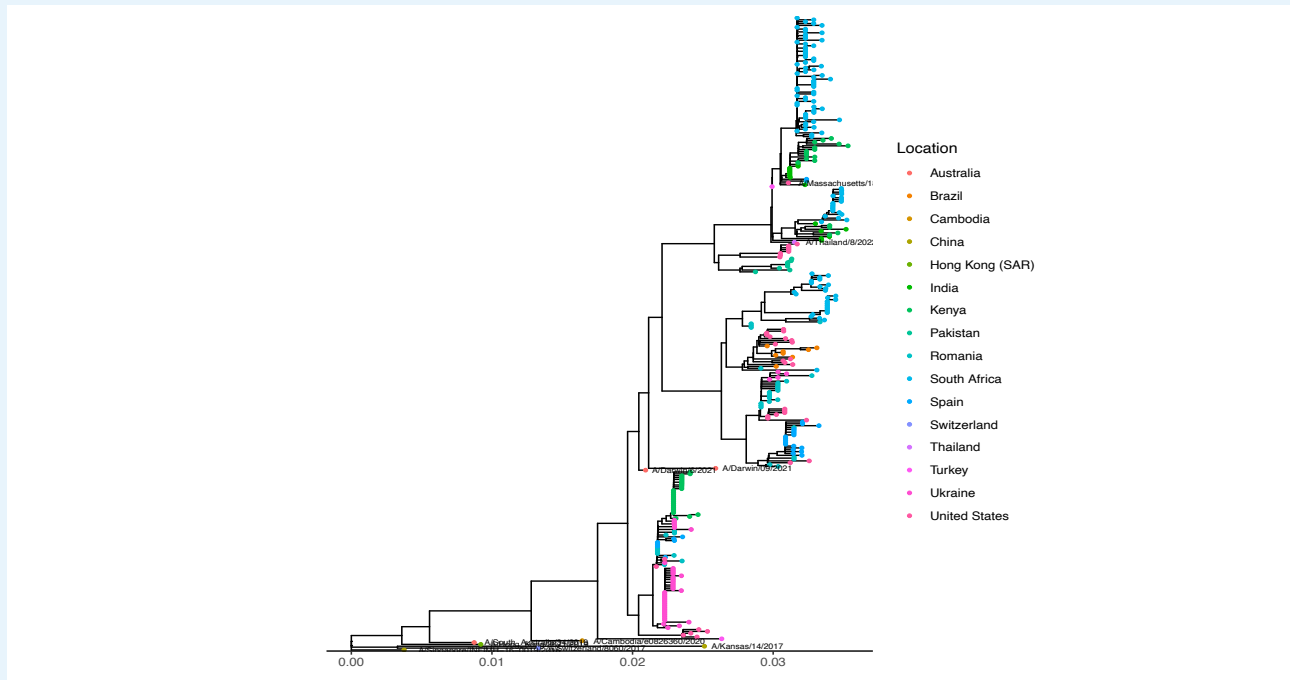
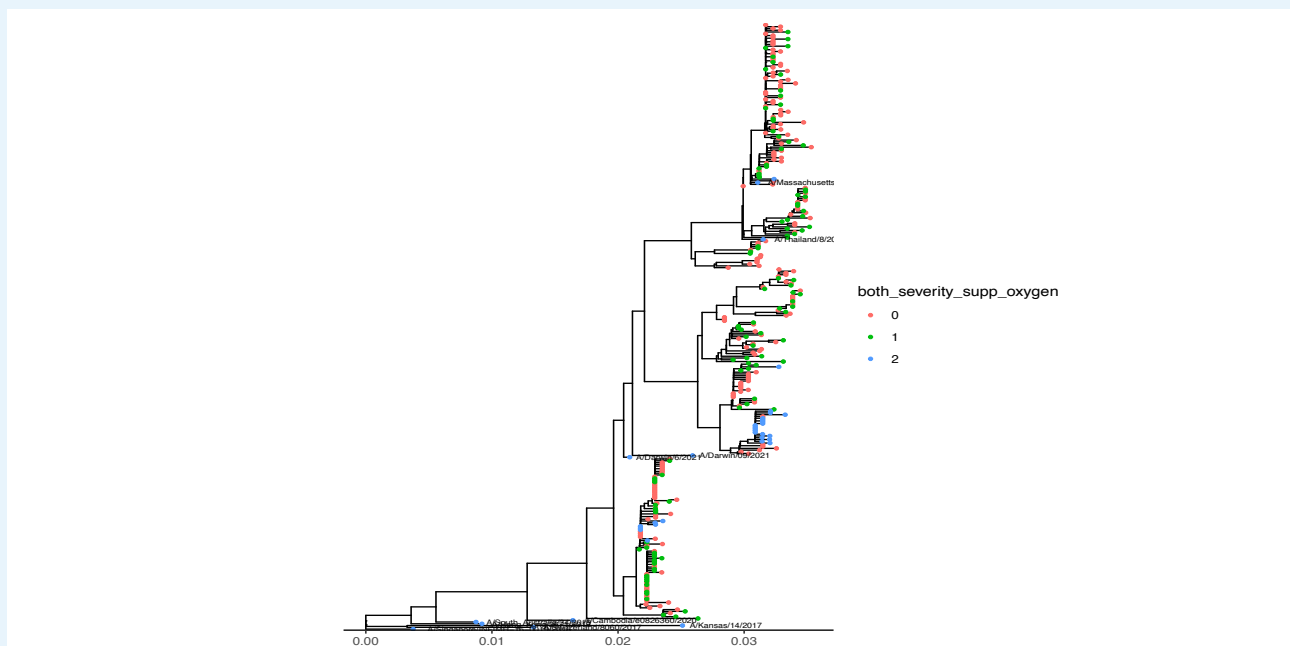


Figure 17 : Phylogenetic tree of the A(H3N2) viruses sampled within the GIHSN network between 1st of November 2022 and 31st of October 2023 (3)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to oxygen requirement (0 = no / 1 = yes / 2 = unknown).



4.d. Description of the influenza B viruses

All influenza B viruses characterized belonged to the B/Victoria/2/87 lineage, and to clade V1A.3a.2 (Figure 18), with diverse geographic origins (Figure 19) and no association with oxygen requirement (Figure 20).

Figure 18 : Phylogenetic tree of the B viruses sampled within the GIHSN network between 1st of November 2022 and 31rd of October 2023 (1)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to clades assignment.

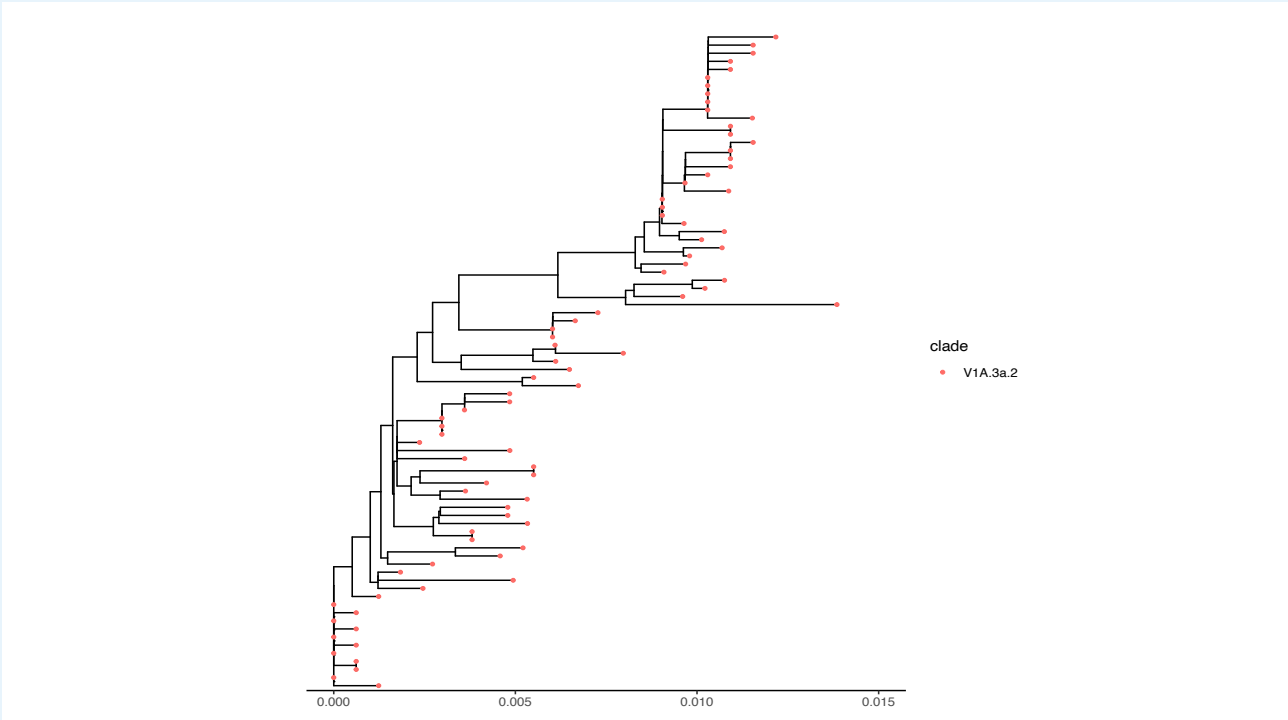


Figure 19 : Phylogenetic tree of the B viruses sampled within the GIHSN network between 1st of November 2022 and 31rd of October 2023 (2)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to samples location.

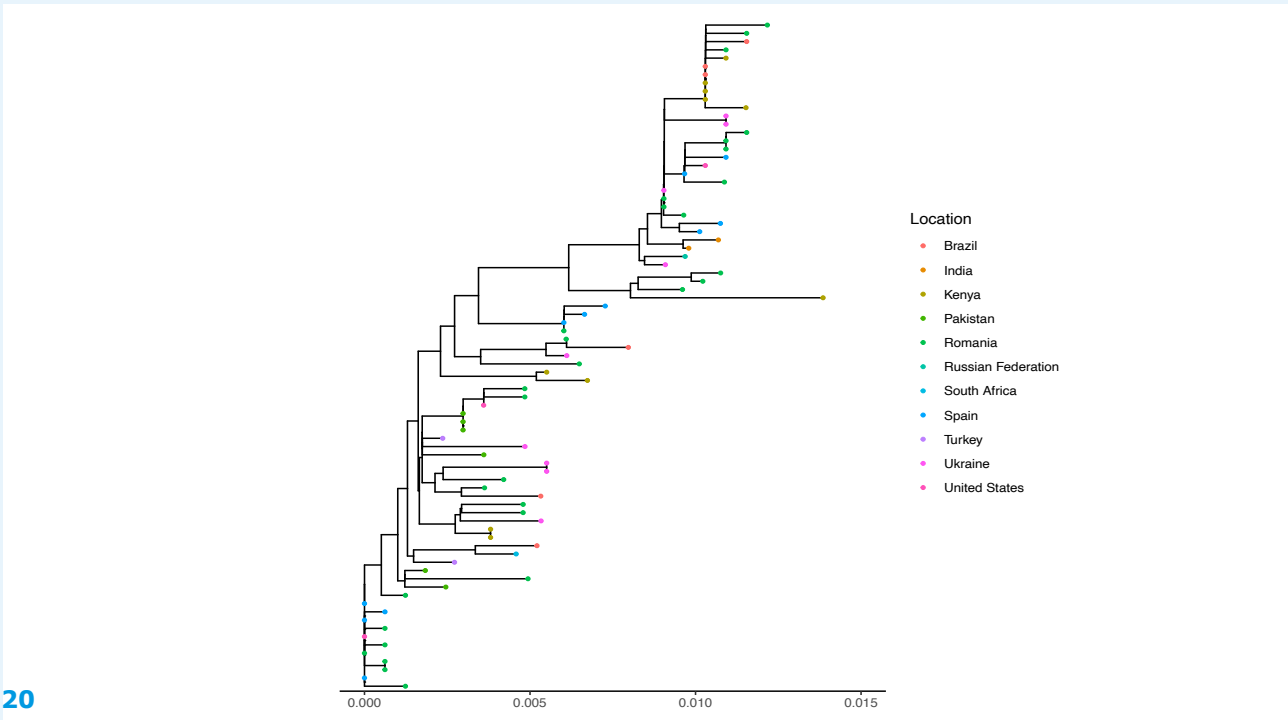
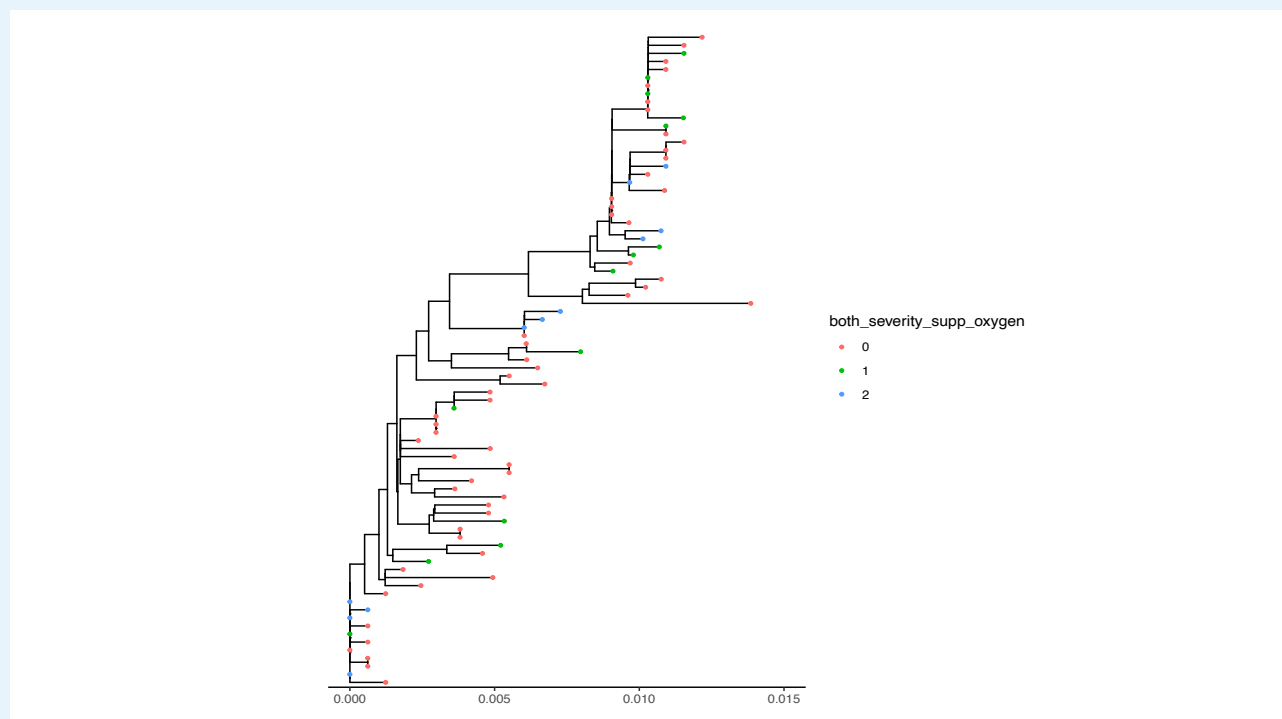


Figure 20 : Phylogenetic tree of the B viruses sampled within the GIHSN network between 1st of November 2022 and 31rd of October 2023 (3)

Vaccine strains were added as references with names provided in the tips. Genetic distances were calculated using the Kimura's two-parameter model (K80) and pairwise deletion. The tree was constructed by the neighbour-joining method using R seqinr and ggtree packages and validated using 1000 bootstrap pseudo-replicates. Tips (samples) colors correspond to oxygen requirement (0 = no / 1 = yes / 2 = unknown).



5. Results overview: SARS-CoV-2, RSV and other respiratory viruses

5.a. SARS-CoV-2

2 864 laboratory-confirmed SARS-CoV-2 cases were detected during the 2022-2023 season in the 17 sites which tested and/or shared data on SARS-CoV-2.

Positivity

Figure 21 shows, for each site, the number of patients who were tested for SARS-CoV-2, and the positivity rate, and, among those who were positive, the number of SARS Cov2 viruses which were sequenced.

Positivity rate is derived from the number of laboratory-confirmed patients with SARS-CoV-2 among all patients tested. Percentage of whole genome sequencing is derived from the total number of SARS-CoV-2 patients.

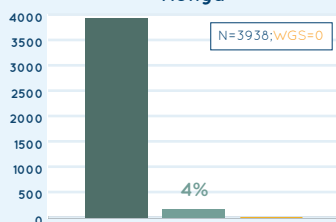
11 sites could provide SARS-CoV-2 Whole Genome Sequencing results for the 2022-2023 season. In all, 621 SARS-CoV-2 WGS results were uploaded on GISAID, contributing to COVID-19 pandemic surveillance.

Figure 21 : Number of patients tested for SARS-CoV-2 (dark green bar), positivity rate (green bar) and percentage of SARS-CoV-2 viruses with whole genome sequencing data available (orange bar)- By site (2022-2023)

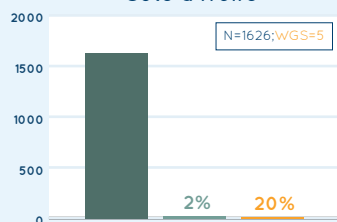
Tested SARS-CoV-2 # SARS-CoV-2 # WGS Sars-CoV-2

AFRICA

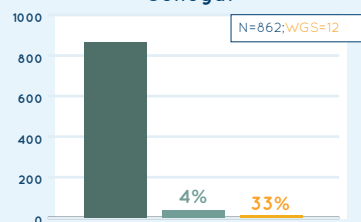
Kenya



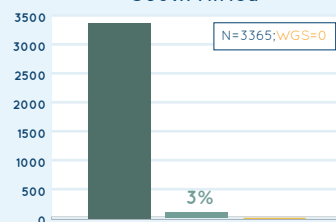
Côte d'Ivoire



Senegal

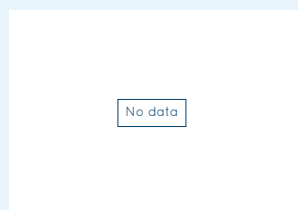


South Africa

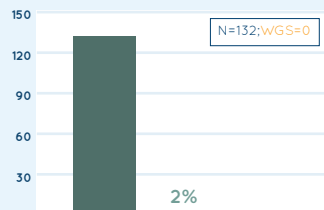


ASIA

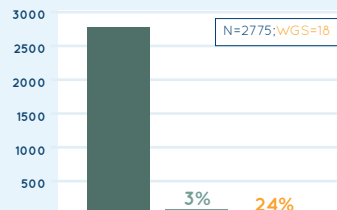
India



Nepal

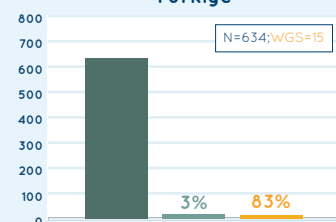


Pakistan

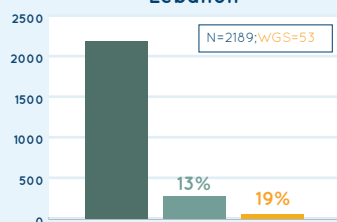


MIDDLE EAST

Türkiye

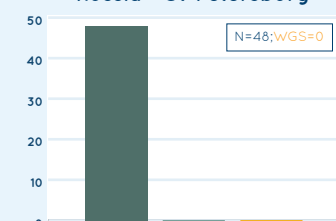


Lebanon

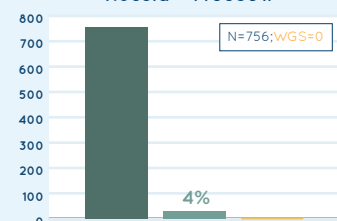


EURASIA

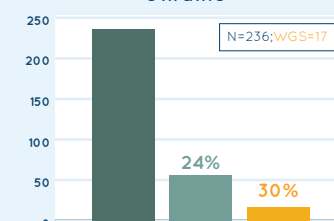
Russia - St-Petersburg



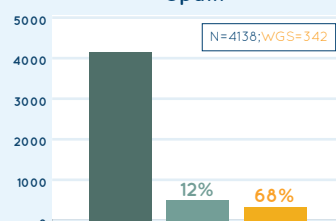
Russia - Moscow



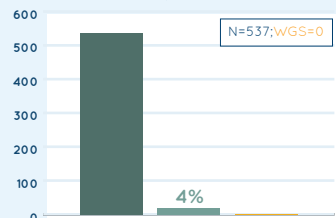
Ukraine*



Spain

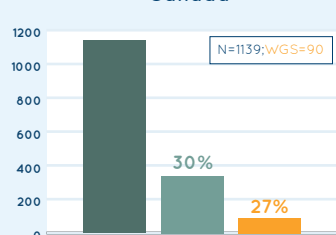


Romania

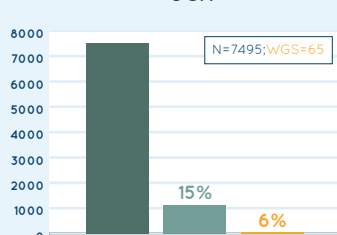


AMERICAS

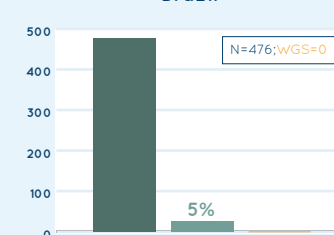
Canada*



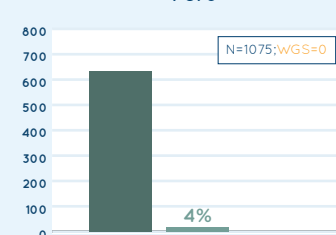
USA



Brazil



Peru

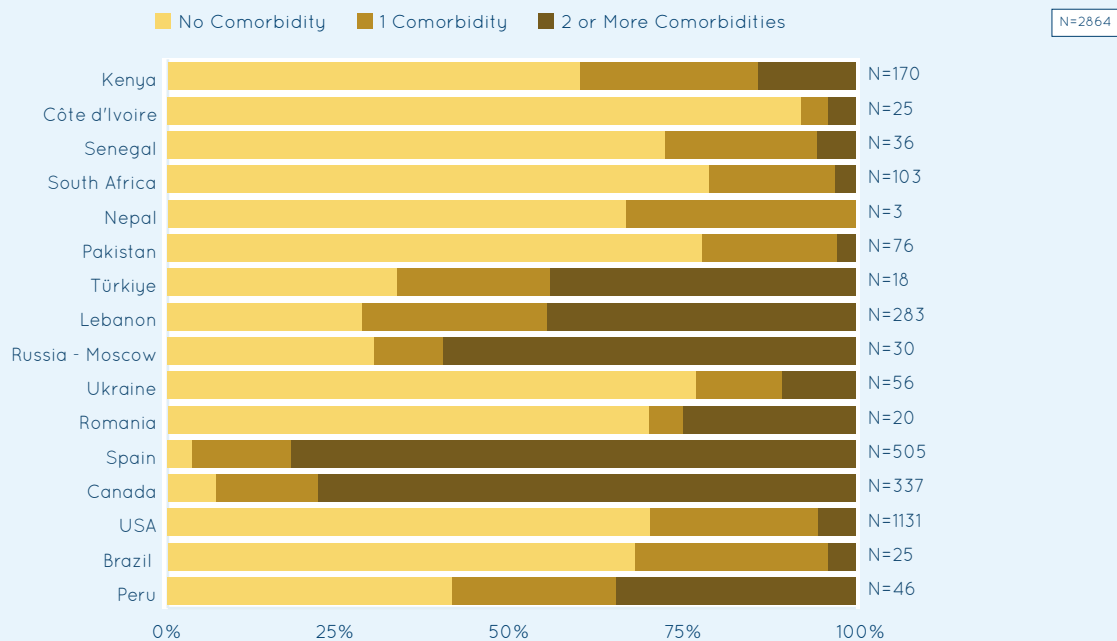


*High positivity rate is partially due to variation on site enrollment strategy

Comorbidities

Figure 22 shows the number of comorbidities (none / 1 / 2 or more) among laboratory-confirmed SARS-CoV-2 cases, by site.

Figure 22 : Presence of comorbidities among laboratory-confirmed SARS-CoV-2 cases - By site (2022-2023)



Severity

Severity is captured and reported similarly to influenza. Figure 23 shows ICU admissions and deaths among laboratory-confirmed SARS-CoV-2 cases, in each participating site.

The percentages on top of the bars represent the number of ICU admissions by total patients with SARS-CoV-2. Deaths represent total deaths by the total number of SARS-CoV-2 cases (not within ICU).

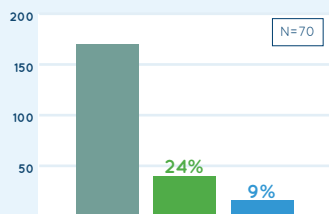


Figure 23 : Intensive care unit admissions and deaths among laboratory-confirmed SARS-CoV-2 cases - By site (2022-2023)

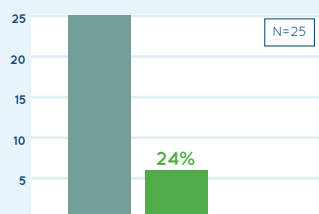
#SARS-Cov-2+ #ICU admissions #Deaths

AFRICA

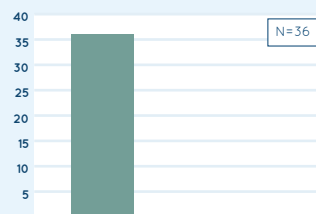
Kenya



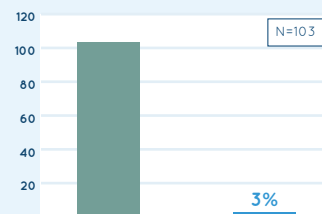
Côte d'Ivoire



Senegal

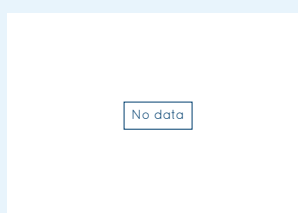


South Africa

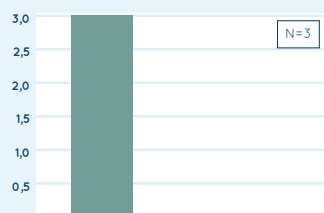


ASIA

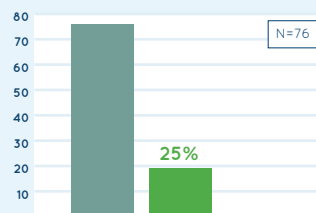
India



Nepal

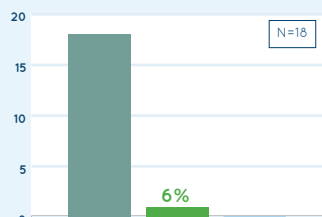


Pakistan

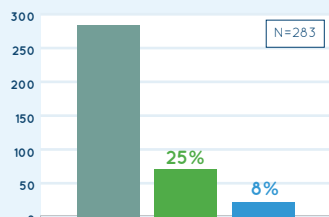


MIDDLE EAST

Türkiye

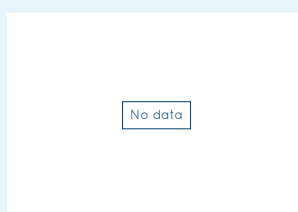


Lebanon

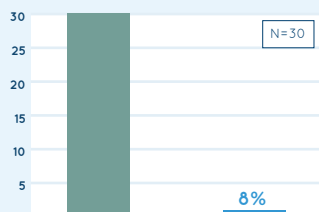


EURASIA

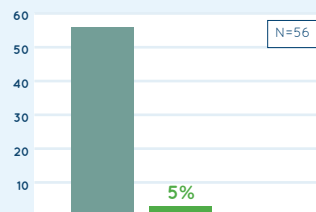
Russia - St-Petersburg



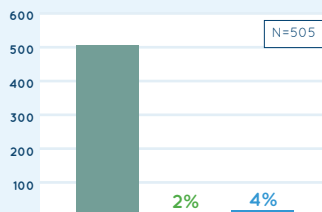
Russia - Moscow



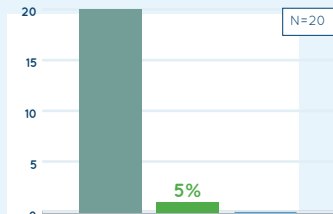
Ukraine



Spain

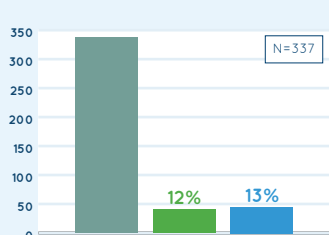


Romania

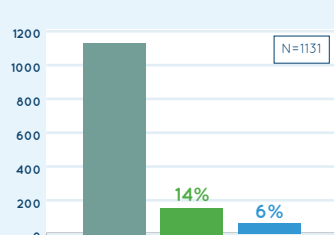


AMERICAS

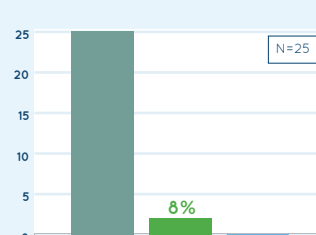
Canada



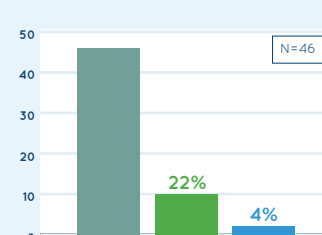
USA



Brazil



Peru



5.b. Respiratory Syncytial Virus (RSV)

2 040 laboratory-confirmed RSV cases were detected during the 2022-2023 season in the 15 sites which tested patients for RSV and/or shared RSV data (Kenya, India and Ukraine did not share data on RSV).

Positivity

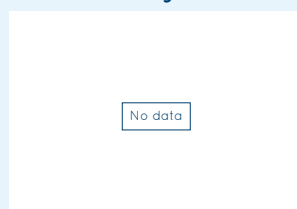
Positivity rates vary substantially by site, from 0,2% in Côte d'Ivoire, 24% in Brazil (this may reflect that the site in Brazil only enrolls children up to 14 years, hence a smaller denominator). **Figure 24** shows, for each site, the number of patients who were tested for RSV, and the positivity rate.

Figure 24 : Number of patients tested for RSV and positivity rate - By site (2022-2023)

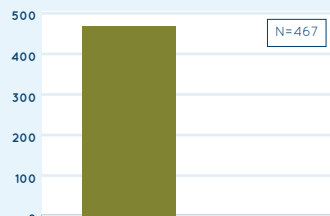
#Tested RSV #RSV+

AFRICA

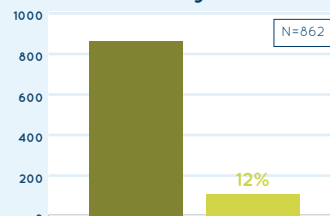
Kenya



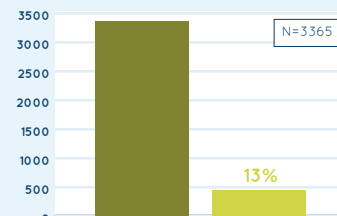
Côte d'Ivoire



Senegal

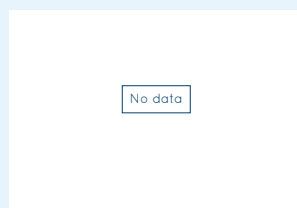


South Africa

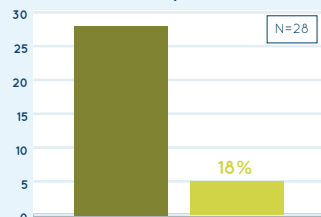


ASIA

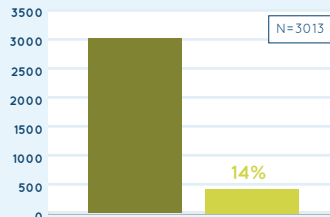
India



Nepal

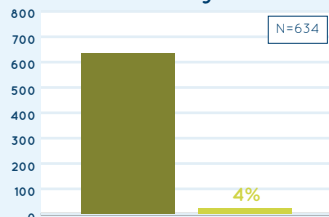


Pakistan

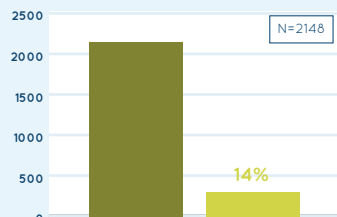


MIDDLE EAST

Türkiye

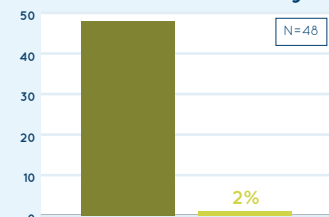


Lebanon

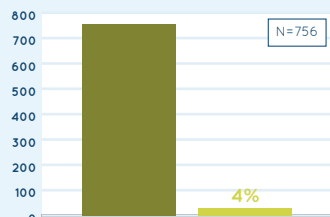


EURASIA

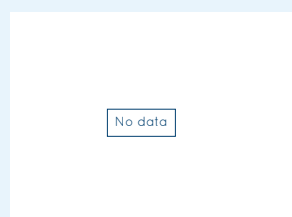
Russia - St-Petersburg



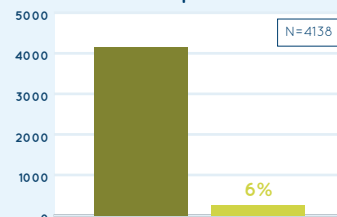
Russia - Moscow



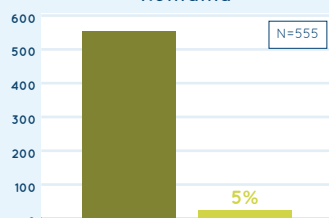
Ukraine



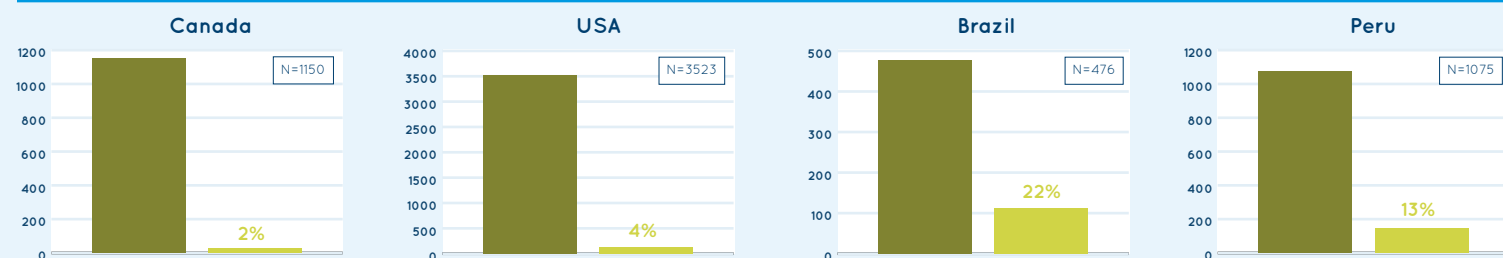
Spain



Romania



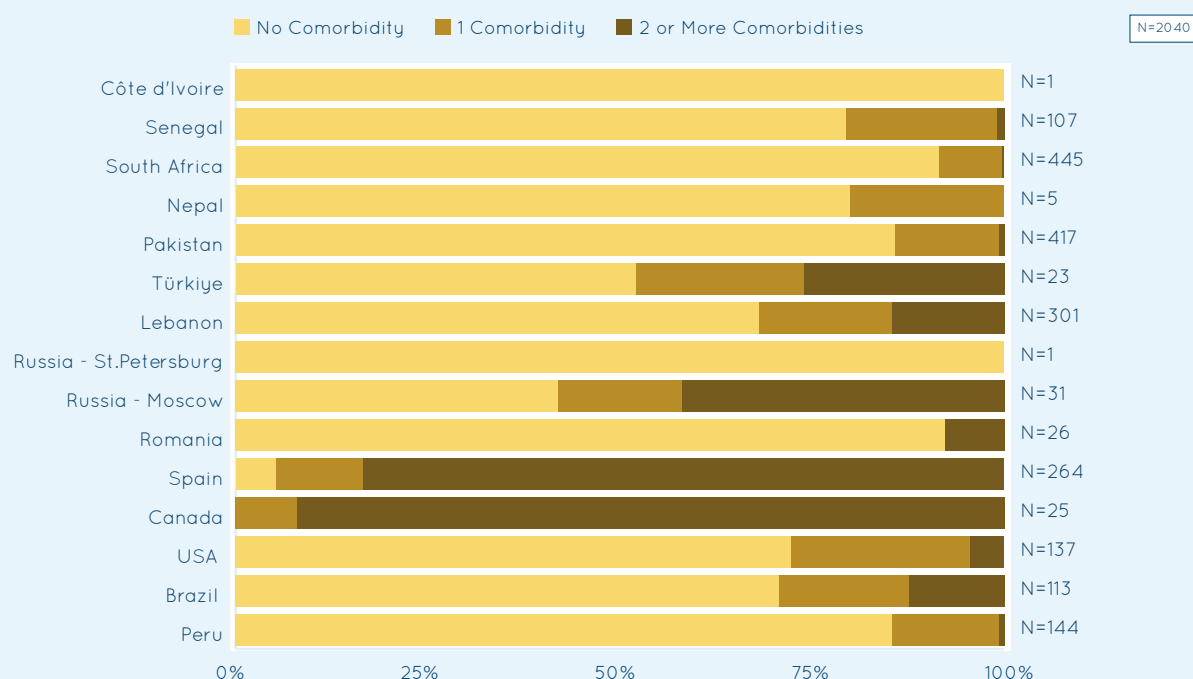
AMERICAS



Comorbidities

Figure 25 shows the number of comorbidities (none / 1 / 2 or more) among laboratory-confirmed RSV cases, by site.

Figure 25 : Presence of comorbidities among laboratory-confirmed RSV cases - By site (2022-2023)



Severity

Severity is captured and reported similarly to influenza. **Figure 26** shows ICU admissions and deaths among laboratory-confirmed RSV cases, in each participating site.

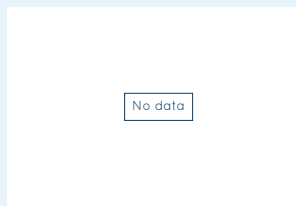
The percentages on top of the bars represent the number of ICU admissions by total patients with RSV. Deaths represent total deaths by the total number of RSV cases (not within ICU).

Figure 26 : Intensive care unit admissions and deaths among laboratory-confirmed RSV cases - By site (2022-2023)

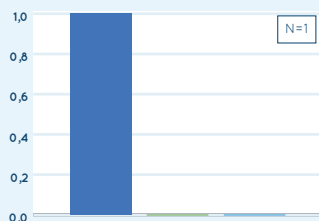
#Enrolled #ICU admissions #Deaths

AFRICA

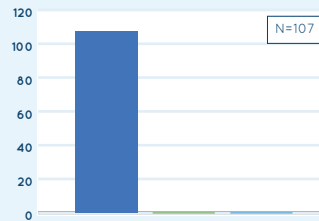
Kenya



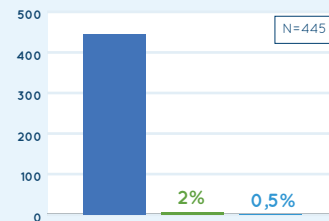
Côte d'Ivoire



Senegal

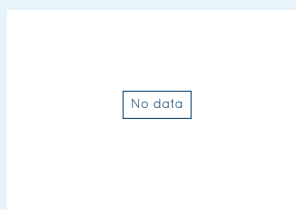


South Africa

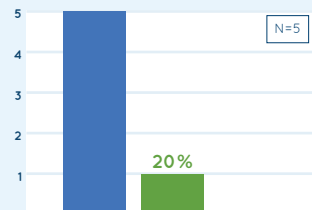


ASIA

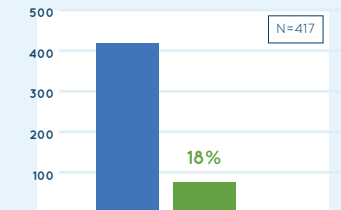
India



Nepal

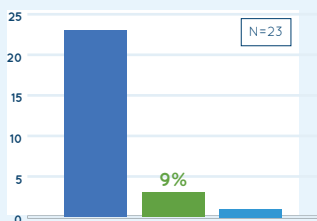


Pakistan

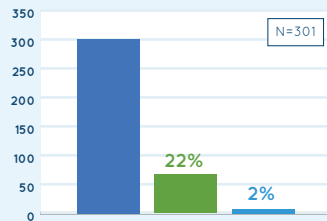


MIDDLE EAST

Türkiye

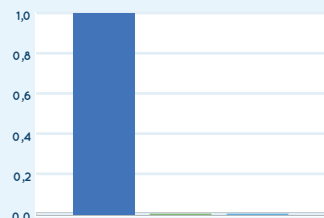


Lebanon

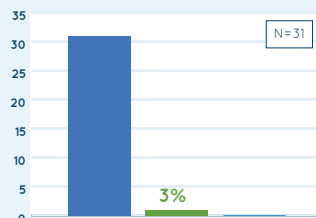


EURASIA

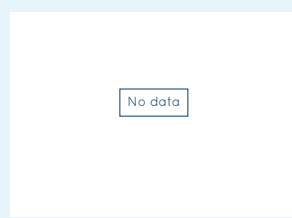
Russia - St-Petersburg



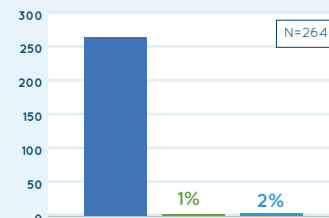
Russia - Moscow



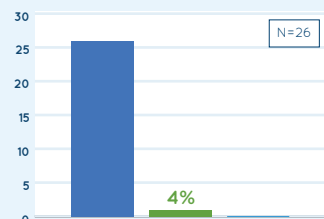
Ukraine



Spain

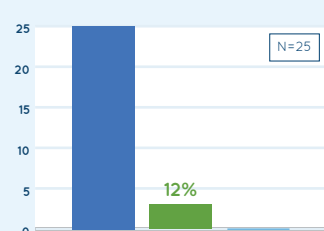


Romania

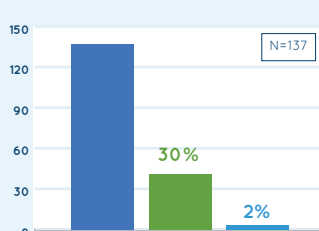


AMERICAS

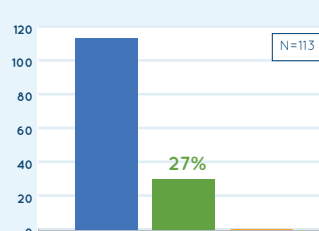
Canada



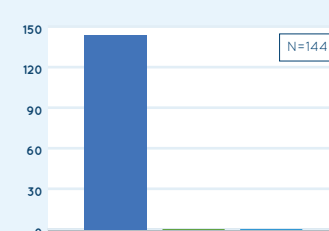
USA



Brazil



Peru



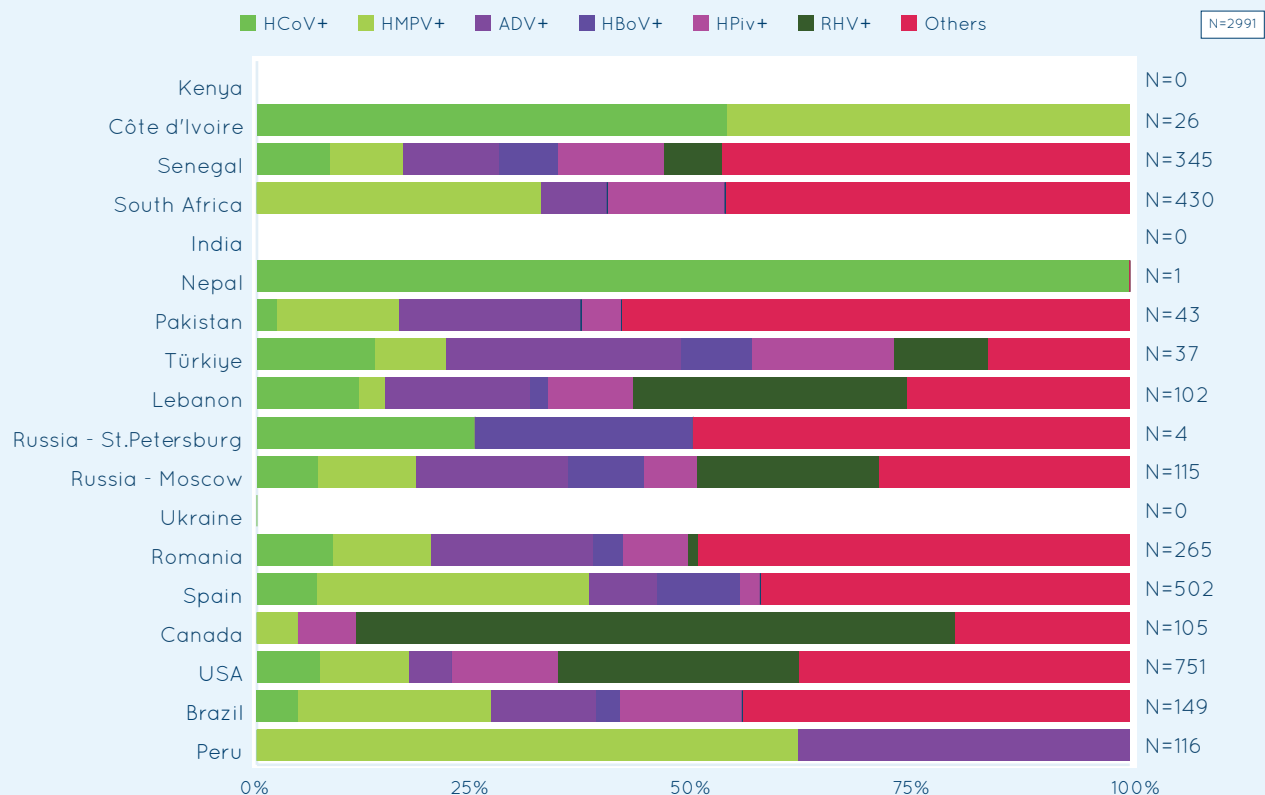
5.c. Other respiratory viruses

2 731 other respiratory viruses were detected during the 2022-2023 season in the 15 sites which tested patients for other respiratory viruses (Kenya, India and Ukraine did not test for other respiratory viruses).

These viruses included: human coronavirus, metapneumovirus, adenovirus, bocavirus, parainfluenza virus, rhinovirus and others.

Figure 27 shows the distribution of viruses tested, for sites which did test.

Figure 27 : Distribution of laboratory-confirmed other respiratory viruses - By site (2022-2023)



PART III.

The Foundation for Influenza Epidemiology governance, data management and research activities

The GIHSN is supported by a dedicated fund, the **Foundation for Influenza Epidemiology** (FIE), which was created in September 2015 by Sanofi under the auspices of **Fondation de France**, a leading philanthropy network in France¹³, to formalize several years of commitment to epidemiological research on severe influenza.

The Foundation for Influenza Epidemiology provides **catalytic funding** to sites, complementary to national and other sources of funding.

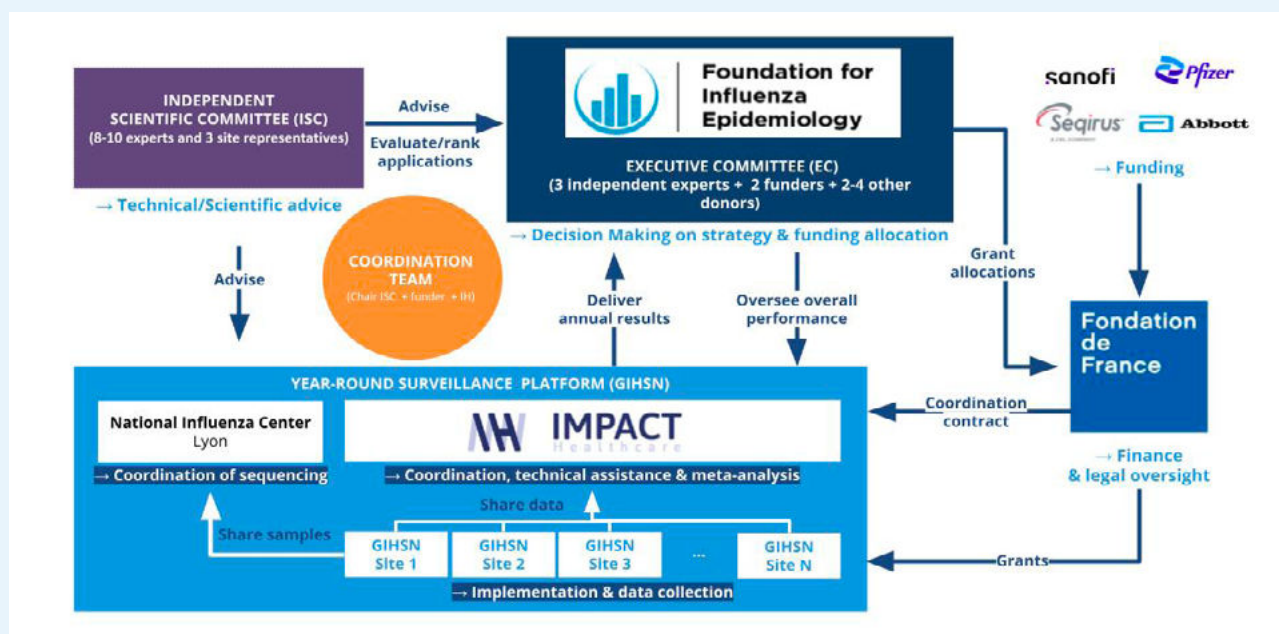
As of February 2024, donors of the Foundation for Influenza include Sanofi, Seqirus, Abbott Diagnostics, Pfizer, Illumina and IFPMA contributed in previous years.

All donations collected through this Foundation are dedicated to epidemiological research in the field of severe influenza and other respiratory viral diseases. Data are published yearly. Donors do not have access to the data and there is no commercial use of the data

1. Governance

Figure 28 presents the governance of the Foundation for Influenza Epidemiology, its committees and stakeholders, with their roles and responsibilities.

Figure 28 : Governance of the Foundation for Influenza Epidemiology



The Executive committee (EC) is responsible for the strategic direction of the foundation, prioritization of activities, allocation of funds, external stakeholders' engagement and communication. This committee is composed of funders, donors and independent scientific experts (members of the Independent Scientific Committee).

¹³ <https://www.fondationdefrance.org/en/homepage>

The Independent Scientific Committee (ISC) is in charge of the scientific oversight; it includes the world's top influenza epidemiology/virology/policy experts from public health institutes, health organizations and academia.

Coordination of the GIHSN network, surveillance implementation, data management and database hosting, is managed by **Impact Healthcare (IH)**, an independent organization based in Paris, France, specializing in the strategic and operational management of large innovative projects in Digital Health and the use of Health data, both in France and internationally; IH is the primary contact for sites and researchers. The **National Influenza Center Lyon (EZUS)** is coordinating laboratory activities with sites (training, technical support, sequencing) and producing sequencing reports for WHO Influenza vaccines composition meetings.

Fondation de France (FDF) ensures all administrative, legal and financial diligence (financial auditing, contracting, and payments). FDF is in direct contact with sites for grants allocation and administrative details.

A Coordination team is ensuring the operational flow and coordination of activities.

Composition of the Executive Committee (as of February 2024)

Funder: 2 seats* for Sanofi representatives

Other donors:

- 1 seat* for Seqirus representative
 - 1 seat* for Abbott-Diagnostics representative
 - 1 seat* for Pfizer representative
 - 3 seats* for Independent Scientific Committee represented by Marta Nunes, John Mc Cauley, and Melissa Andrew
- * with voting right

Participants to EC meetings:

- Fondation de France represented by Aurélie Mercier
- Foundation for Influenza Epidemiology represented by Sandra Chaves, Laurence Torcel-Pagnon and Myriam Beigeaud
- Impact Healthcare represented by Catherine Commaille-Chapus

Members of the Independent Scientific Committee (ISC) members

Independent Experts*:



Marta Nunes,
CERP, University of Lyon, France (Chair)



Bruno Lina,
University of Lyon, France (Former Chair)



Joseph Bresee,
Task Force for Global Health, USA



John McCauley,
Crick Institute, London, UK



Justin Ortiz,
University of Maryland, USA



Cecile Viboud,
Fogarty International Center at the National Institutes of Health (NIH), USA



Wenqing Zhang,
Head of GIP, WHO, Geneva (Observer)



Sandra S Chaves,
Foundation for Influenza Epidemiology, Paris, France (Observer)

Site Representatives:



Melissa K Andrew,
Canadian Serious Outcomes Surveillance Network, Halifax, Canada



Sonia M Raboni
Virology Laboratory, Infectious Diseases Division, Universidade Federal do Paraná, Brazil



Xavier Lopez Labrador,
Virology Laboratory, Genomics and Health, FISABIO, Spain

*John PAGET (Netherlands Institute for Health Services Research, Utrecht) has been an important historical member

2. Site selection process

All investigating sites participating in the GIHSN are selected on a yearly basis, through an annual Call for Proposal. published in May on the GIHSN website¹⁴.

14 See last Call for Proposal: <https://www.gihsn.org/join-the-gihsn/call-for-proposal>

Applications from institutions meeting the eligibility criteria are reviewed and evaluated by the Independent Scientific Committee of the Foundation according to predefined quality criteria.

These include scientific and technical criteria, such as the robustness of study settings, case ascertainment strategy/sampling strategy, lab capacities, commitment to timeliness sharing of data besides considerations regarding geographic representativeness.

Final decision is made by the Executive Committee of the Foundation.

3. Data management and ethics

3.a. Data sharing

To comply with regulations of data access and privacy, the Foundation set up a data warehouse and a data access framework. Impact Healthcare is Data Controller for the GIHSN (jointly with Fondation de France), handling the data collection process and supervising the GIHSN data warehouse.

The GIHSN database is hosted in a secured environment (certified secured hosting for health personal data).

Data are processed in full accordance with the European General Data Protection Regulation (GDPR) and French data protection regulations.

A data sharing agreement is signed by each site before field implementation starts. Sites implementing the GIHSN protocol should be compliant with their ethical and national regulations for the conducting of the surveillance. Any obligation related to data protection and data transfer to the Impact Healthcare platform should be anticipated.

Sites are strongly encouraged to share data with WHO's Global Influenza Surveillance and Response System (GISRS) and with local health authorities in ongoing bases.

3.b. Data analysis

A yearly pooled analysis is proposed, describing the season, or combining data from various sites and/or years for pooled analyses.

A yearly manuscript is developed under the responsibility of the Independent Scientific Committee. Additional analyses can be performed by research teams after review and approval of their research proposal by the Independent Scientific Committee and the Foundation.

Data access (anonymised and/or aggregated data only) is granted to research teams through a dedicated interface. The data catalogue is available on the platform, together with sites description. This provides a high-level fingerprinting of the GIHSN database and allows researchers to assess the feasibility of their research question.

Sites are informed upfront of any analysis, and they have the possibility to opt out.

3.c. Ethics

The GIHSN design and protocol has to be approved by local Research Ethics Committee before field implementation starts.

Informed written consent is required for enrolment. No intervention, apart respiratory specimens (e.g., nasopharyngeal, nasal and oropharyngeal) is associated with the study.

4. Publications and communications 2022-2023

Scientific papers

Analyses of GIHSN season data and results are performed on a yearly basis. All analyses results are submitted for publication to a peer reviewed journal, under the supervision of a member of the Independent Scientific Committee.

Other than yearly analysis, the following papers were published in 2023:



Predictors of severity of influenza-related hospitalizations: Results from the Global Influenza Hospital Surveillance Network (GIHSN)

Lily E Cohen, Chelsea L Hansen, Melissa K Andrew, Shelly A McNeil, Philippe Vanhems, Jan Kyncl, Javier Díez Domingo, Tao Zhang, Ghassan Dbaibo, Victor Alberto Laguna-Torres, Anca Draganescu, Elsa Baumeister, Doris Gomez, Sonia M Raboni, Heloisa I G Giamberardino, Marta C Nunes, Elena Burtseva, Anna Somnina, Snežana Medić, Daouda Coulibaly, Afif Ben Salah, Nancy A Otieno, Parvaiz A Koul, Serhat Unal, Mine Durusu Tanriover, Marie Mazur, Joseph Bresee, Cecile Viboud, Sandra S Chaves

National Library of Medicine – 01 Aug 2023



Age Differences in Comorbidities, Presenting Symptoms, and Outcomes of Influenza Illness Requiring Hospitalization: A Worldwide Perspective From the Global Influenza Hospital Surveillance Network

Melissa K Andrew, Henrique Pott, Lisa Staadegaard, John Paget, Sandra S Chaves, Justin R Ortiz, John McCauley, Joseph Bresee, Marta C Nunes, Elsa Baumeister, Sonia Mara Raboni, Heloisa I G Giamberardino, Shelly A McNeil, Doris Gomez, Tao Zhang, Philippe Vanhems, Parvaiz A Koul, Daouda Coulibaly, Nancy A Otieno, Ghassan Dbaibo, Maria Lourdes Guerrero Almeida, Victor Alberto Laguna-Torres, Anca Cristina Drăgănescu, Elena Burtseva, Anna Somnina, Daria Danilenko, Snežana Medić, Javier Díez-Domingo, Bruno Lina

National Library of Medicine – 27 May 2023

Sites are also very much encouraged to publish on their own, using the data they generated as part of their contribution in the GIHSN. The following paper was published by the site of Senegal in 2023:



Respiratory syncytial virus in pediatric patients with severe acute respiratory infections in Senegal: findings from the 2022 sentinel surveillance season

Mamadou Malado Jallow, Moussa Moise Diagne, Samba Niang Sagne, Fatime Tall, Jean Baptiste Niokhor Diouf, Djibril Boiro, Marie Pedapa Mendy, Ndiendé Koba Ndiaye, Davy Kiori, Sara Sy, Déborah Goudiaby, Cheikh Loucoubar, Gamou Fall, Mamadou Aliou Barry & Ndongo Dia.

Nature Portfolio (www.nature.com/scientificreports) - 2023.

All publications are shared on the GIHSN website¹⁵.

Communications & posters

The GIHSN participated in the 7th Meeting of the Africa Network for Influenza Surveillance and Epidemiology (ANISE), Johannesburg, 11-13 September 2023, and presented one poster:



The Global Influenza Hospital Surveillance Network (GIHSN): Data Sharing for Action.

Marta C Nunes, Nancy A Otieno, John Paget, Justin Ortiz, Melissa K Andrew, Shelly McNeil, Philippe Vanhems, Jan Kyncl, Javier Díez Domingo, Tao Zhang, Ghassan Dbaibo, Victor Alberto Laguna Torres, Anca Draganescu, Elsa Baumeister, Doris Gomez, Sonia M Raboni, Heloisa Giamberardino, Vicky Baillie, Elena Burtseva, Anna Somnina, Snežana Medić, Daouda Coulibaly, Afif Ben Salah, Liem Binh Luong, Bruno Lina, Parvaiz Koul, Serhat Unal, Mine Durusu Tanriover, Joseph Bresee, Cecile Viboud, John McCauley, Sandra S Chaves.

A poster was also presented by the site in Ukraine at the 9th ESWI Influenza Conference, 17-20 September 2023, Valencia:



Influenza during COVID-19 pandemic and war in Ukraine

Mironenko A., Holbka O., Radchenko L., Teteriuk N., Zakharchuk I., Kravchuk I., Potienko L., Rezvykh V., Palichuk O., Taranenko S., Ralets N.

9th ESWI Influenza Conference, 17-20 September, 2023, Valencia.

Links to the oral presentation and posters are available on the GIHSN website¹⁶.

¹⁵ <https://www.gihsn.org/publications/scientific-papers>

¹⁶ <https://www.gihsn.org/publications/oral-presentations-and-posters>



5. Current research activities associated with the GIHSN

Severity scale for influenza cases reported to GIHSN. This project supported by Nivel, Utrecht, the Netherlands, aims to develop a severity scale that is age-specific and based on the GIHSN patient questionnaire which would be used for surveillance purposes (e.g. uploaded to GISAID with the whole genome sequence data). The data have been analyzed and an algorithm developed to assign level of severity to influenza hospitalized cases in the network. The manuscript is under development and should be submitted for publication this year.

Association of severity indicators and influenza virus genome sequencing. This analytical project has been taken by the CERP - Center of Excellence in Respiratory Pathogens. Epidemiologic and clinical data collected from hospitalized patients are linked to whole genome sequencing of influenza viruses identified in those patients. The analysis will explore any pattern of disease severity associated with changes in the viruses or with specific clades.

Enterovirus D68 (EV-D68) retrospective analysis leveraging GIHSN platform. The US Centers for Disease Control and Prevention (CDC) are working with GIHSN sites that have information on EV-D68 cases from the years before the COVID-19 pandemic for a retrospective investigation on epidemiological and clinical characteristics of cases. This initiative may set up the stage for a possible prospective surveillance of this viruses to be included in the network.

Identify hospital-based catchment areas to estimate influenza disease burden and characterize changes in healthcare seeking behavior during and after the COVID-19 pandemic: A pilot initiative in LMIC. The National Institutes of Health (NIH) approached the GIHSN for a possible collaboration to identify hospital-based catchment areas to estimate influenza disease burden. GIHSN sites represent a unique data source for characterizing influenza virus infection associated hospitalizations and the risk of in-hospital mortality in different settings. Prior analysis of these data has highlighted increased severity of influenza-related hospitalizations in lower-income hospitals, compared to higher income sites. However, population denominators are lacking and these data cannot be used for disease burden estimates and direct comparison across settings. The project is supported by CERP - Center of Excellence in Respiratory Pathogens, and will initially focus on 3 or 4 sites for a proof of concept analysis.

Trends in influenza antiviral use among hospitalized influenza cases: real-world evidence from a global perspective. Early antiviral treatment can reduce influenza-associated complications including lower respiratory tract infections and death in hospitalized patients. In the US, antivirals are recommended for all hospitalized patients with suspected or confirmed influenza. Recommendation policies for other parts of the world may differ slightly from that in the US, but mostly support the use of antivirals and clinicians can consider treatment for people at higher risk of severe disease from influenza empirically. This data should serve as a benchmark and could provide insight on the use of influenza antivirals before and during the COVID-19 pandemic. Analytical proposal has been approved by the independent scientific committee and the GIHSN investigators. Analysis will start in 2024.

Influenza hospitalization among children <5 years: Retrospective data analysis from 20+ countries. There are effective and safe vaccines against influenza licensed for children as young as 6 months. A 2018 Cochrane review reported a pooled vaccine efficacy for 2 doses of inactivate influenza vaccine (IIV) against influenza of 64% (RR 0.4, 95%CI 0.3–0.5) in healthy children over 2 years of age – Jefferson T et al. Yearly vaccination being the most effective way to protect those at risk of influenza related complications. Nonetheless, despite data documenting the impact of influenza in young children, the World Health Organization (WHO) updated their recommendations for the use of influenza vaccine and removed young children from the high priority groups for vaccination. Data analysis have been initiated, leveraging 8 years of data and contrasting clinical outcomes and demographics by country and small age brackets.



PART IV.

Financial report

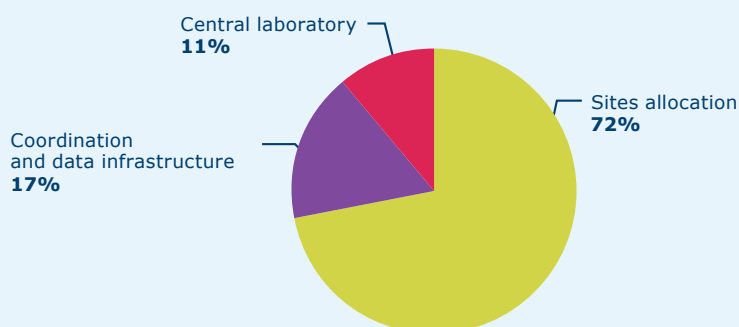
To date, the Foundation for Influenza Epidemiology (FIE) has invested more than 17 M€ to set up and scale up the GIHSN platform over the past 11 years. The yearly FIE budget allocation is endorsed by the Executive Committee in October.

Each year the Foundation invests part of its budget in new sites to continue building worldwide surveillance capacity and expands its network for a better representativeness. Geographical repartition of the sites translates also grants allocation by country income level (high, upper middle, lower middle). The FIE covers each year around 25% of the overall cost of the GIHSN platform which relies on existing national capacity and infrastructure (co-funding from sites or other sources).

FIE budget spent for 2022-23 (see **Figure 29**):

- 1, 2 M€ was committed for sites implementation of the year-round surveillance from 1st November 2022 to 31 October 2023.
 - 10% of this budget was dedicated to pilot the implementation of the GIHSN surveillance in new sites.
- 285 K€ was spent to ensure the coordination and data infrastructure of the GIHSN platform; 180k€ was used for centralized laboratory activities and sequencing.

• **Figure 29 : FIE funds repartition for 2022-2023** •



PART V.

Collaboration with WHO

The GIHSN relies on existing national assets and is complementary to the Global Influenza Surveillance and Response System (GISRS), which celebrated in 2022 its 70 years collaboration with 148 National Influenza Centers, seven WHO CC, four Essential Regulatory Laboratories, and 13 H5 Reference Laboratories. For the 2022-23 season, 12 GIHSN sites are integrated into their national influenza surveillance systems and most of them are themselves or are close to their National Influenza Centers which contribute to GISRS. What makes the GIHSN unique and complementary to GISRS is the linkage of clinical data on influenza severity with virology and virus sequencing.

In October 2023, the Foundation signed a Memorandum of Understanding with WHO. This necessary condition to engage in official relations and exchange resources with WHO is the recognition of the value of GIHSN and of the strong governance, transparency, and audit processes of the Foundation

Few priorities area of collaboration have been highlighted:

- **Virus co-circulation and alert mechanisms**

GIHSN can provide useful information to describe a wide range of respiratory virus circulation at the level of hospitalized patients (case-based data vs. aggregated data). It can also potentially trigger an alert by identifying unexpected cluster of cases.

Focus will be put on the improvement of the timeliness of the reporting, case-based reporting modalities, potential for real time reporting of some variables, data reporting flow at country, regional and global level.

The expansion of the GIHSN (with recruitment of new sites) will also be coordinated with WHO to ensure better geographical representativeness.

- **Combination of severity and WGS for strain selection**

Currently, some of the GIHSN sites without local capacities send samples for whole genome sequencing (WGS) to the Lyon NIC. WHO CCs and NICs may be able to support the GIHSN sites by receiving specimens for WGS, to increase volume of data and timeliness of sequencing sharing to support decision on strain selection for flu vaccine. The collaboration will focus on stressing the link with NIC and WHO CC to be able to perform more and timely WGS and/or provide access to probes/reagents, develop further the collaboration with GISAID and potentially sequencing for other viruses (RSV, SARS-Cov2,...)

- **Burden of disease estimation and other research activities**

In terms of research perspectives, the GIHSN relies on 3 pillars: a motivated and diverse researchers/clinicians' community, an hospital/lab infrastructure able to carry strong quality research, rich and unique data generated every year. This infrastructure should be leveraged to address specific research questions. It could include evaluation of catchment area for burden of disease evaluation, POC for preparedness, etc.



Acknowledgements

Investigating sites:

- **Brazil:** Hospital Pequeno Principe, Curitiba (Sonia Mara Raboni, MD, PhD; Heloisa Isle Giamberardino, MD, PhD)
- **Canada:** The CIRN Serious Outcomes Surveillance (SOS) Network, Halifax (Shelly A. McNeil, MD and Melissa K Andrew)
- **China:** School of Public Health, Fudan University, Shanghai (Tao Zhang, PhD)
- **Côte d'Ivoire:** Institut National d'Hygiène Publique (INHP), Abidjan (Daouda Coulibaly, MD)
- **France:** ANRS-MIE, Paris (Odile Launay; Liem Binh Luong; Louise Lefrançois)
- **India:** Sher-i-Kashmir Institute, Srinagar (Parvaiz A Koul, MD)
- **Kenya:** Kenya Medical Research Institute (KEMRI), Nairobi (Nancy A. Otieno, PhD)
- **Lebanon:** American University of Beirut, Beirut, (Dr Ghassan Dbaibo, MD)
- **Nepal:** Patan Academy of Health Sciences (Kedar Baral)
- **Pakistan:** National Institute of Health, Islamabad (Dr Muhammad Salman; Nazish Badar)
- **Peru:** Instituto de Medicina Tropical Universidad Nacional Mayor de San Marcos, Lima (Victor Alberto Laguna-Torres, MD)
- **Romania:** National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest (Anca Cristina Draganescu, MD, PhD; Oana Sandulescu)
- **Russian Federation:** Federal Research Budgetary Institute "National Research Center of Epidemiology and Microbiology named after honorary academician N.F. Gamaleya, Moscow (Elena Burtseva, MD, PhD)
- **Russian Federation:** Smorodintsev Research Institute of Influenza, St Petersburg (Anna Sominina, MD, PhD; Daria Danilenko)
- **Senegal:** Institut Pasteur of Dakar (IPD), Dakar (Ndongo Dia, MD)
- **South Africa:** Vaccines and Infectious Diseases Analytics Research Unit, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg (Marta Nunes, PhD)
- **Spain:** Fisabio-Public Health, Valencia (Javier Diez-Domingo, MD, PhD; Ainara Mira Iglesias)
- **Türkiye:** Turkish Society of Internal Medicine, Ankara (Serhat Unal, MD; Mine Durusu Tanriover)
- **Ukraine:** SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine, Kyiv (Alla Mironenko; Nataliia Teteriuk)
- **USA:** Icahn School of Medicine at Mount Sinai, NYC (Viviana Simon, MD)

Members of the Independent Scientific Committee, Members of the Executive Committee, Fondation de France (Aurélien Mercier), **Foundation for Influenza Epidemiology** (Cedric Mahe; Laurence Torcel-Pagnon; Sandra S Chaves).

National Influenza Center, Lyon, France: Bruno Lina; Antonin Bal; Nathalie Bergaud; Gwendolyne Burfin; Gregory Queromes; Hadrien Regue; Quentin Semanas.

Impact Healthcare: Catherine Commaille-Chapus; Camille Hunsinger; Jean-Yves Robin.



Annex

Annex 1: Distribution of patients by site: number of enrolled patients and viruses tested and detected (2022-

Country	Site/Institution	#Enrolled*	#Influenza +	#Tested SARS-CoV2	#SARS-CoV2 +	#Tested RSV	#RSV +	#Tested ORV**	#ORV +	#WGS Total	#WGS Influenza	#WGS SARS-CoV2
Africa												
Kenya	Kenya Medical Research Institute (KEMRI), Nairobi	3948	286	3938	170	0	-	0	-	124	124	0
Côte d'Ivoire	Institut National d'Hygiène Publique (INHP), Abidjan	1656	39	1626	25	467	1	1505	24	10	5	5
Senegal	Institut Pasteur of Dakar (IPD), Dakar	862	33	862	36	862	107	862	290	31	19	12
South Africa	University of the Witwatersrand, Johannesburg	3366	200	3365	103	3365	445	3365	409	119	119	0
Asia/Pacific												
India	Sher-i-Kashmir Institute, Srinagar	1207	54	0	-	0	-	0	-	29	29	0
Nepal	Patan Academy of Health Sciences	256	7	132	3	28	5	123	1	0	-	-
Pakistan	National Institute of health Islamabad Pakistan	3355	499	2775	76	3013	417	96	43	80	62	18
Middle East												
Türkiye	Turkish Society of Internal Medicine, Ankara	640	14	634	18	634	23	631	37	28	13	15
Lebanon	American University of Beirut, Beirut	2225	205	2189	283	2148	301	90	70	100	47	53
Eurasia												
Russia - St Petersburg	Smorodintsev Research Institute of Influenza, St Petersburg, Russia	48	48	48	0	48	1	48	4	48	48	0
Russia - Moscow	FSBI "N.F. Gamaleya NRCEM" Ministry of Health, Moscow	756	132	756	30	756	31	756	108	15	15	0
Ukraine	SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine, Kyiv	244	151	236	56	0	-	0	-	83	66	17
Romania	National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest	560	189	537	20	555	26	547	230	140	140	0
Spain	FISABIO, Valencia	4138	345	4138	505	4138	264	4138	488	462	120	342
France	ANRS MIE, Paris	0	-	-	-	-	-	-	-	-	-	-
North America												
Canada	The CIRN Serious Outcomes Surveillance (SOS) Network, Halifax	1155	554	1139	337	1150	25	1150	104	90	0	90
USA	Icahn School of Medicine at Mount Sinai, NYC	7930	374	7495	1131	3523	137	2219	669	118	53	65
South America												
Brazil	Hospital Pequeno Principe, Curitiba	476	79	476	25	476	113	476	138	28	28	0
Peru	Instituto de Medicina Tropical, Lima	1075	76	1075	46	1075	144	1075	116	0	-	-
Total		33897	3285	31421	2864	22238	2040	17081	2731	1505	888	617

* All tested for influenza

** Tests varies by sites and can include any of the following : Adenovirus, Bocavirus, Human Coronavirus, Metapneumovirus, Parainfluenzavirus, Rhinovirus, or other respiratory viruses not predefined

«Abbreviations :
WGS - Whole Genome Sequencing ;
ORV - Other Respiratory Viruses ;
RSV - Respiratory Syncytial Virus »



Global Influenza
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GIHSN Annual Report

SEASON 2022-23

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