Global Influenza
Hospital Surveillance
Network

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Healthcare

GIHSN 11TH GLOBAL ANNUAL MEETING

16-17 November 2023

Foundation for
Influenza
Epidemiology

Sous l'égide de
Fondation
de
France

WELCOME TO THE GIHSN GLOBAL ANNUAL MEETING 2023

GIHSN GLOBAL ANNUAL MEETING 2023

16 – 17 November 2023

WHO HQ, Geneva

Global Influenza Hospital Surveillance Network

Global Annual Meeting 2023

AGENDA DAY 1 PM

13:30 - 14:45	**GIHSN contribution to influenza vaccine selection** *Presentations & discussion* - **Perspectives and challenges for influenza vaccine selection** - **Role and contribution of GIHSN** - **GISAID and GIHSN**	Moderator: J McCauley, Crick Institute N Lewis, Crick Institute B Lina, CIRI S Maurer-Stroh, GISAID
14:45 - 16:00	**Leveraging on the GIHSN database & network** *Presentations & discussion* - **Enterovirus surveillance and proposed collaboration with the GIHSN** *(25' presentation & discussion)* - **The importance of denominator for burden of disease estimates and how it could be implemented in the GIHSN** *(25' presentation & discussion)* - **The SevScale project** *(25' presentation & discussion)*	Moderator: S Chaves, FIE M Delahoy, US CDC C Viboud, NIH B Boudewijns, Nivel
16:00 - 16:30	Coffee break	
16:30 - 17:45	**Collaboration with WHO, based on the Memorandum of Understanding between WHO and the Foundation** *Presentations & discussion* - **Virus co-circulation and alert mechanisms** *(25' presentation & discussion)* - **Combination of severity and WGS for strain selection** *(25' presentation & discussion)* - **Burden of disease estimation** *(25' presentation & discussion)*	Moderators: W Zhang, WHO & C Mahé, FIE JM Heraud, WHO M Samaan & W Zhang, WHO S Tempia, WHO
17:45 - 18:00	**Wrap-up & Closing of Day 1**	

WEBINAR RULES

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

Thank you all for cooperation.

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GIHSN CONTRIBUTION TO INFLUENZA VACCINE SELECTION

Moderator: John Mc CAULEY, The Francis Crick Institute

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-Nicola LEWIS, Worldwide Influenza Centre at the Francis Crick Institut
-Bruno LINA, CIRI, Lyon
-Sebastian MAURER-STROH, GISAID

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GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

PERSPECTIVES AND CHALLENGES FOR INFLUENZA VACCINE SELECTION

Nicola S LEWIS , Director, Worldwide Influenza Centre at the Francis Crick Institute

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Perspectives and challenges for influenza vaccine selection

Opportunities for GIHSN and GISRS

Nicola S. Lewis BSc BVetMed PhD PGCert VetEd FHEA MRCVS

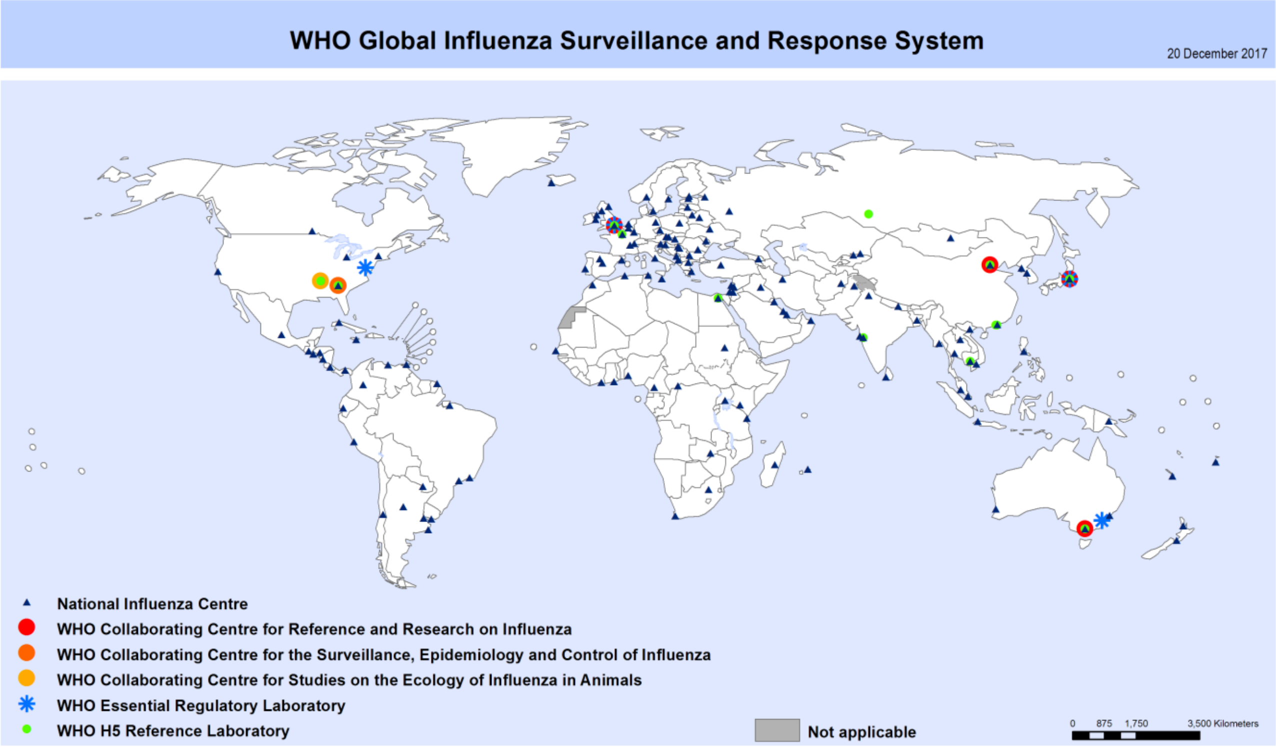
- Director: Worldwide Influenza Centre at the Francis Crick Institute.

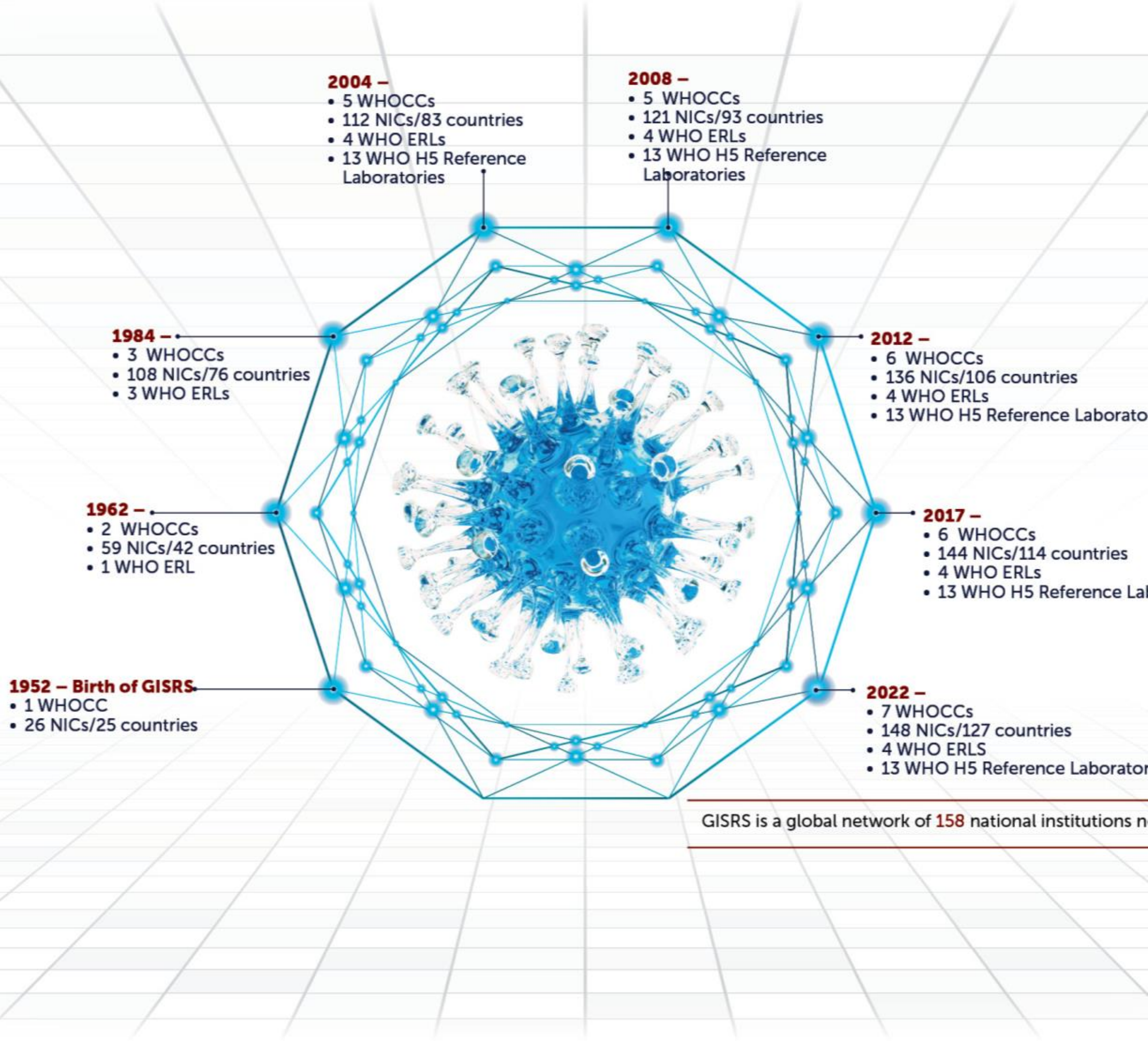
The WHO Collaborating Centre for Influenza Research and Response

- Professor in One Health Evolutionary Biology: Royal Veterinary College, University of London

The WHO Global Influenza Surveillance and Response System

- Created in 1952, the Global Influenza Surveillance and Response System,
- or GISRS as it is known now, is celebrating 70 years of success as a worldwide network,
- highlighting its value to broad respiratory virus threats including influenza and
- SARS-CoV-2 and setting its sights to the future.
- TO expanded GISRS





The role of the Worldwide Influenza Centre

Characterisation

- fully characterize & preserve representative influenza viruses from outbreaks in different parts of the world.

Vaccine recommendation

- provide guidance and advise as and when appropriate on the viruses that should be included in influenza vaccines.

Reference viruses and reagents

- collect & distribute virologic and epidemiological information about the prevalence of influenza in different parts of the world and to develop and distribute reference viruses.

Training

- provide training as and when appropriate to experts from WHO National Influenza Centres and other GISRS laboratories in specialized techniques.

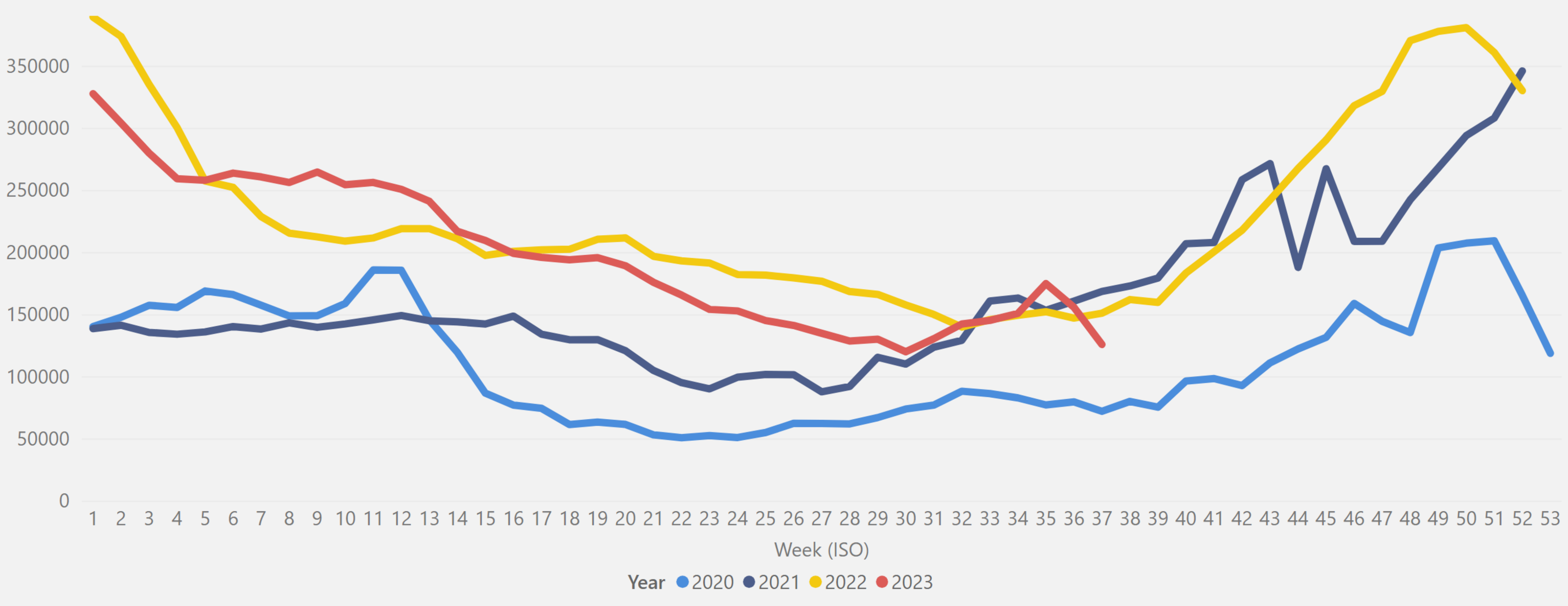
Research

- research related to the properties of influenza viruses and reference activities as prioritized by the WHO Research Agenda for influenza.

Pandemic preparedness

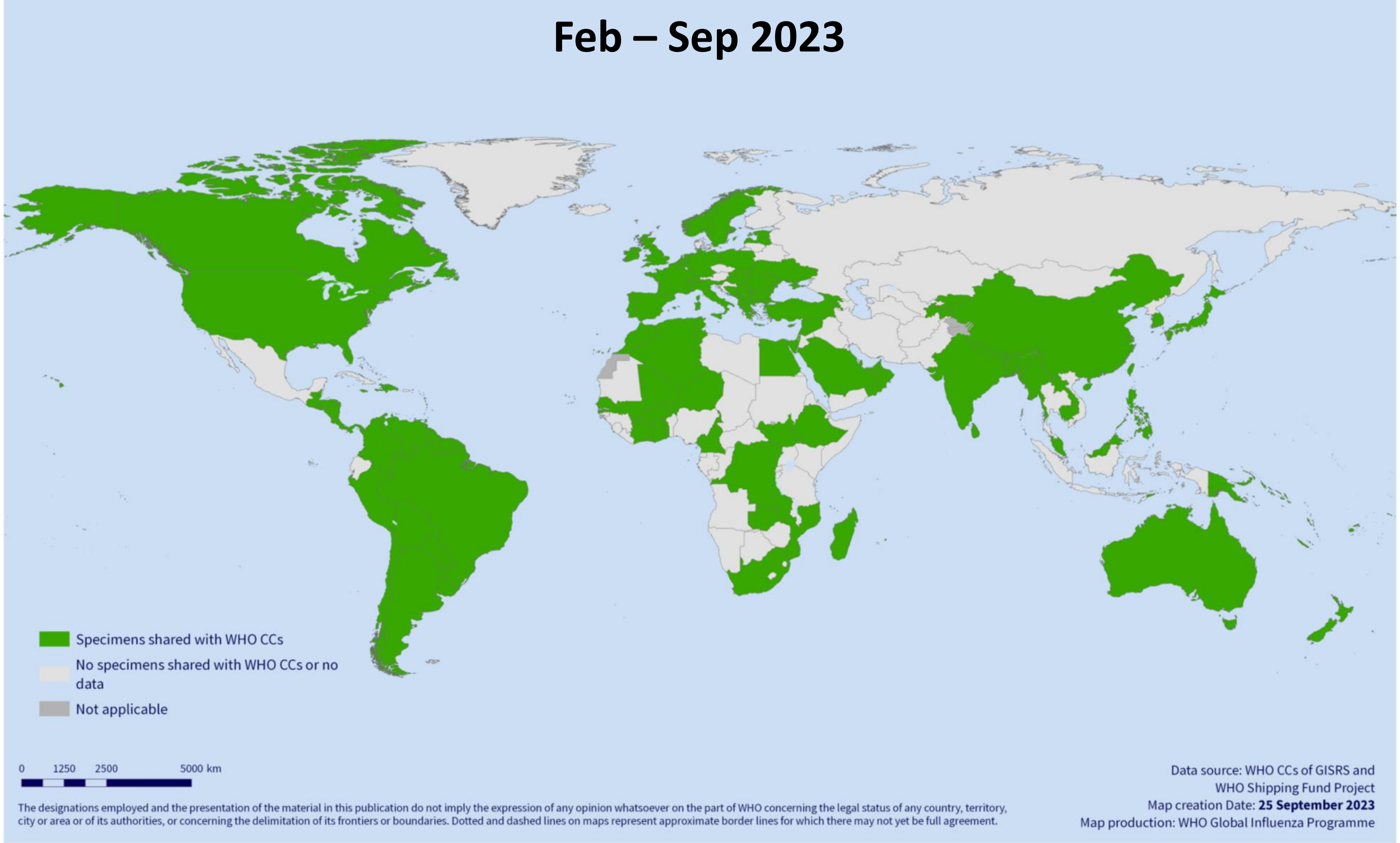
- receive, handle and distribute influenza viruses of pandemic potential according to the rules set out by the WHO Pandemic Influenza Preparedness (PIP) Framework

Number of specimens processed by GISRS by week



Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (GISRS)

Countries, areas and territories shared viruses with WHO CCs


Feb – Sep 2023

🟩 Specimens shared with WHO CCs

⬜ No specimens shared with WHO CCs or no data

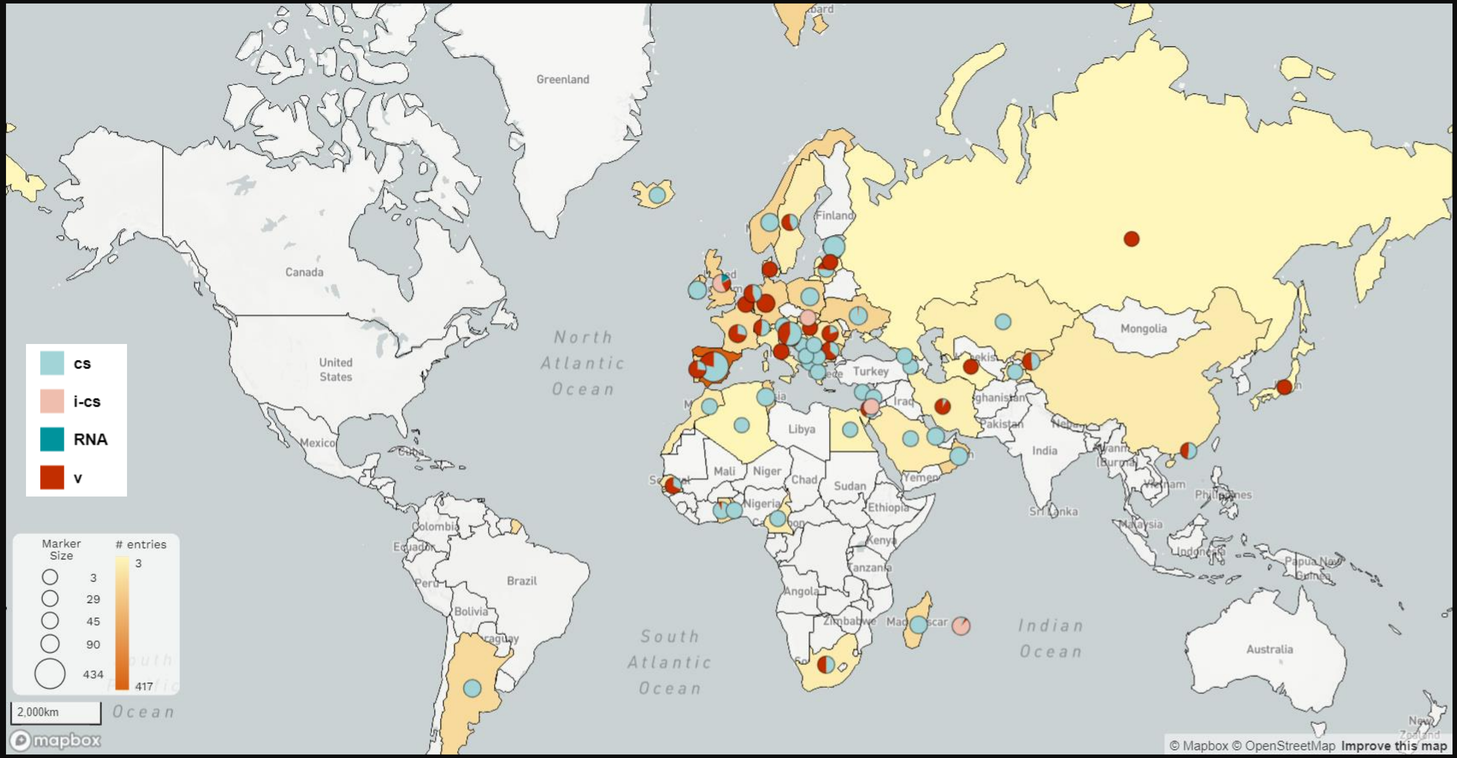
▨ Not applicable

The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data source: WHO CCs of GISRS and
WHO Shipping Fund Project
Map creation Date: **25 September 2023**
Map production: WHO Global Influenza Programme

Sample type & numbers received at the WIC

Collection dates week 21-2022 / 20-2023

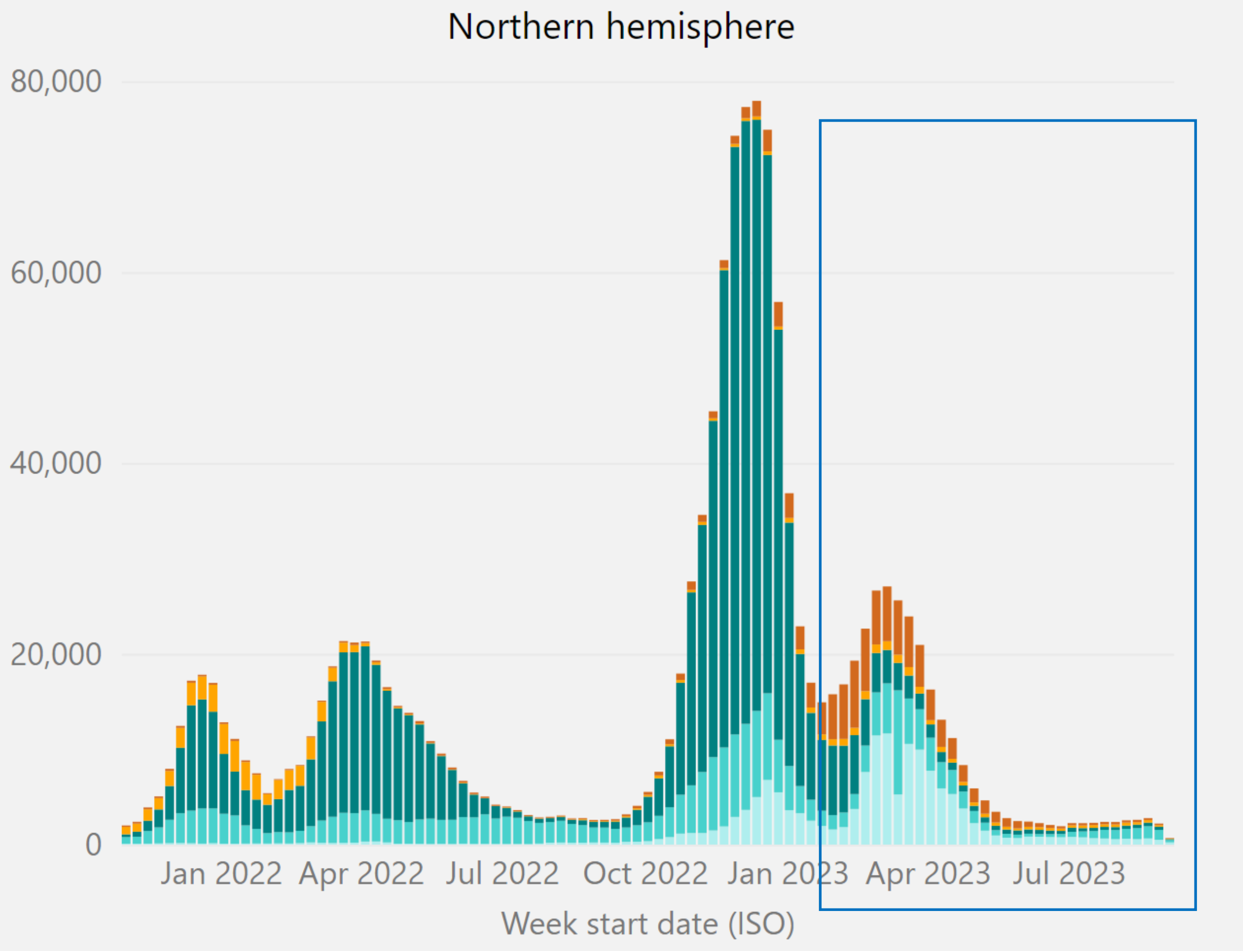


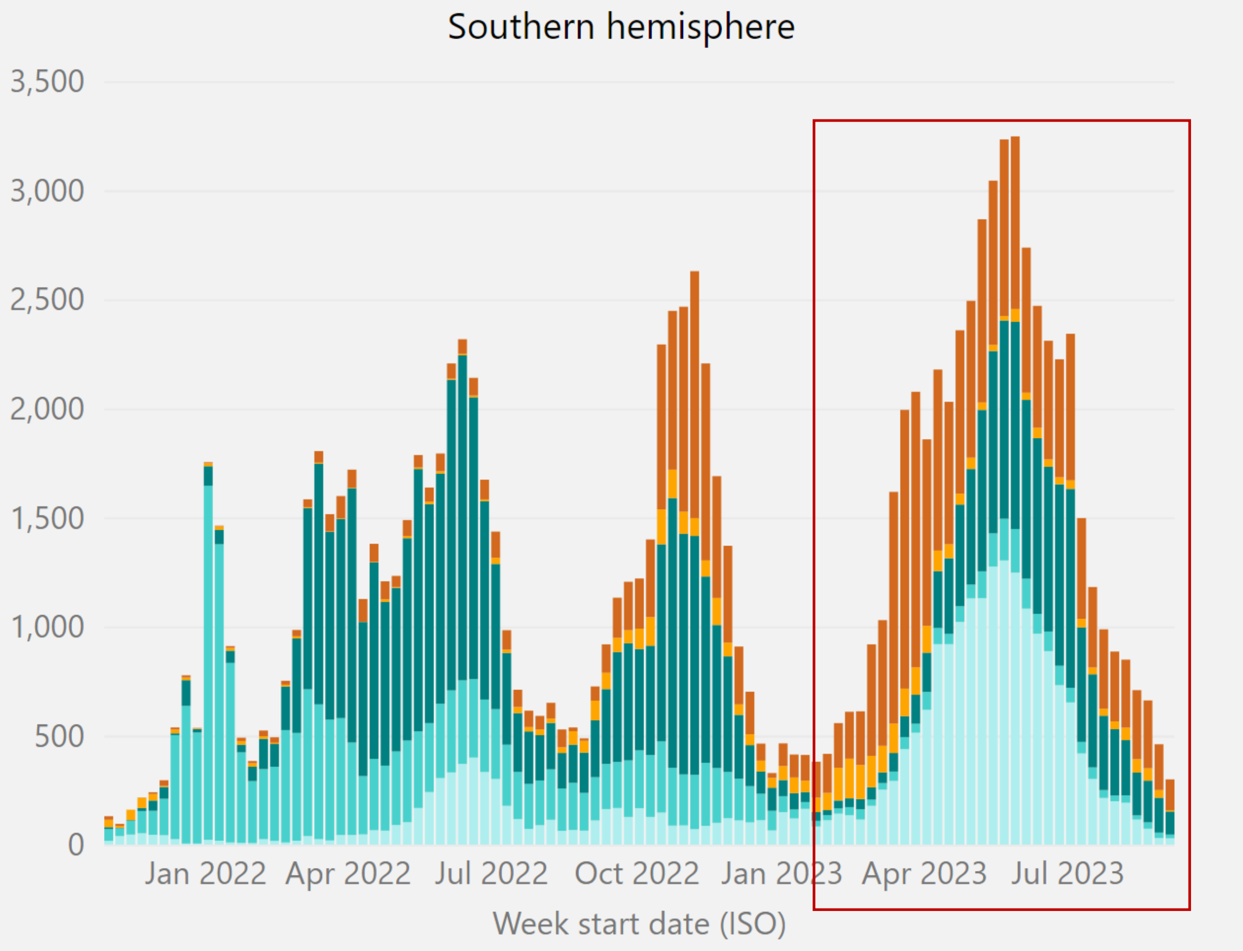
3811 samples received:

- 2605 clinical samples
- 976 virus isolates
- 14 RNAs
- 216 clinical samples in lysis buffer

246 CS + VI pairs

Circulation of influenza viruses by hemisphere





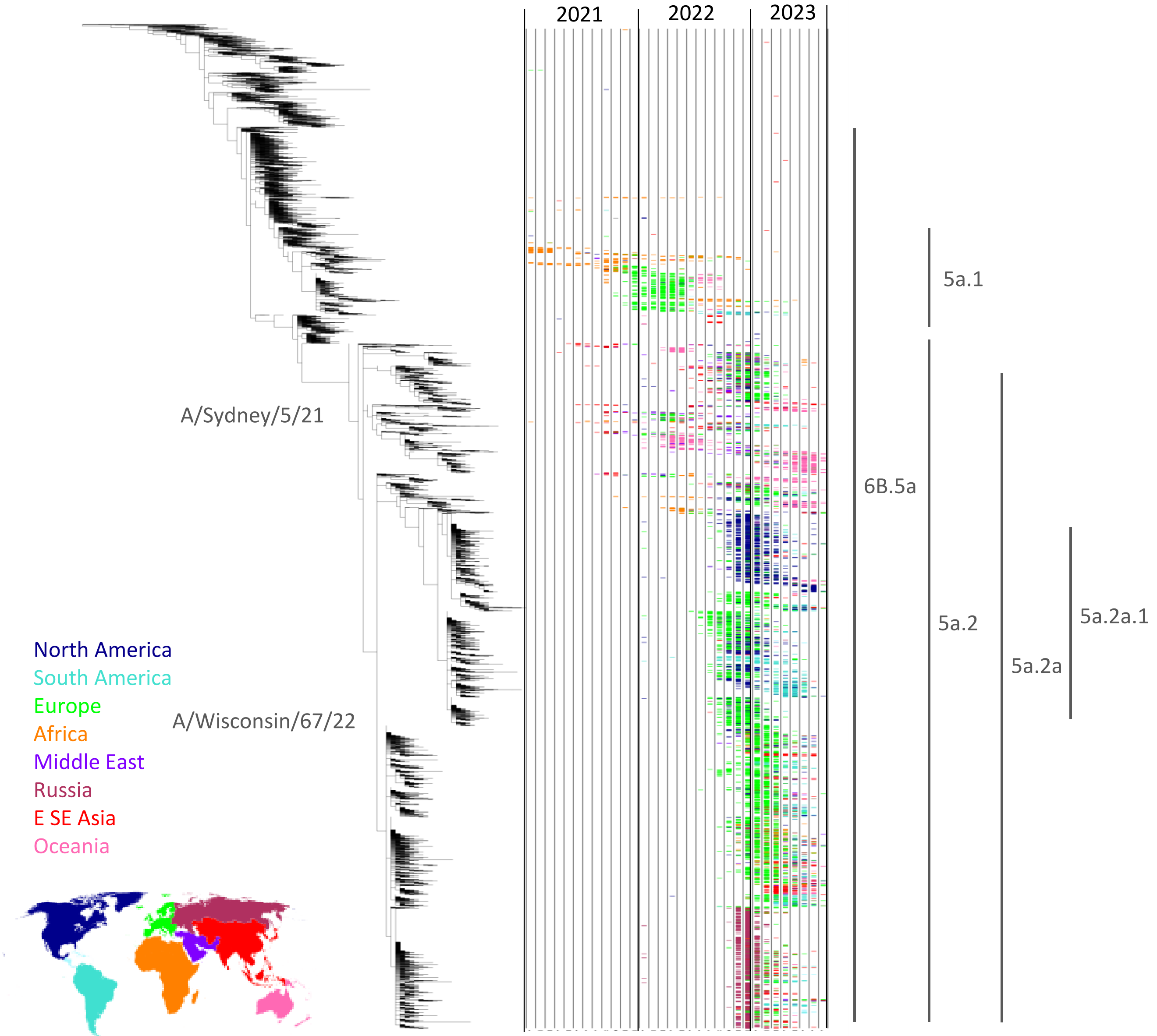
Virus type name ● A(H1N1)pdm09 ● A(H3) ● A (Not subtyped) ● B (Victoria lineage) ● B (Yamagata lineage) ● B (Lineage not determined) ● A(H1) ● A(H5)

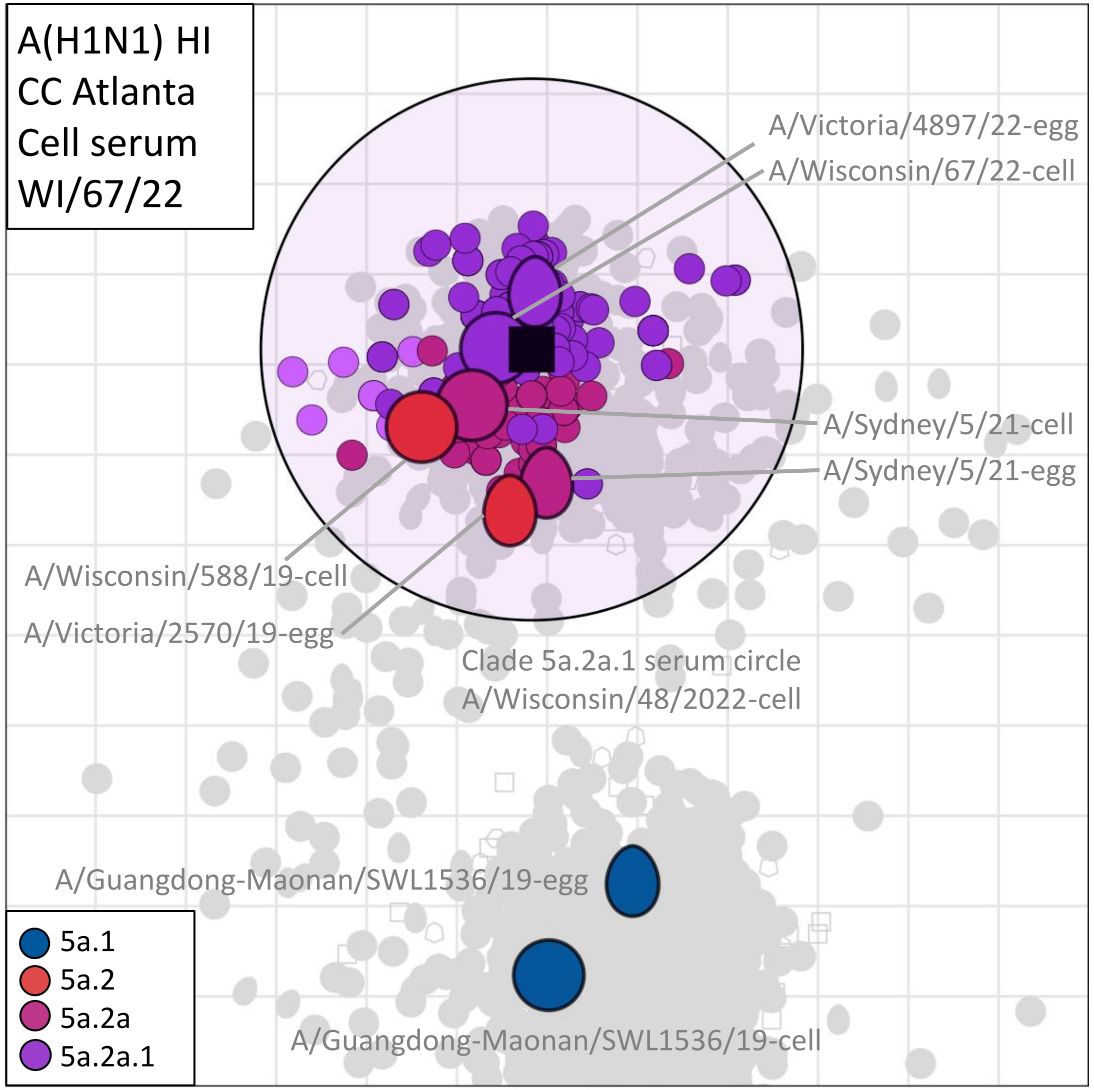
Select week start date (ISO)

11/1/2021 9/4/2023

Data source: FluNet, (https://www.who.int/tools/flunet), Global Influenza Surveillance and Response System (GISRS)

A(H1N1)pdm09 phylogenetic tree and antigenic map





Since 1st February 2023 (older viruses in grey)
Antiserum circles (within 8-fold of homologous titers)

Source: S. James and D. Smith, Cambridge, UK

Recommendation

It is recommended vaccines for use in the 2024 southern hemisphere influenza season contain the following:

Trivalent: Egg-based Vaccines

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Thailand/8/2022 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Trivalent: Cell- or recombinant-based Vaccines

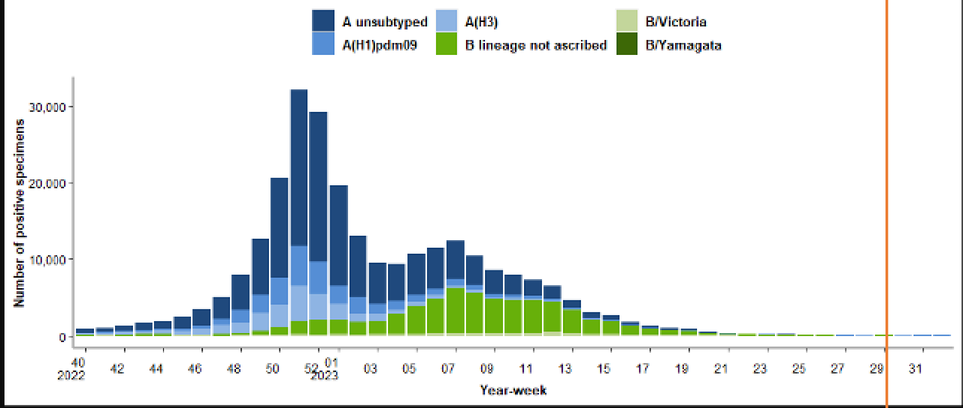
- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/Massachusetts/18/2022 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

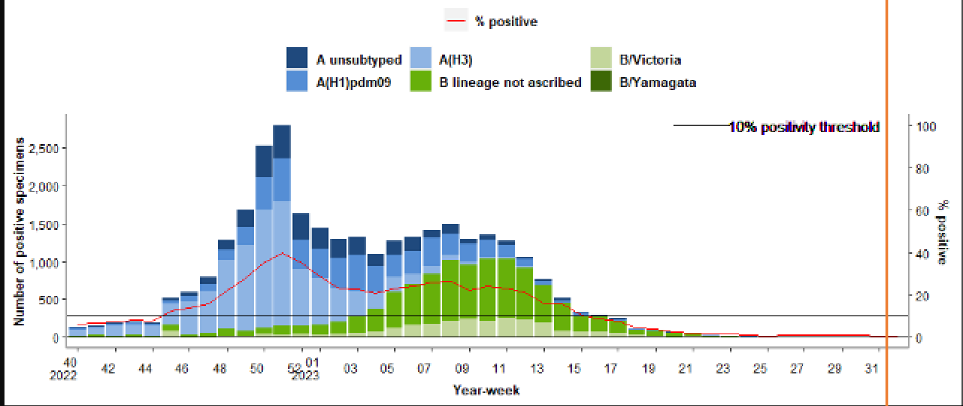
Quadrivalent: egg- or cell culture- or recombinant-based vaccines

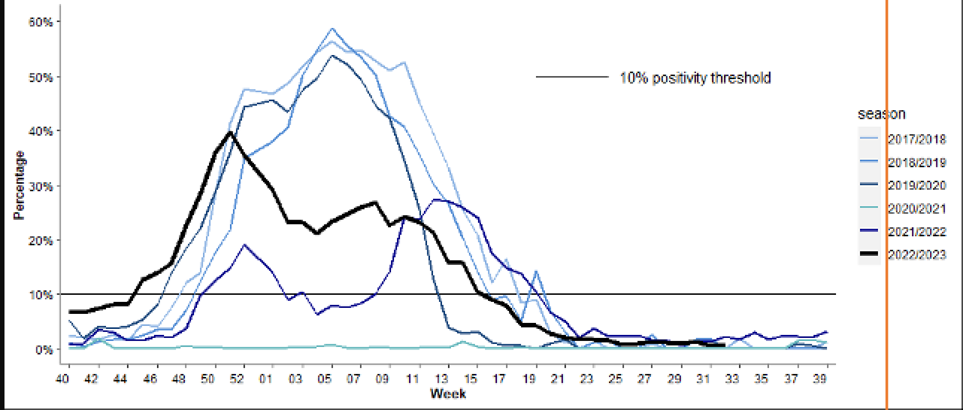
- Above 3 components; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Surveillance

- Timely sharing of specimens with the CC’s
- Genetic and phenotypic characterization including antiviral sensitivity and serology
- Two vaccine composition meetings a year
- Take data from a set time period so encourage multiple shipments throughout season from sentinel systems/sites via NICs


C. Non-sentinel specimens testing positive for influenza by week, (sub)type and percentage positive, 2022/23 season


B. Sentinel specimens testing positive for influenza by week, (sub)type and percentage positive, 2022/23 season


A. Percentage of sentinel ILI/ARI specimens testing positive for influenza by season

Opportunities for GIHSN and GISRS

- Enhanced linkage between GIHSN sentinel network and GISRS
  - Through NICs
  - Through bilateral collaboration between sentinel node and WHO CC

- Metadata fields from sequence submission identify GIHSN samples for higher resolution analyses
- Options for increased sequence generation through WHOCC's if GIHSN node has limited capacity to generate with timeliness
- Multi-pathogen e.g. SARS-CoV2 for eGISRS

- Other partnership opportunities for discussion with network

With thanks:

WHO National Influenza Centres
WHO Collaborating Centres
WHO HQ and
WHO Regional Offices
ECDC
University of Cambridge

Royal Veterinary College

THE
FRANCIS
CRICK
INSTITUTE

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GIHSN SEQUENCING ANALYSIS 2022-23

Bruno LINA – Virseq platform HCL, Lyon

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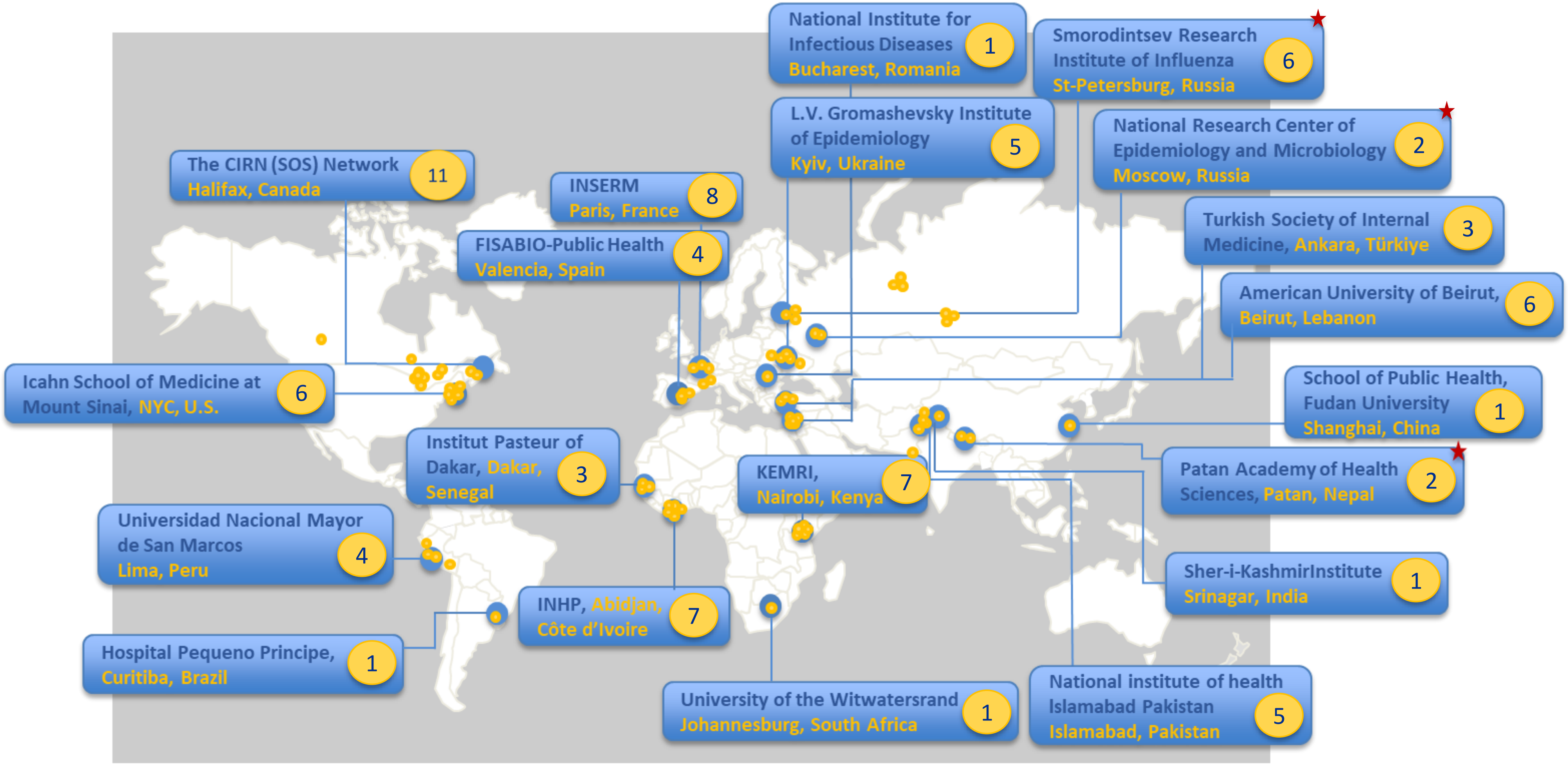
20 SITES IN 19 COUNTRIES PARTICIPATED IN THE GIHSN IN 2022_23



The CIRN (SOS) Network **Halifax, Canada** 11

Icahn School of Medicine at Mount Sinai, **NYC, U.S.** 6

Universidad Nacional Mayor de San Marcos **Lima, Peru** 4

Hospital Pequeno Principe, **Curitiba, Brazil** 1

INSERM **Paris, France** 8

FISABIO-Public Health **Valencia, Spain** 4

Institut Pasteur of Dakar, **Dakar, Senegal** 3

INHP, **Abidjan, Côte d'Ivoire** 7

National Institute for Infectious Diseases **Bucharest, Romania** 1

L.V. Gromashevsky Institute of Epidemiology **Kyiv, Ukraine** 5

KEMRI, **Nairobi, Kenya** 7

University of the Witwatersrand **Johannesburg, South Africa** 1

Smorodintsev Research Institute of Influenza **St-Petersburg, Russia** 6 ★

National Research Center of Epidemiology and Microbiology **Moscow, Russia** 2 ★

Turkish Society of Internal Medicine, **Ankara, Türkiye** 3

American University of Beirut, **Beirut, Lebanon** 6

School of Public Health, Fudan University **Shanghai, China** 1

Patan Academy of Health Sciences, **Patan, Nepal** 2 ★

Sher-i-KashmirInstitute **Srinagar, India** 1

National institute of health Islamabad Pakistan **Islamabad, Pakistan** 5

● GIHSN sites (2022-23) ● Hospital location

x Number of hospitals per site ★ No fund allocated

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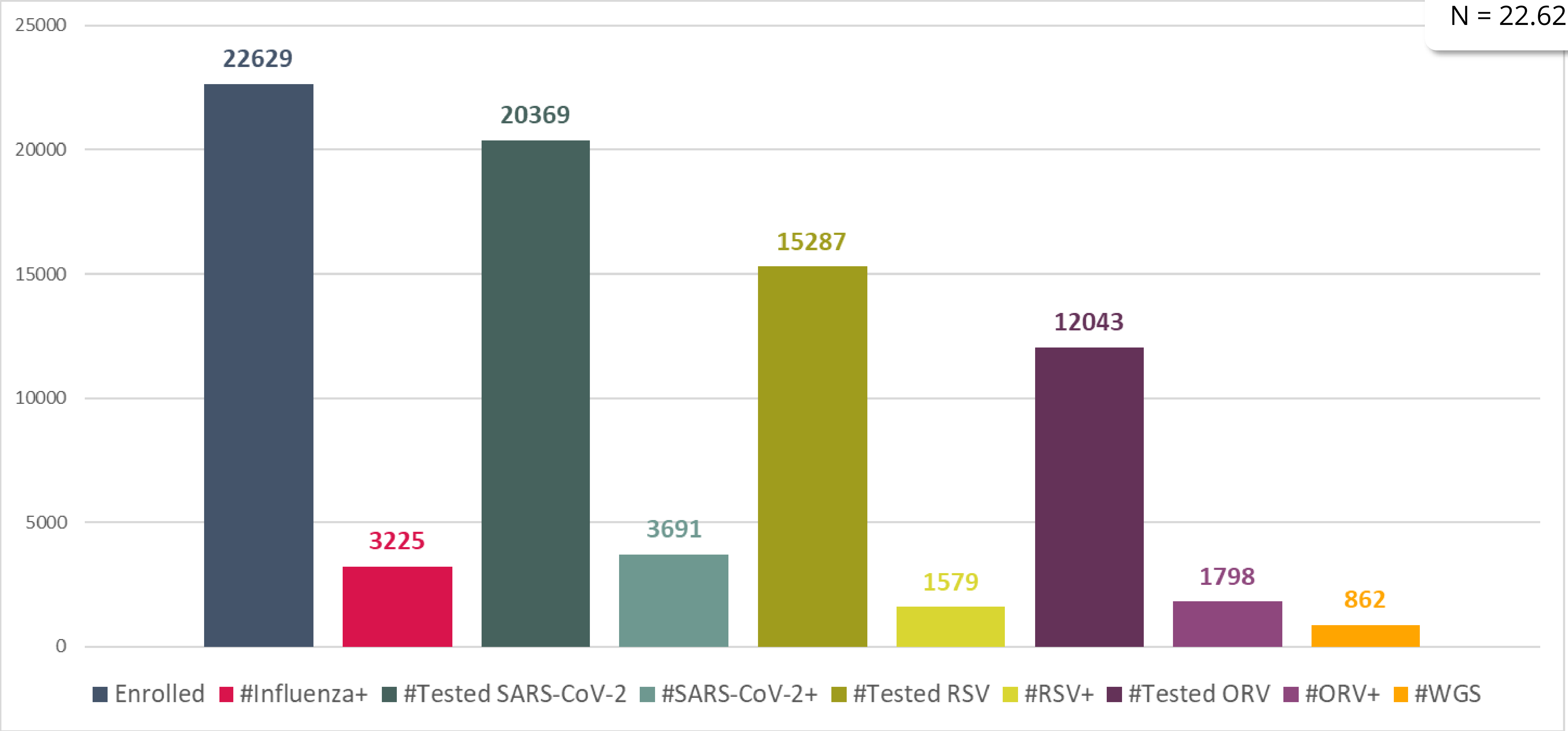
OVERALL NB OF PATIENTS ENROLLED AND POSITIVE CASES OF INFLUENZA, SARS-COV2, RSV AND ORV (2022-23) (#)

(AS OF NOVEMBER 3RD, 2023)

N = 22.629



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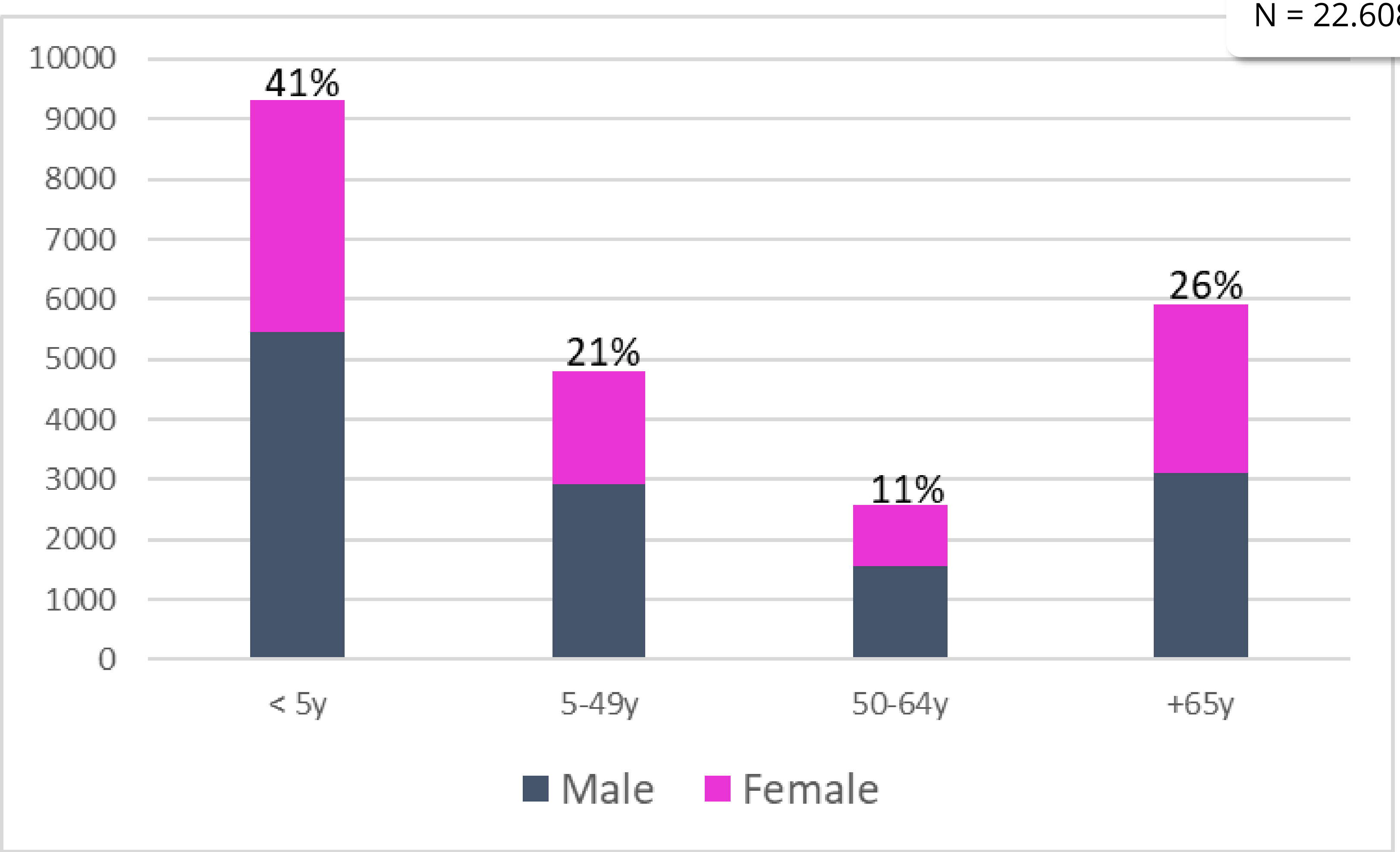
DISTRIBUTION OF ENROLLED PATIENTS BY AGE GROUP AND SEX – ALL SITES (2022-23) (#)

(AS OF NOVEMBER 3RD, 2023)

N = 22.608*



*No age completed for 21 patients

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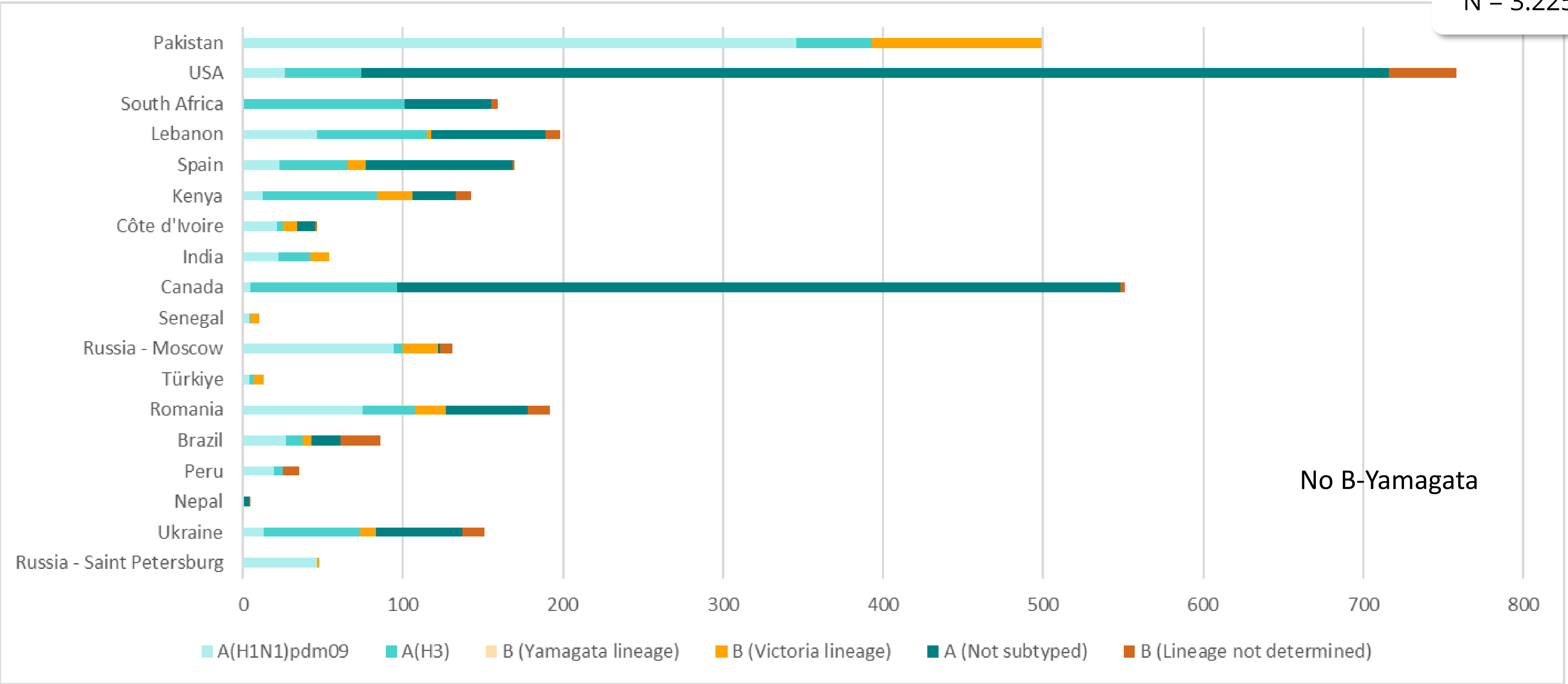
DISTRIBUTION OF LAB CONFIRMED INFLUENZA CASES BY VIRUS SUBTYPE AND LINEAGE (22-23) (#) (AS OF NOVEMBER 3RD, 2023)

N = 3.225



No B-Yamagata

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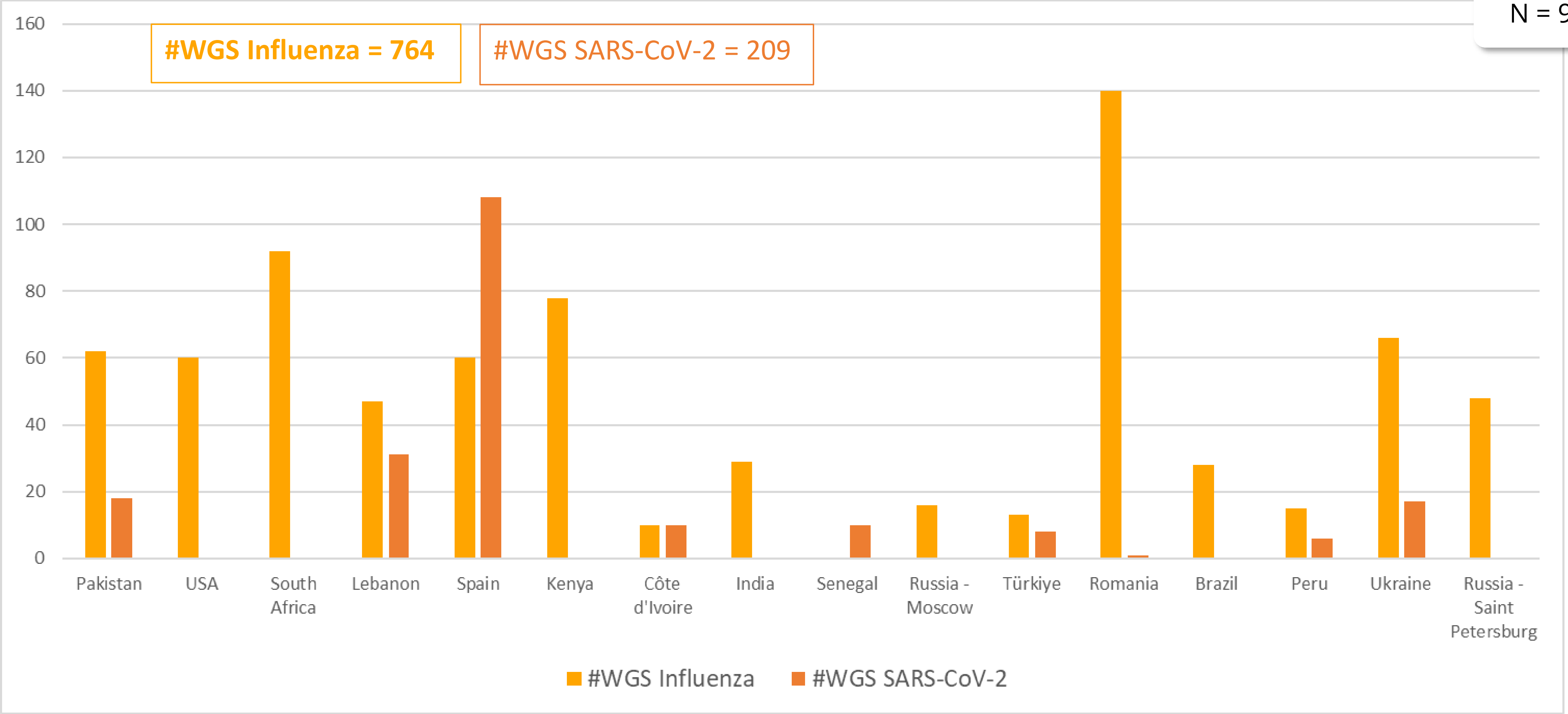
WGS BY SITE (2022_23) (#)
(AS OF NOVEMBER 3RD, 2023)

N = 961*



*99 not yet in the GIHSN database

Global Influenza Hospital Surveillance Network

GIHSN reports provided to the WHO prior to the 2 VCM

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GIHSN report of activity prior to the WHO Consultation on the Composition of Influenza Virus Vaccines for use in the 2023-2024 Northern Hemisphere Influenza Season.

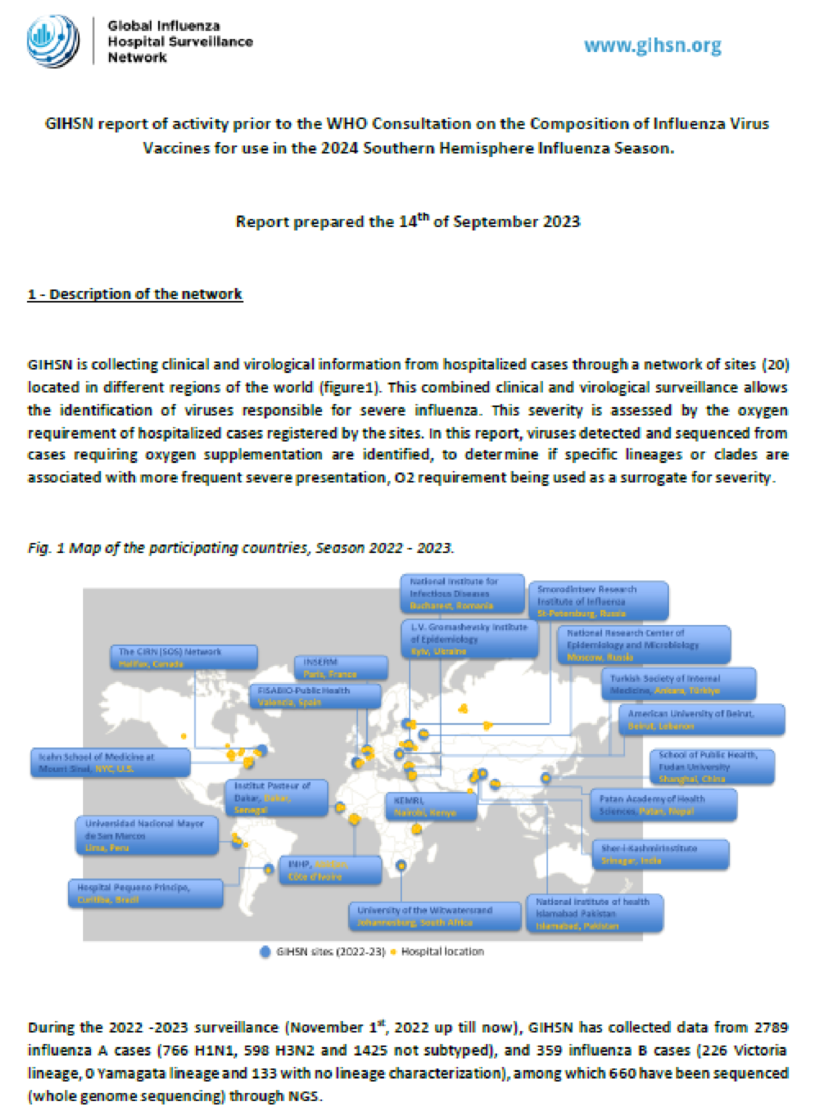
GIHSN is collecting clinical and virological information from hospitalized cases through a network of sites located in different regions of the world (figure1). This combined clinical and virological surveillance allows the identification of viruses responsible for severe influenza. This severity is 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, to determine if specific lineages or clades are associated with more frequent severe presentation.

For the 2022-2023 surveillance in GIHSN, influenza activity was detected earlier than usual, increasing rapidly in November in many Northern Hemisphere countries. Overall, influenza A (H3N2) has accounted for the majority of detections reported, followed by A(H1N1)pdm09 viruses. Fewer influenza B/Victoria lineage virus detections have been reported so far, but there are ongoing outbreaks observed in some countries. No B/Yamagata/16/88 viruses have been detected by the GIHSN.

This report is colliding the sequencing data from 11 sites (Türkiye (3), Spain (13), USA-NYC (3), Senegal (6), Russia-St Petersburg (48), Romania (25), South Africa (19), Pakistan (7), Ukraine (43), Lebanon (40) and India (19)). All 226 sequences, from hospitalized cases only, have been uploaded in the GISAID database with a GIHSN tag.

Specimens from Peru (38) were delivered to the sequencing lab in Lyon after February 1, 2023. These additional sequences will be shared to the community in a next update of this report.

Fig. 1 Map of the participating countries, between September 2022 and January 2023.



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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 Southern Hemisphere Influenza Season.

Report prepared the 14th of September 2023

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 (figure1). This combined clinical and virological surveillance allows the identification of viruses responsible for severe influenza. This severity is assessed by the oxygen requirement of hospitalized cases registered by the sites. In this report, viruses detected and sequenced from cases requiring oxygen supplementation are identified, to determine if specific lineages or clades are associated with more frequent severe presentation, O2 requirement being used as a surrogate for severity.

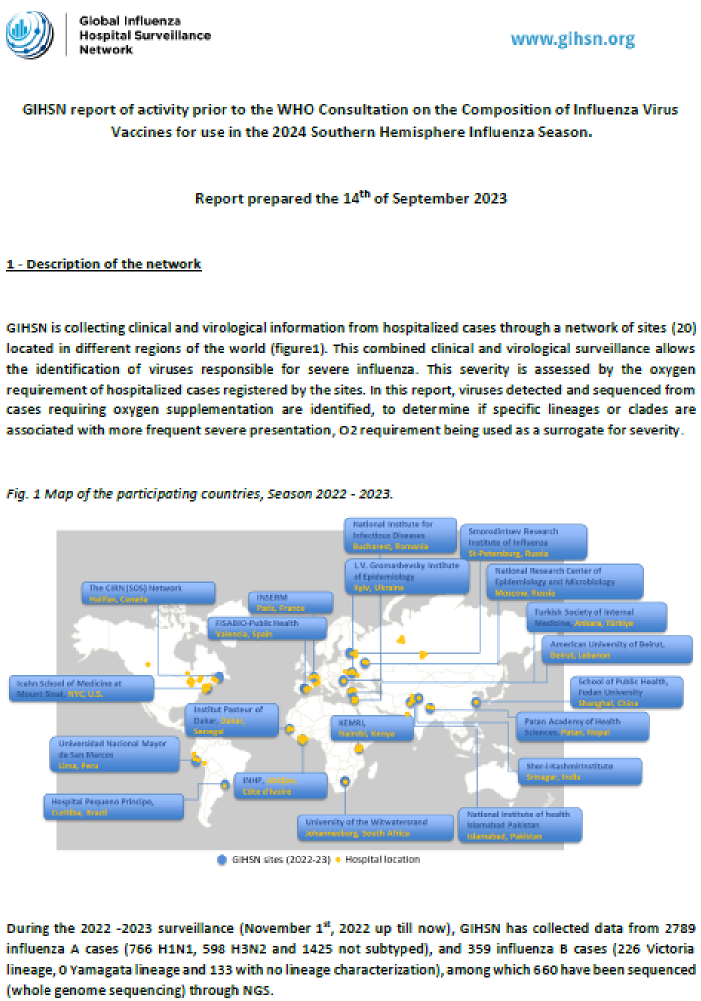
Fig. 1 Map of the participating countries, Season 2022 - 2023.

During the 2022 -2023 surveillance (November 1st, 2022 up till now), GIHSN has collected data from 2789 influenza A cases (766 H1N1, 598 H3N2 and 1425 not subtyped), and 359 influenza B cases (226 Victoria lineage, 0 Yamagata lineage and 133 with no lineage characterization), among which 660 have been sequenced (whole genome sequencing) through NGS.

KEY VACCINE AND SEVERITY INDICATORS COLLECTED BY THE SITES (2022-2023)

	Total #enrolled	Influenza vaccination for the current season both_influ_vac_current_season			Supplemental oxygen without mechanical ventilation both_severity_supp_oxygen			ICU admission (at any time during hospitalization) both_icu_adm		
		% completed	% missing	% unknown	% completed	% missing	% unknown	% completed	% missing	% unknown
Kenya	1694	100	0	0	100	0	0	100	0	0
Côte d'Ivoire	1482	100	0	0	100	0	4	100	0	0
Senegal	632	100	0	40	100	0	39	100	0	85
South Africa	2336	100	0	0	100	0	1	100	0	23
India	1207	100	0	0	100	0	0	100	0	0
Pakistan	3295	100	0	0	100	0	33	100	0	0
Nepal	243	100	0	0	100	0	0	100	0	0
Türkiye	549	100	0	1	100	0	1	100	0	2
Lebanon	1896	100	0	0	100	0	0	100	0	0
Russia - Saint Petersburg	48	100	0	0	100	0	0	100	0	0
Russia - Moscow	558	100	0	0	0	100*	0	100	0	0
Ukraine	244	100	0	0	100	0	0	100	0	0
Spain	1878	100	0	0	100	0	100*	100	0	1
Romania	540	100	0	1	100	0	0	100	0	0
Canada	869	100	0	32	100	0	1	100	0	0
USA	3128	100	0	0	100	0	0	100	0	0
Brazil	496	99	1	0	99	1	0	96	4	0
Peru	422	100	0	1	100	0	0	100	0	0

Focus on the GIHSN report provided prior to the SH VCM



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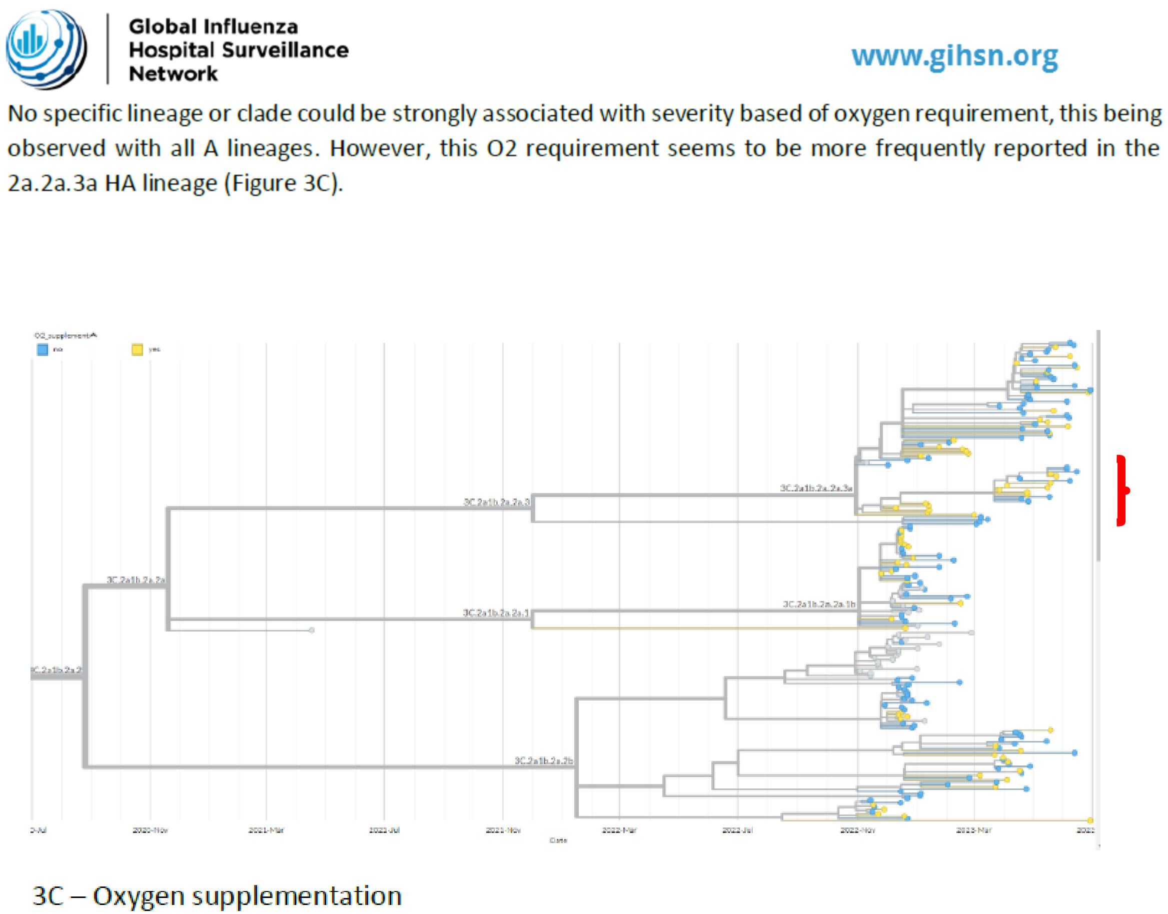

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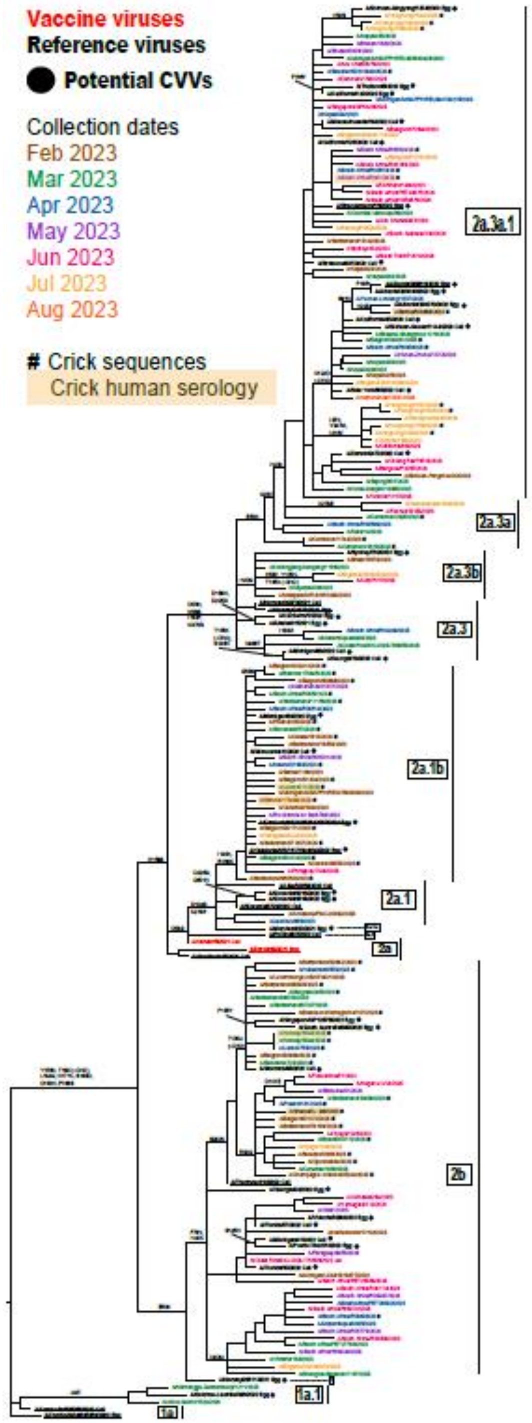
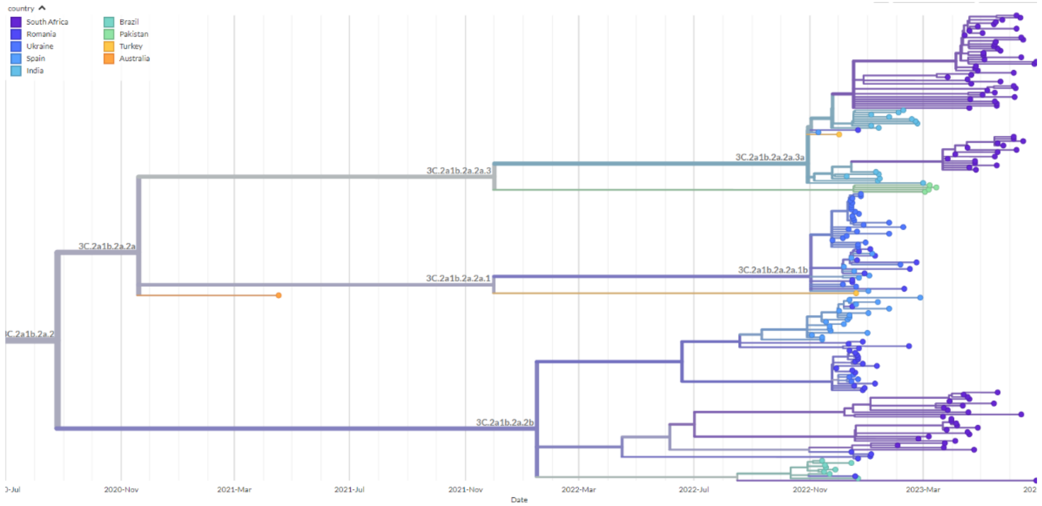
No specific lineage or clade could be strongly associated with severity based of oxygen requirement, this being observed with all A lineages. However, this O2 requirement seems to be more frequently reported in the 2a.2a.3a HA lineage (Figure 3C).

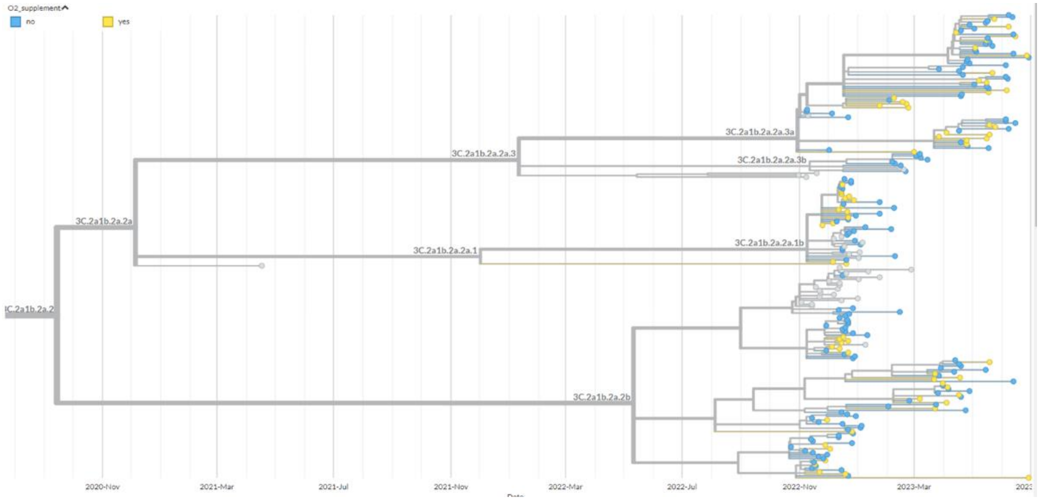
3C – Oxygen supplementation

H3N2



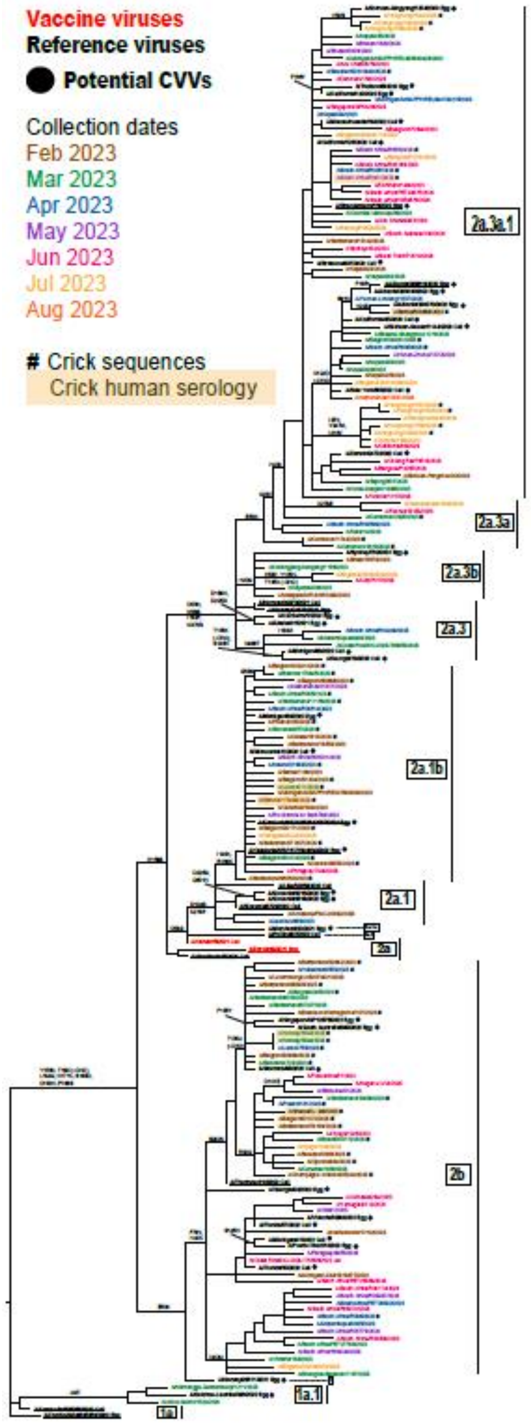


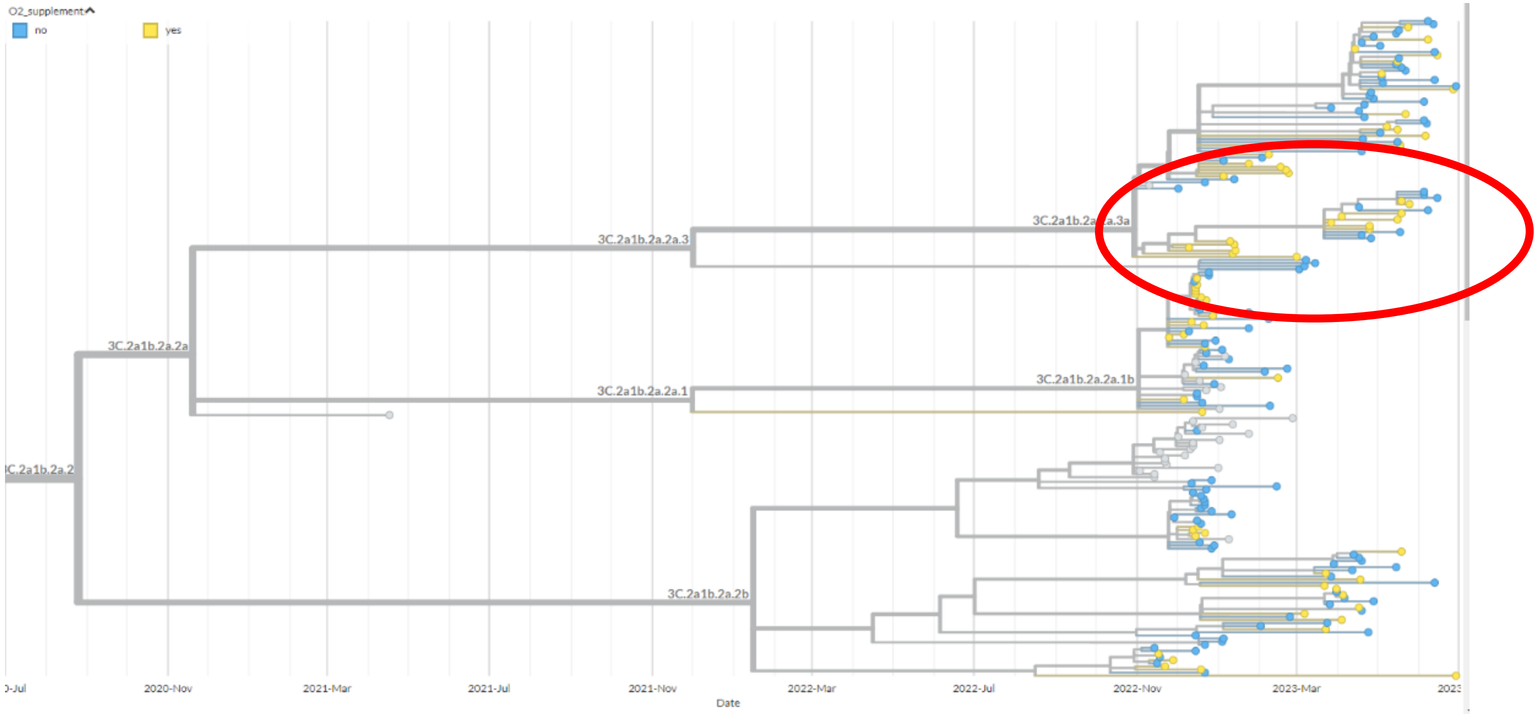
3A – Geographic distribution



3B – Clade distribution

H3N2

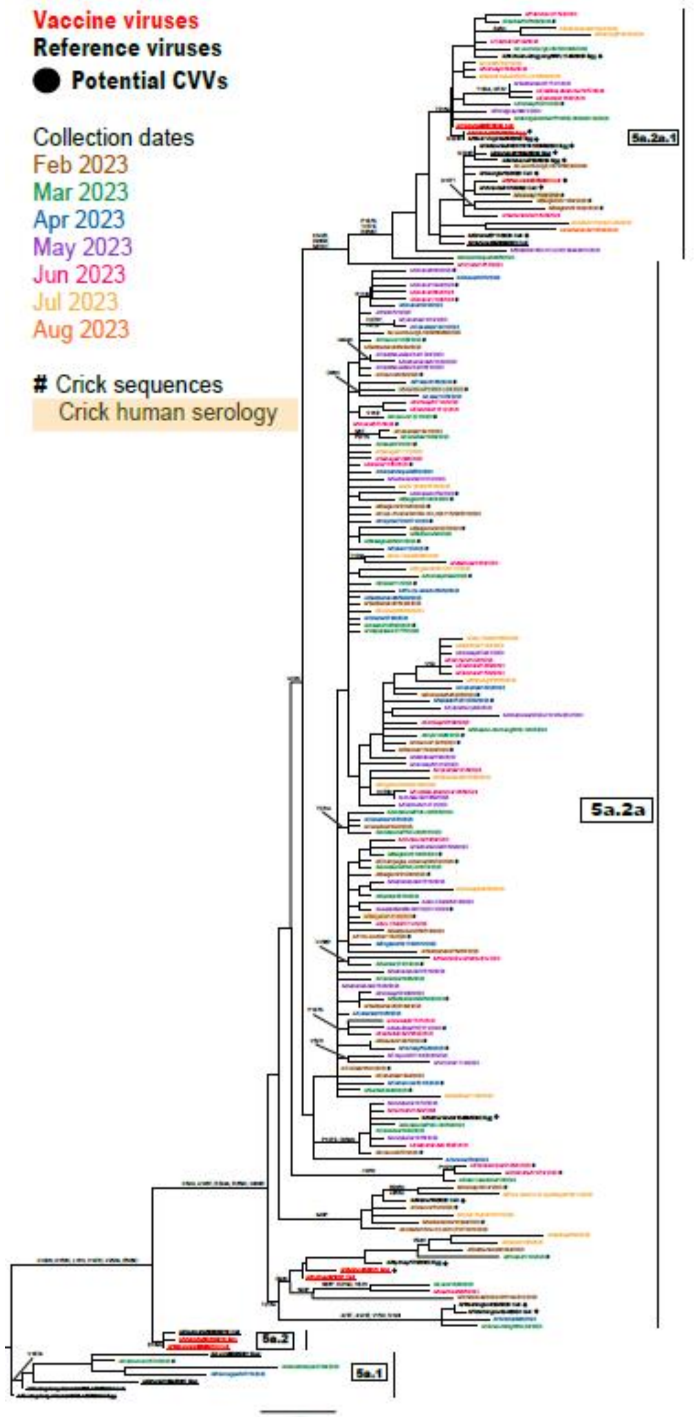


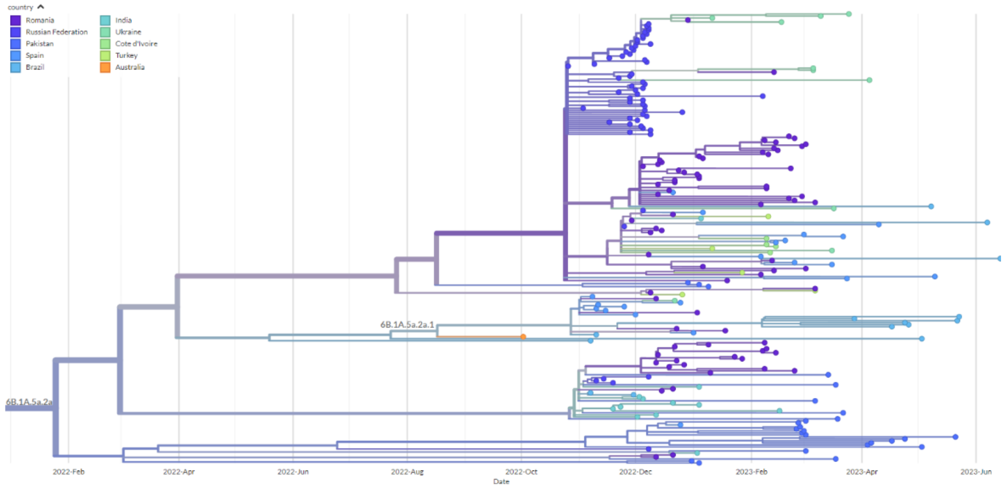


3C – Oxygen supplementation

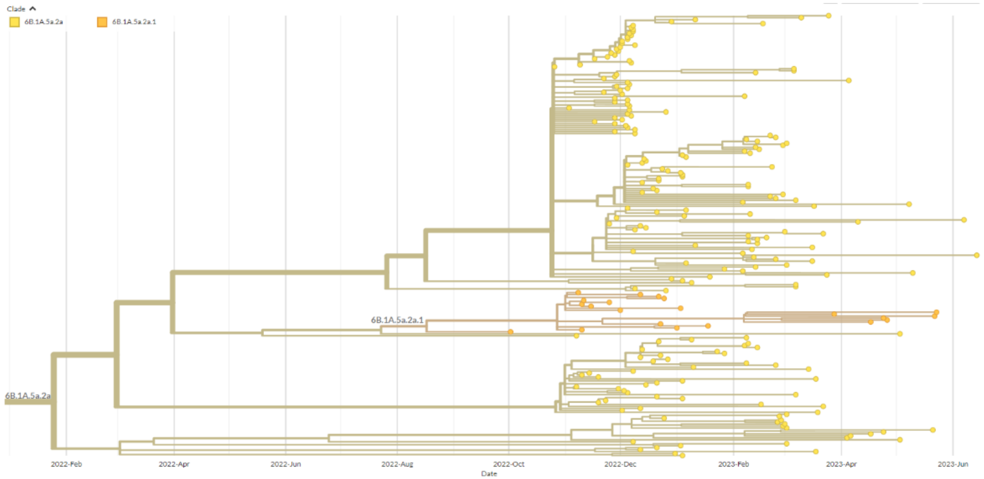
No specific lineage or clade could be strongly associated with severity based of oxygen requirement, this being observed with all A lineages. **However, this O2 requirement seems to be more frequently reported in the 2a.2a.3a HA lineage**.

H1N1pdm09



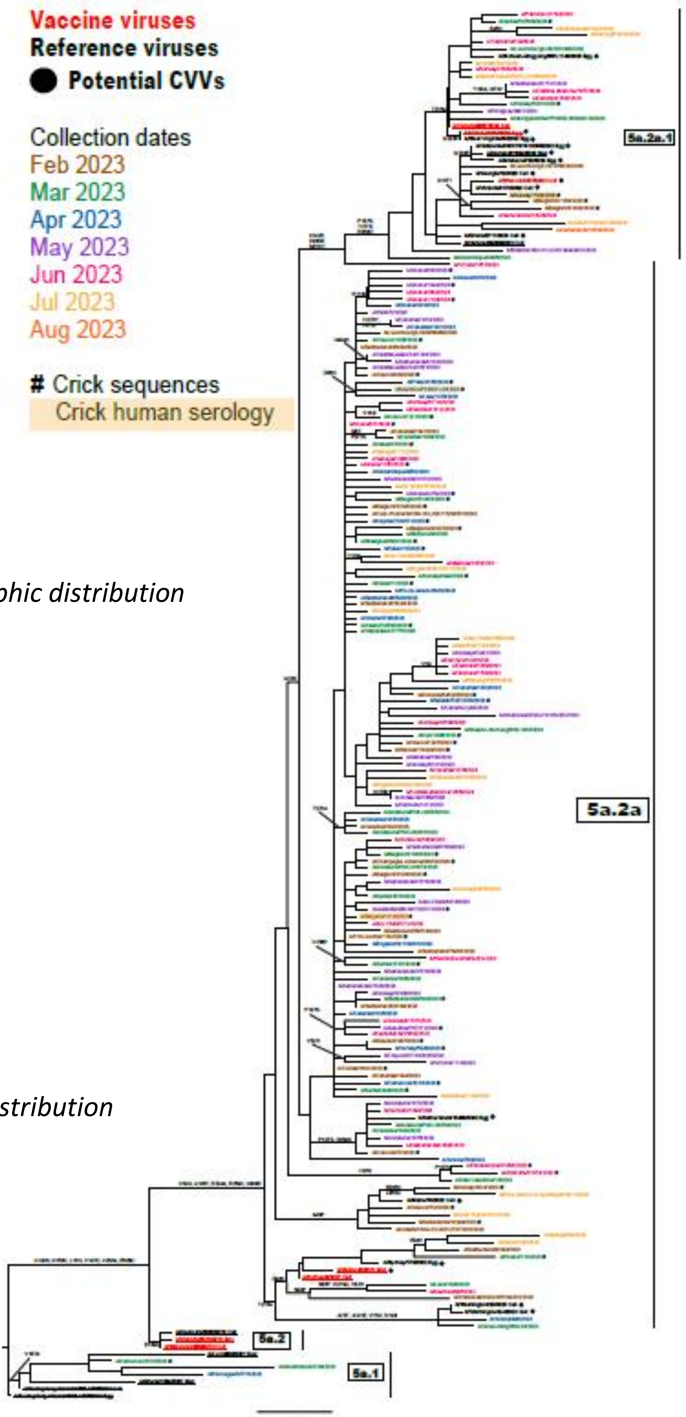


2A – Geographic distribution



2B – Clade distribution

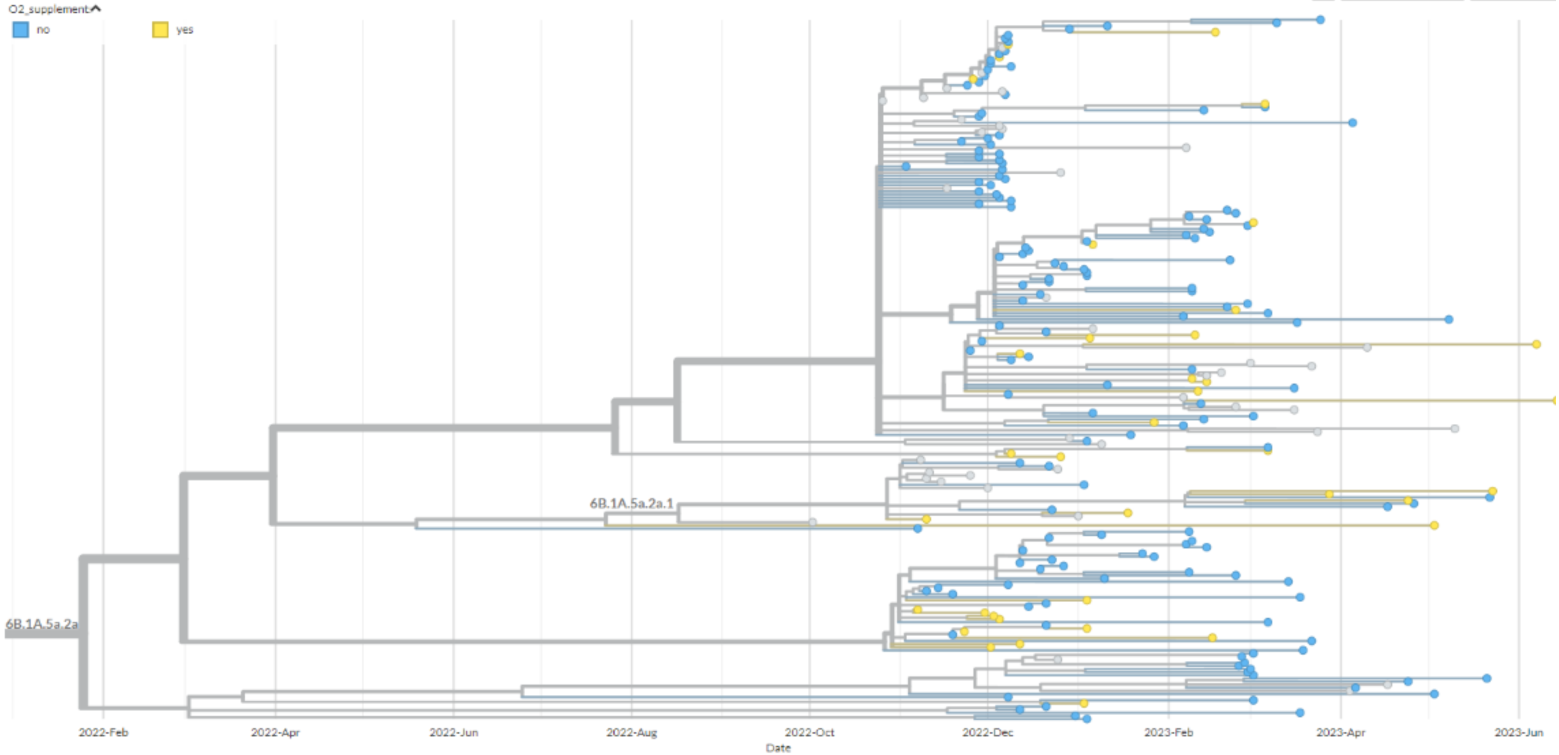
H1N1pdm09



2A – Geographic distribution

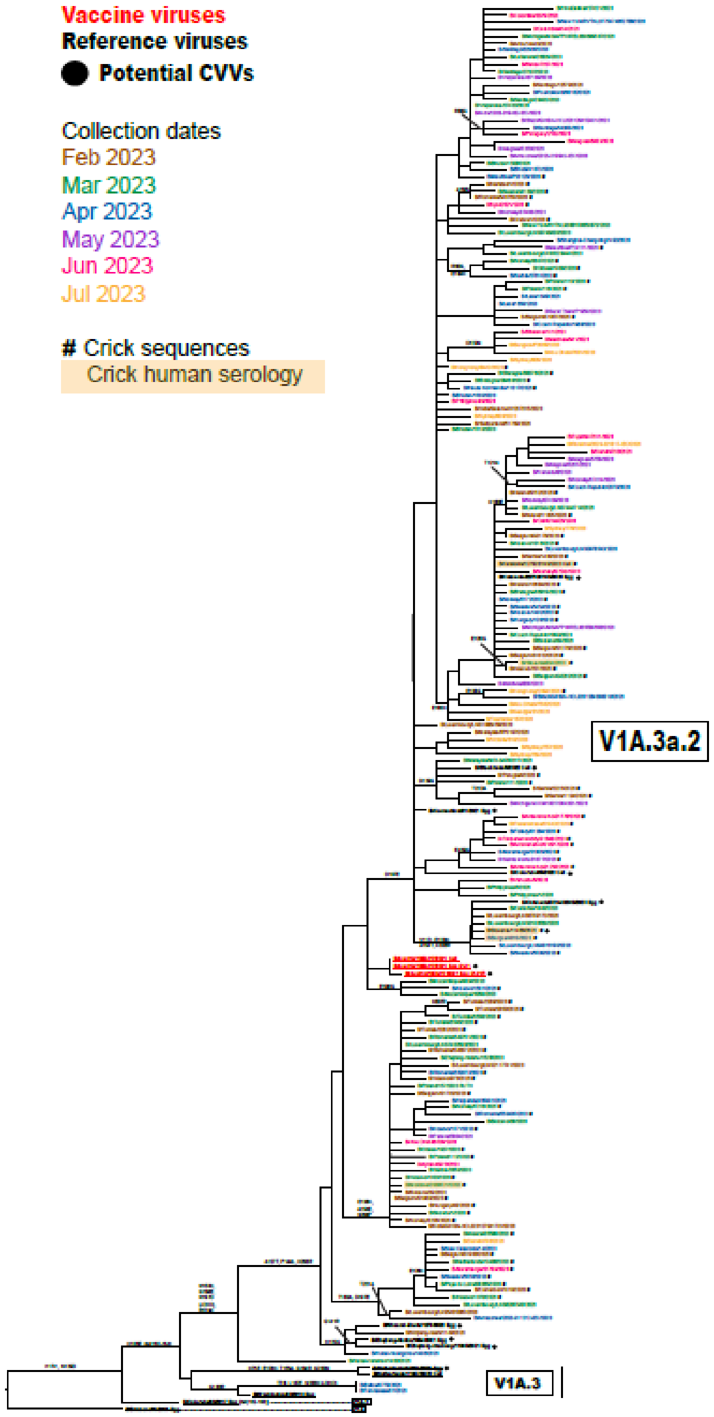
.

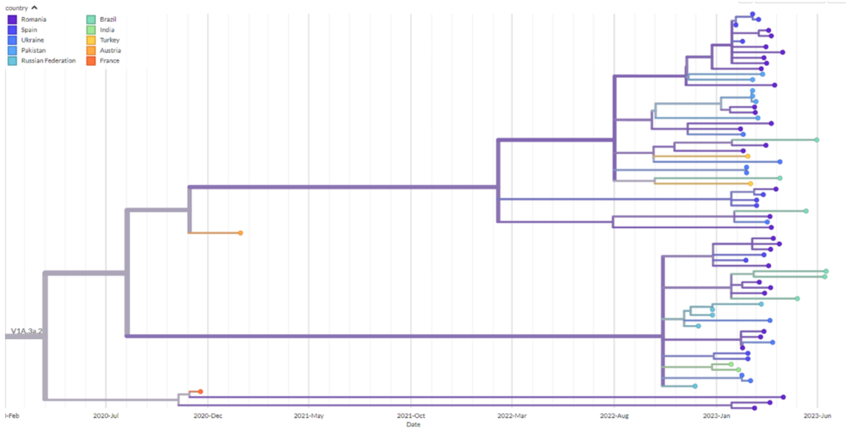
2B – Clade distribution



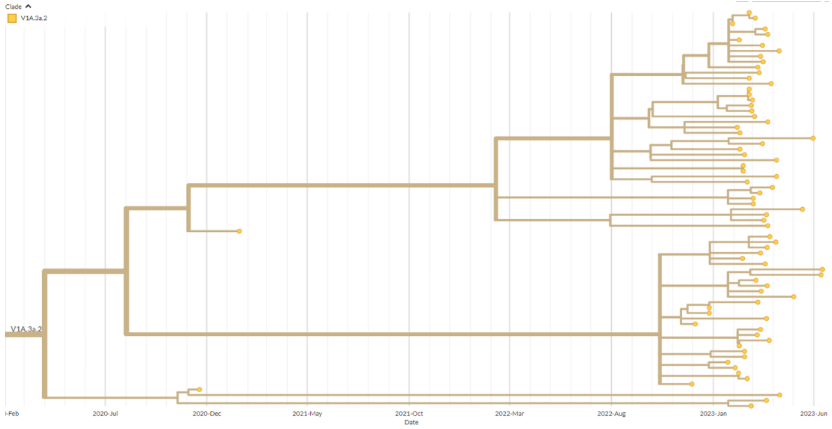
2C – Cases requiring Oxygen supplementation.

B Victoria

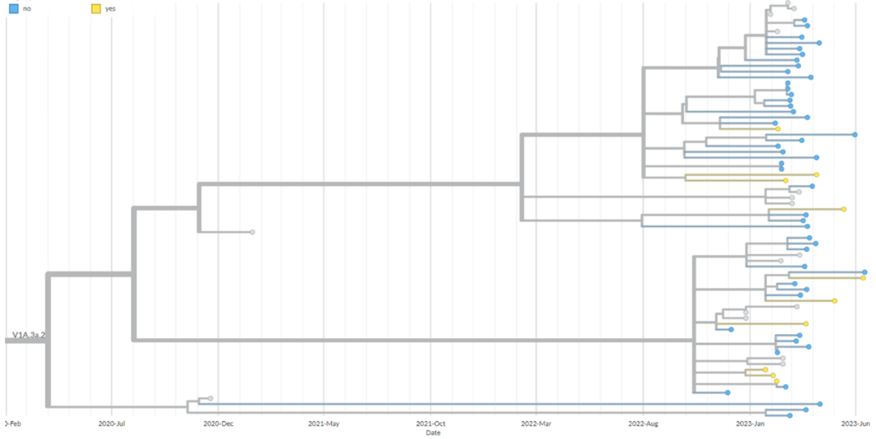




4A – Geographic distribution,



4B – Clade distribution



4C – Oxygen supplementation in yellow

GIHSN assets for specific severity data from hospitalized cases

Geographic diversity of investigated cases

Standardized clinical data set for all patients of all sites

Increased sequencing capacity with standardized analysis (capacity building)

In 2023, a memorandum of understanding has been signed between GIHSN and WHO

Further ongoing analysis to confirm the possible increased severity of clade 3c.2a1b.2a.2a.3a

THANK YOU!

contact@gihsn.org

www.gihsn.org

Global Influenza
Hospital Surveillance
Network

Global Influenza
Hospital Surveillance
Network

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coordination

IMPACT
Healthcare

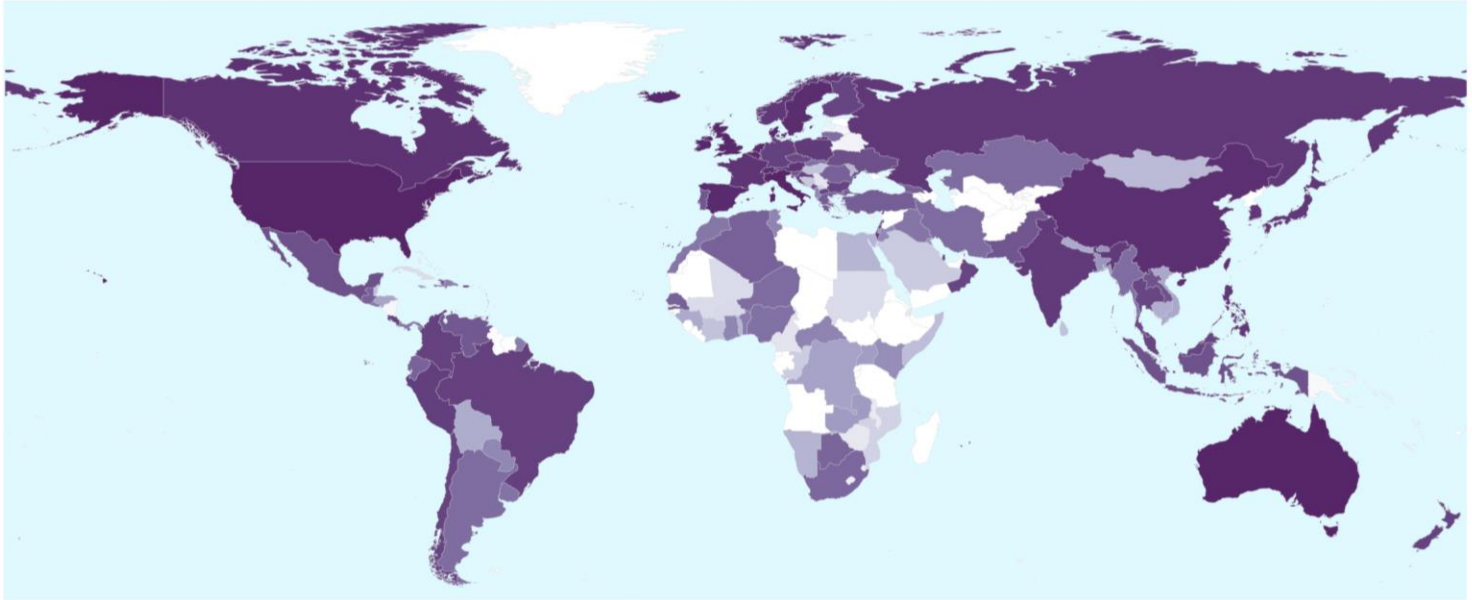
GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

GISAID AND GIHSN

Sebastian MAURER-STROH, GISAID

Foundation for
Influenza
Epidemiology

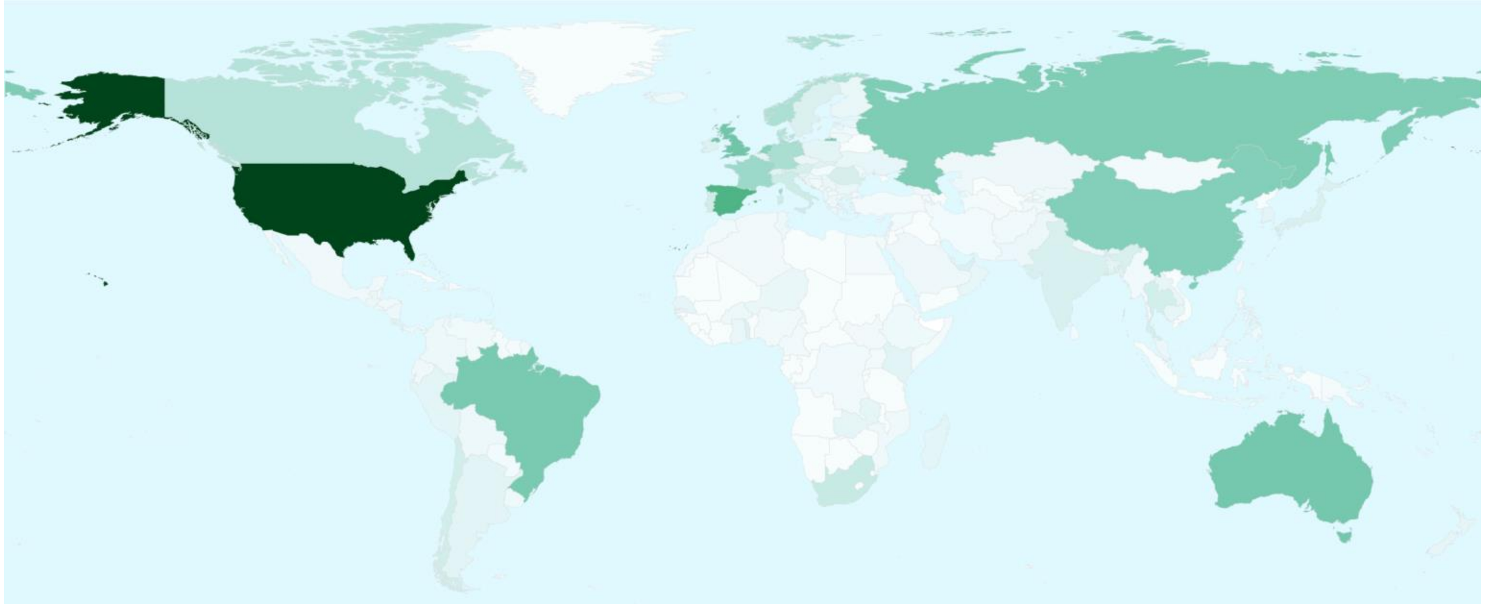
GISAID analytics and display updates



16,217,407 SARS-CoV-2
sequences since 2020

751,915 influenza
sequences since 2020

(2,224,752 sequences in total)



The secret sauce

TRUST

QUALITY

INSIGHTS

One platform,
one ecosystem

TRUST - GISAID Data Sharing Principles

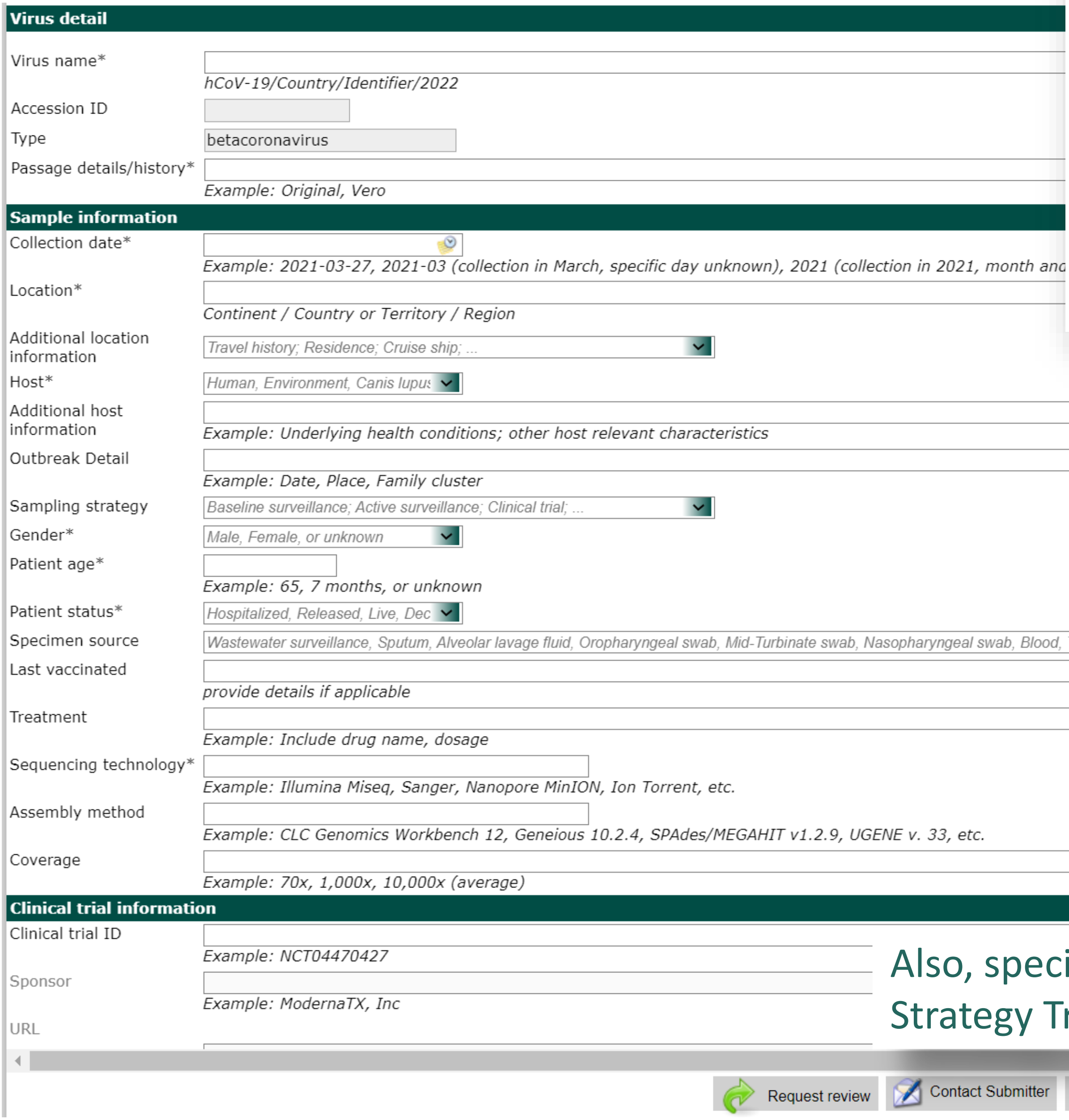
- **Data Providers** grant **Data Users** a license for the use of their Data, providing legal certainty for use in research and publications, and for the development, testing and dissemination of interventions such as vaccines, diagnostics and therapeutics.

- Access to GISAID is **free-of-charge** and **open to everyone** provided they identify themselves in order to foster collaboration and to permit an effective oversight to uphold the sharing principles enshrined;

- The guiding principle for those using Data in publications is the **need to acknowledge the contribution of Data Providers**;

- While all the Data are publicly accessible, Data Providers do not forfeit their Rights to the Data they share through GISAID.

QUALITY - rich meta-data and curation



Virus detail

Virus name* ☐
hCoV-19/Country/Identifier/2022

Accession ID ☐

Type: betacoronavirus

Passage details/history* ☐
Example: Original, Vero

Sample information

Collection date* ☐
Example: 2021-03-27, 2021-03 (collection in March, specific day unknown), 2021 (collection in 2021, month and

Location* ☐
Continent / Country or Territory / Region

Additional location information: Travel history; Residence; Cruise ship; ...

Host*: Human, Environment, Canis lupus

Additional host information ☐
Example: Underlying health conditions; other host relevant characteristics

Outbreak Detail ☐
Example: Date, Place, Family cluster

Sampling strategy: Baseline surveillance; Active surveillance; Clinical trial; ...

Gender*: Male, Female, or unknown

Patient age* ☐
Example: 65, 7 months, or unknown

Patient status*: Hospitalized, Released, Live, Dec

Specimen source: Wastewater surveillance, Sputum, Alveolar lavage fluid, Oropharyngeal swab, Mid-Turbinate swab, Nasopharyngeal swab, Blood, Tracheal swa

Last vaccinated ☐
provide details if applicable

Treatment ☐
Example: Include drug name, dosage

Sequencing technology* ☐
Example: Illumina Miseq, Sanger, Nanopore MinION, Ion Torrent, etc.

Assembly method ☐
Example: CLC Genomics Workbench 12, Geneious 10.2.4, SPAdes/MEGAHIT v1.2.9, UGENE v. 33, etc.

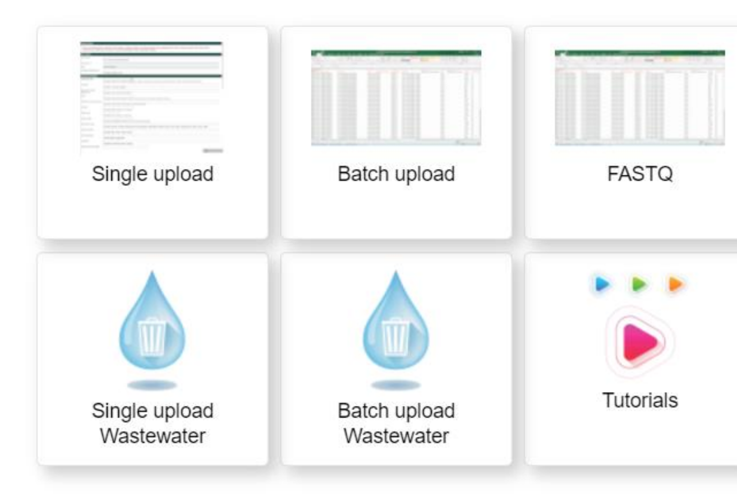
Coverage ☐
Example: 70x, 1,000x, 10,000x (average)

Clinical trial information

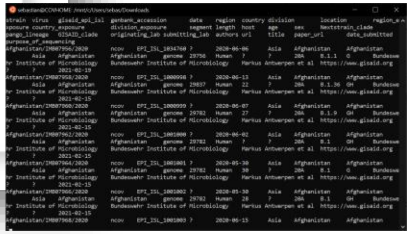
Clinical trial ID ☐
Example: NCT04470427

Sponsor ☐
Example: ModernaTX, Inc

URL ☐



plus CLI (command line interface)



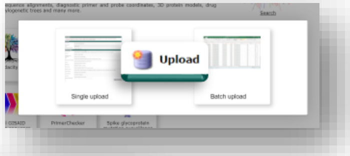
24/7 curation and user/submitter interaction

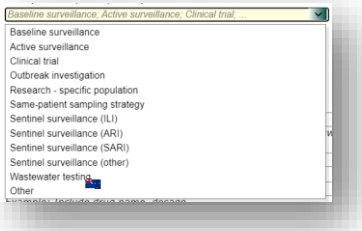
All timezones covered

Also, special fields for: Sequencing technology, Sampling Strategy Travel History, Clinical Trial info and Wastewater

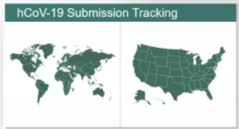
INSIGHTS - GISAID tool ecosystem

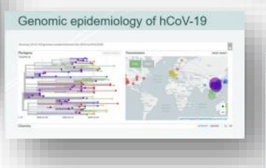
- Submission/Curation
  - New fields: sampling strategy
- Tools on the outside:
  - Submission tracker map
  - Genomic epidemiology
  - Variant tracking
- Tools on the inside:
  - Reporting:
    - Analysis reports and downloads
    - Audacity
    - PrimerChecker
    - EpiCoV search
  - New variants: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

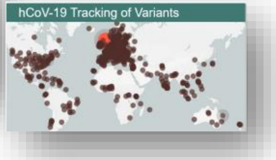


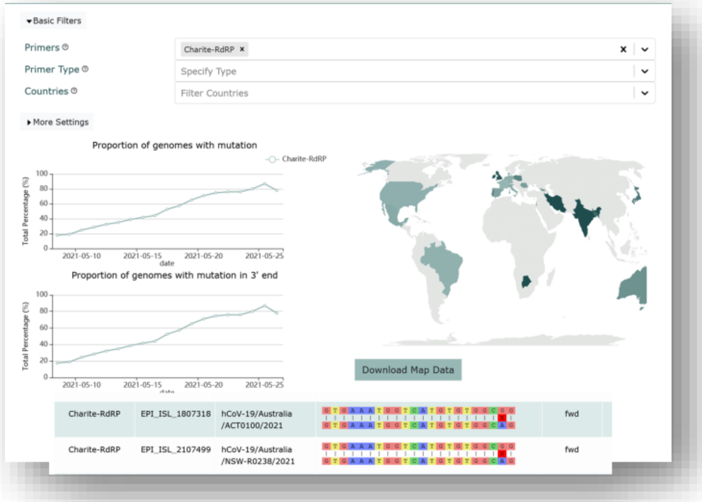

Baseline surveillance; Active surveillance; Clinical trial;

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








Basic Filters

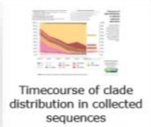
Primers: Charite-RdRP

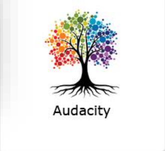
Primer Type: Specify Type

Countries: Filter Countries

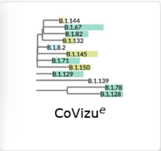
More Settings

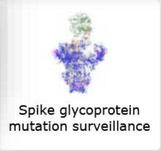
Charite-RdRP	EPI_ISL_1807318	hCoV-19/Australia/ACT0100/2021		fwd
Charite-RdRP	EPI_ISL_2107499	hCoV-19/Australia/NSW-R0238/2021		fwd

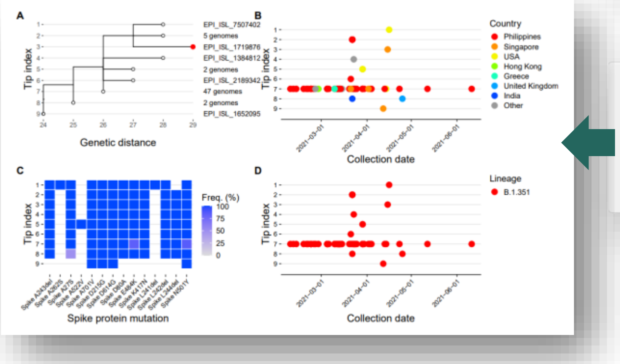


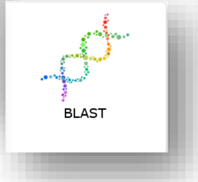


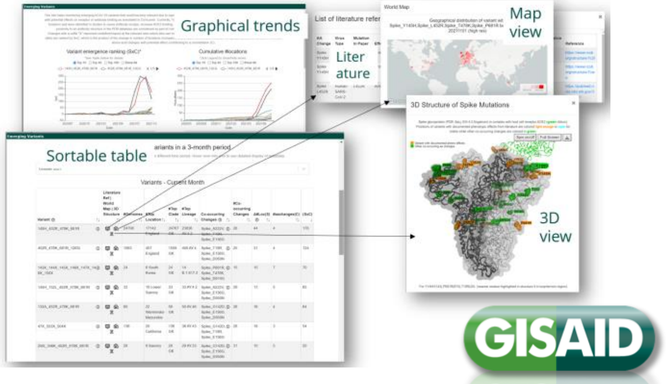
+ enabler for **hundreds** of other tools and sites

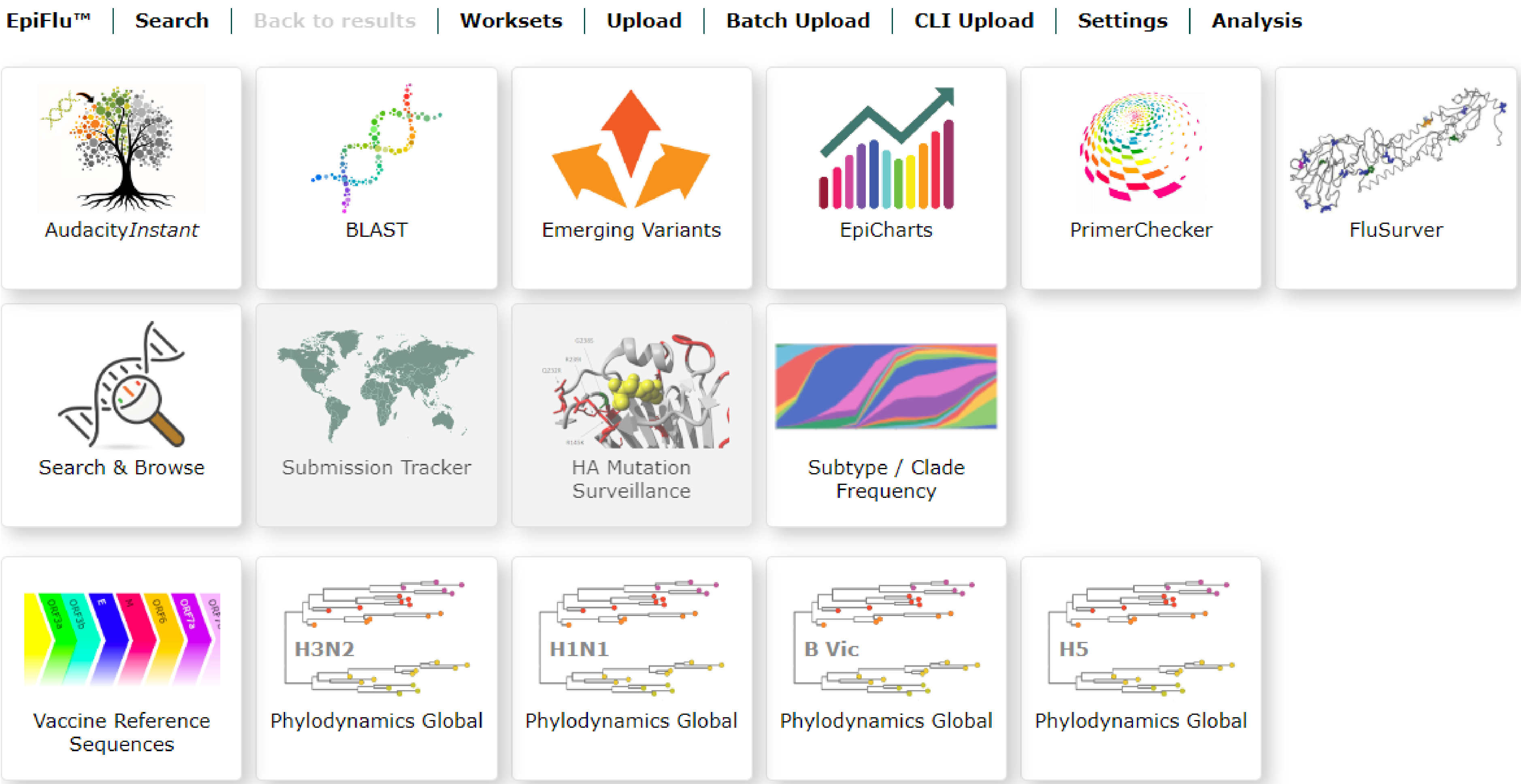




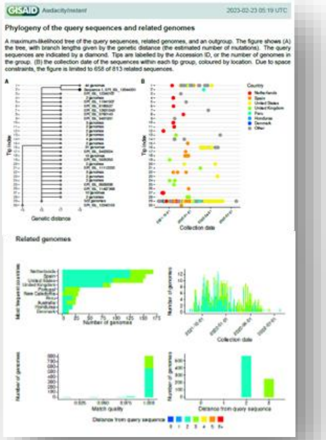




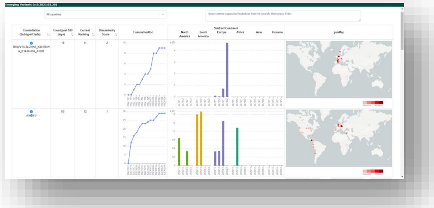




The same tools new in EpiCoV have been implemented in EpiFlu in order to automatically annotate incoming sequences with clade info as well as identification of new variants via mutation constellations and annotation of effects of new mutations.

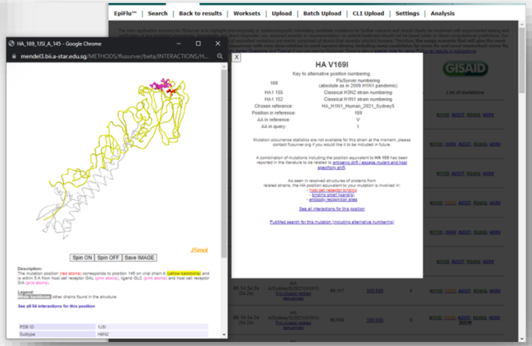


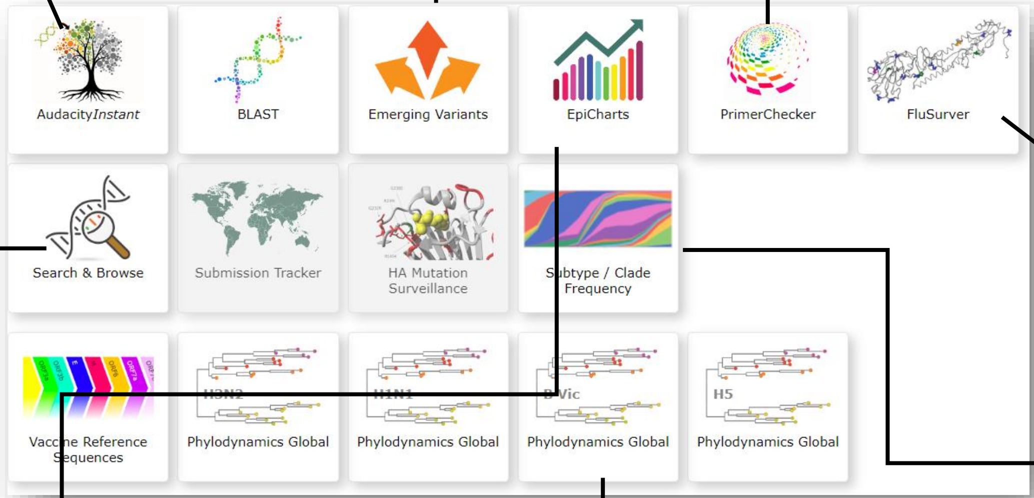
Question:
Which sequences in the database are most similar to my own sequence?
=> **AudacityInstant** tool



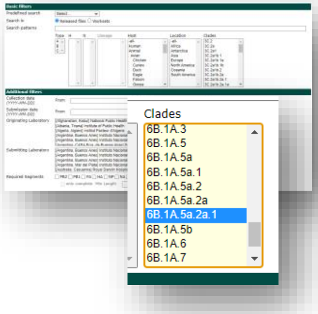
Question:
Any emerging variant with unique constellation of mutations?
=> **EmergingVariants** tool

Question:
Any mutation affecting common or my primers?
=> **PrimerChecker** tool



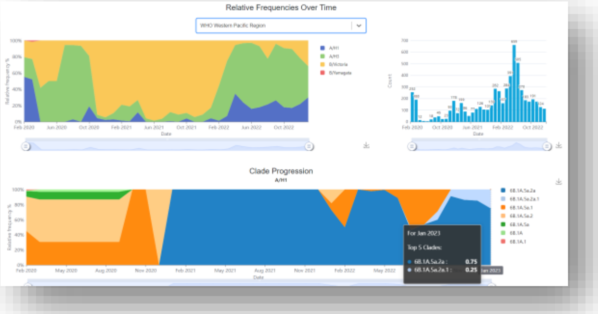


Question:
Any phenotypically important mutation in my sequences (host specificity, antibody binding, drug resistance, glycosylation, virulence?
=> **FluSurver** tool

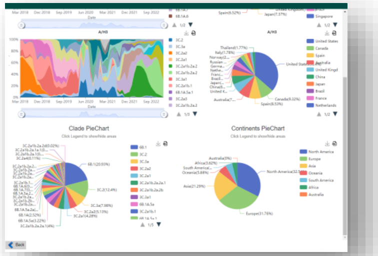


Question:
Can I browse, search and filter entries by clade in the database?
=> **Search & Browse** tool

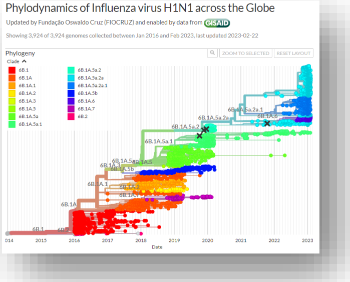
Question:
Which clades are currently dominant or rising in my country/region?
=> **Clade Frequency** tool



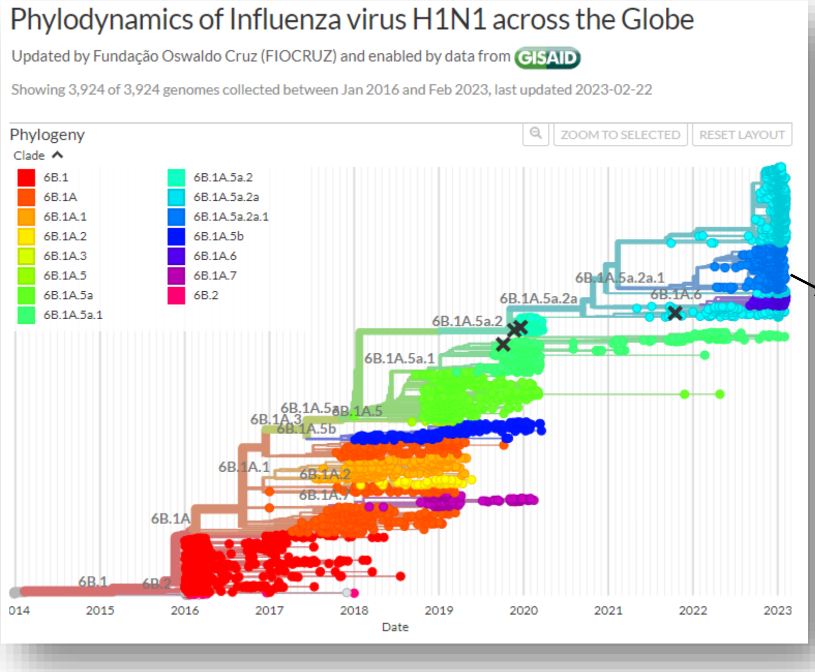
Question:
How can I create summary graphs for hits from a custom database search?
=> **EpiCharts** tool



Question:
Summary of phylogenetic evolution in subsampled tree?
=> **Phylodynamics** tool



Seamless integration of tools inside the GISAID platform (log-in once) provides you comprehensive views from multiple angles and all info in one place



Phylodynamics of Influenza virus H1N1 across the Globe

Updated by Fundação Oswaldo Cruz (FIOCRUZ) and enabled by data from GISAID

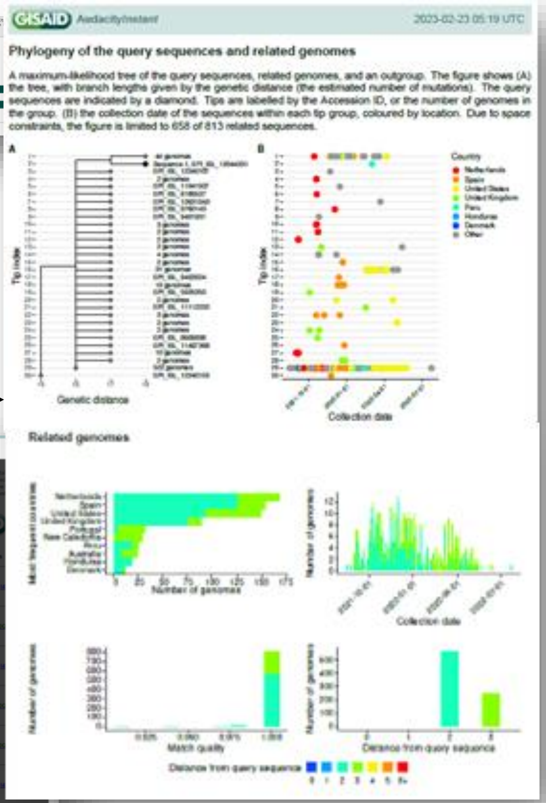
Showing 3,924 of 3,924 genomes collected between Jan 2016 and Feb 2023, last updated 2023-02-22

A/Norway/01839/2023

Collection date 2023-01-26
Submitting laboratory Norwegian Institute of Public Health
Continent Europe
Host Human
Country Norway
Gender Male
GISAID ID EPI_ISL_16986282
Originating laboratory Norwegian Institute of Public Health
Clade 6B.1A.5a2a.1
Age 65 Y

Subsampled summary tree

Full entry meta-data

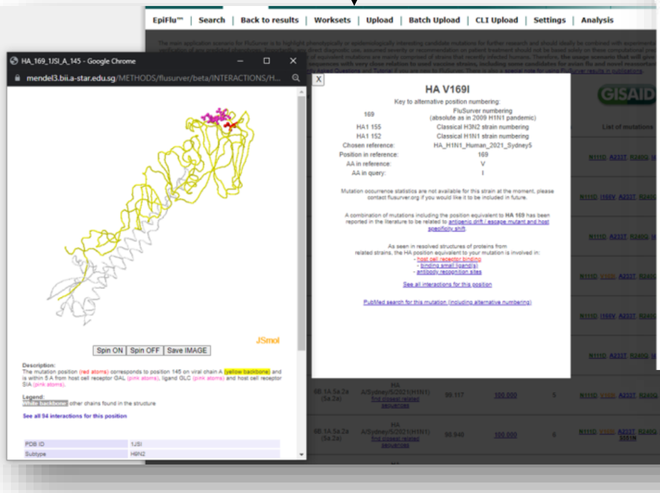


GISAID AudacityInstant 2023-02-23 05:19 UTC

Phylogeny of the query sequences and related genomes

A maximum-likelihood tree of the query sequences, related genomes, and an outgroup. The figure shows (A) the tree, with branch lengths given by the genetic distance (the estimated number of mutations). The query sequences are indicated by a diamond. Tips are labelled by the Accession ID, or the number of genomes in the group. (B) the collection date of the sequences within each tip group, coloured by location. Due to space constraints, the figure is limited to 658 of 813 related sequences.

Full list and summary of all related sequences in the database (not just subsample)



Full mutation phenotype annotation

A scale-free view of virus evolution

Connected levels in GISAID's integrated tool ecosystem

Subtype

↓

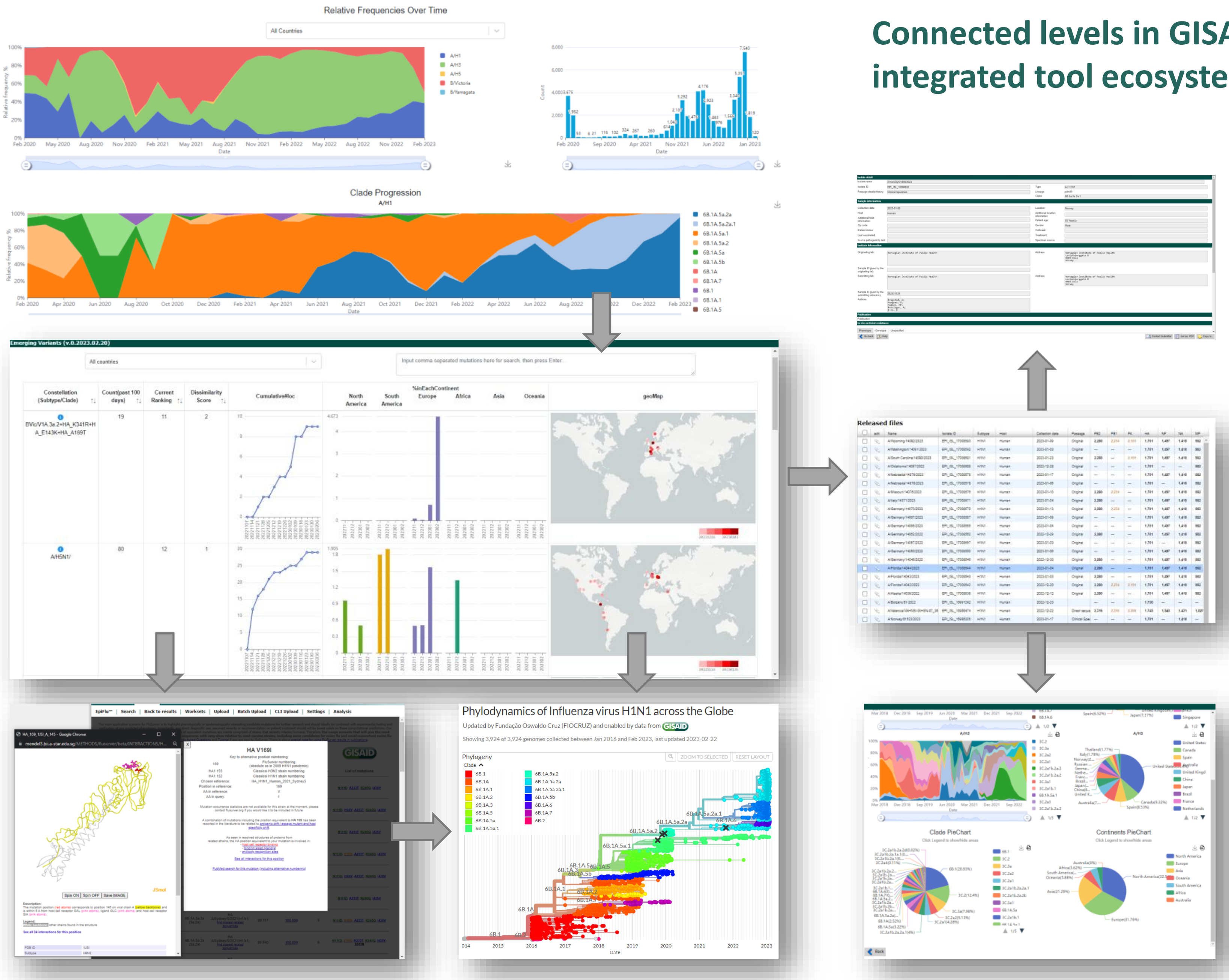
Clade

↓

Emerging Variant
(unique set of mutations)

↓

Individual mutation



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Updated by Fundação Oswaldo Cruz (FIOCRUZ) and enabled by data from GISAID

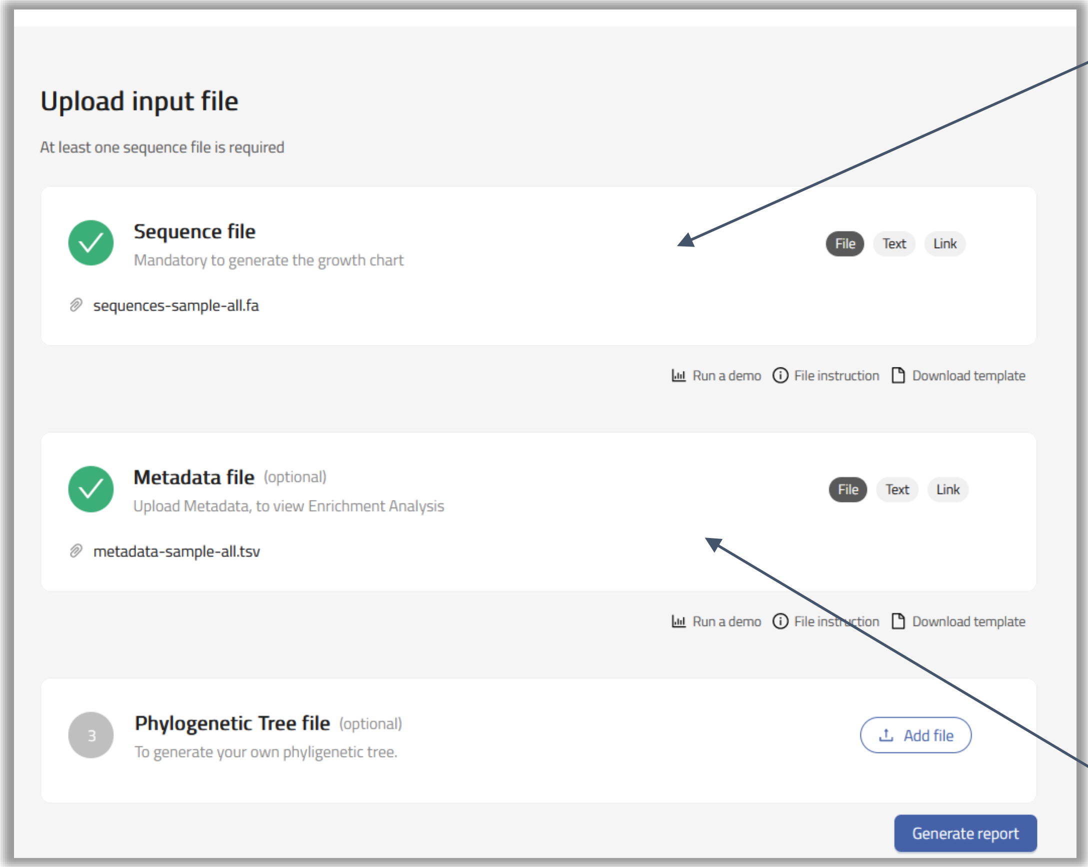
Showing 3,924 of 3,924 genomes collected between Jan 2016 and Feb 2023, last updated 2023-02-22

Single
entry
detail

Set of
entries in
the database

Set of
entries
graphical
summary

GISAID FluCluster-AI – map clinical data to emerging virus variants



Upload input file

At least one sequence file is required

Sequence file

Mandatory to generate the growth chart

sequences-sample-all.fa

Metadata file (optional)

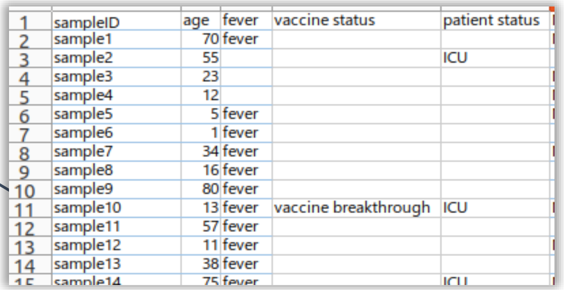
Upload Metadata, to view Enrichment Analysis

metadata-sample-all.tsv

Phylogenetic Tree file (optional)

To generate your own phyligenetic tree.

fasta file(.fasta,.fa)



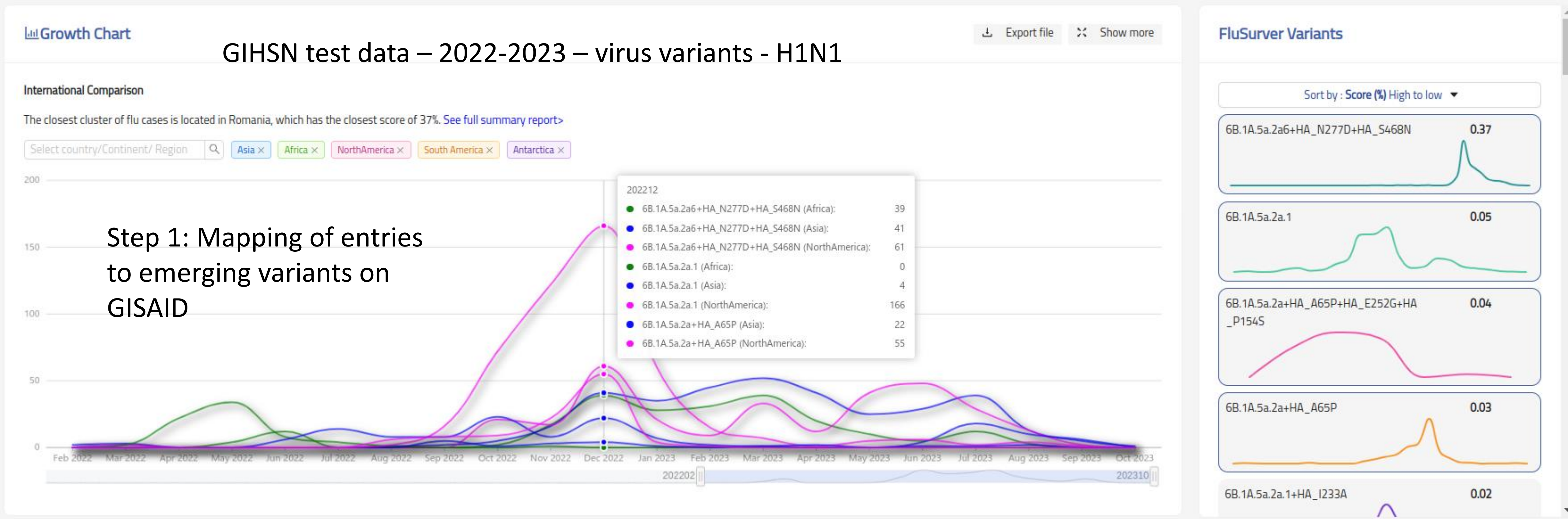
1	sampleID	age	fever	vaccine status	patient status
2	sample1	70	fever		
3	sample2	55			ICU
4	sample3	23			
5	sample4	12			
6	sample5	5	fever		
7	sample6	1	fever		
8	sample7	34	fever		
9	sample8	16	fever		
10	sample9	80	fever		
11	sample10	13	fever	vaccine breakthrough	ICU
12	sample11	57	fever		
13	sample12	11	fever		
14	sample13	38	fever		
15	sample14	75	fever		ICU

metadata file(tsv/csv/json)

- ❖ User uploads sequencing fasta files or GISAID accessions and metadata files(in tsv/csv/json formats) in the landing page.
- ❖ Clinical data never leaves the user's computer, analysis happens in local browser

GIHSN test data – 2022-2023 – virus variants - H1N1

Step 1: Mapping of entries to emerging variants on GISAID



Growth Chart

Export file
Show more

International Comparison

The closest cluster of flu cases is located in Romania, which has the closest score of 37%. See full summary report>

Select country/Continent/ Region

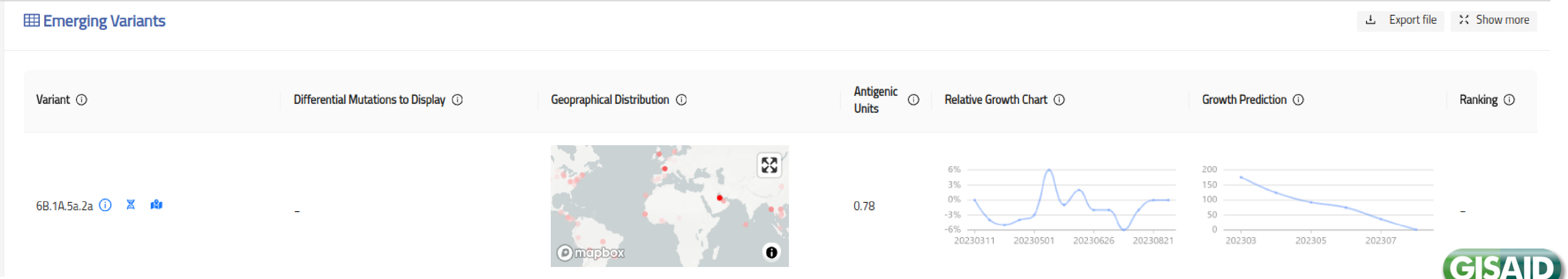
Asia × Africa × NorthAmerica × South America × Antarctica ×

202212
- ● 6B.1A.5a.2a6+HA_N277D+HA_S468N (Africa): 39
- ● 6B.1A.5a.2a6+HA_N277D+HA_S468N (Asia): 41
- ● 6B.1A.5a.2a6+HA_N277D+HA_S468N (NorthAmerica): 61
- ● 6B.1A.5a.2a.1 (Africa): 0
- ● 6B.1A.5a.2a.1 (Asia): 4
- ● 6B.1A.5a.2a.1 (NorthAmerica): 166
- ● 6B.1A.5a.2a+HA_A65P (Asia): 22
- ● 6B.1A.5a.2a+HA_A65P (NorthAmerica): 55

FluSurver Variants

Sort by : **Score (%)** High to low

6B.1A.5a.2a6+HA_N277D+HA_S468N	0.37
6B.1A.5a.2a.1	0.05
6B.1A.5a.2a+HA_A65P+HA_E252G+HA_P154S	0.04
6B.1A.5a.2a+HA_A65P	0.03
6B.1A.5a.2a.1+HA_I233A	0.02



Emerging Variants

Export file
Show more

Variant	Differential Mutations to Display	Geographical Distribution	Antigenic Units	Relative Growth Chart	Growth Prediction	Ranking
6B.1A.5a.2a	-		0.78			-

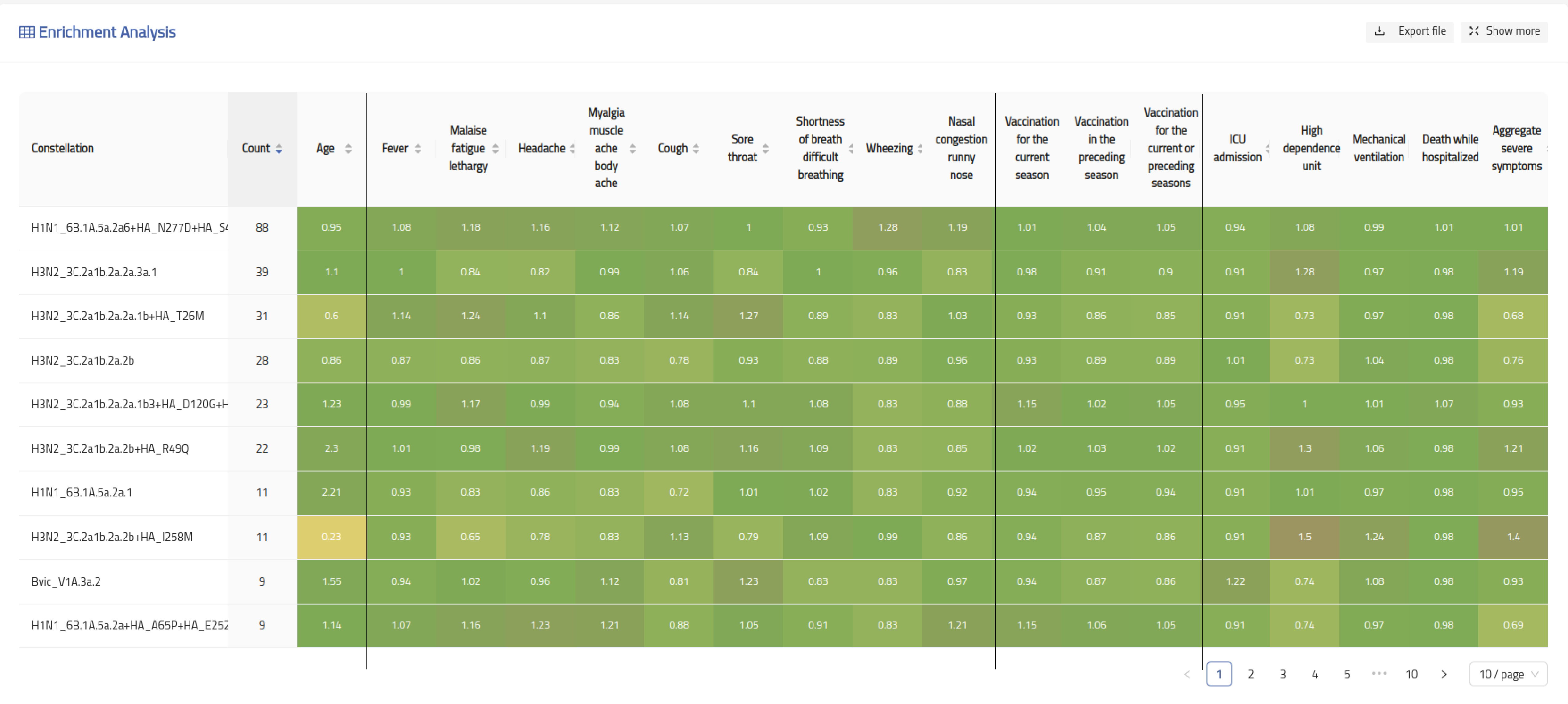
GIHSN test data – 2022-2023 – Clinical correlations - H1N1

FluCluster 6B.1A.5a.2a is associated with higher values of ICU admission (Odds Ratio:1.55), indicating that this FluCluster has a higher representation of patients with ICU admission. FluCluster 6B.1A.5a.2a.1+HA_I233A is associated with low values of Fever (Odds Ratio:0.56), indicating that this FluCluster has a higher ... more

Constellation	Count	Age	Fever	Malaise fatigue lethargy	Headache	Myalgia muscle ache body ache	Cough	Sore throat	Shortness of breath difficult breathing	Wheezing	Nasal congestion runny nose	Vaccination for the current season	Vaccination in the preceding season	Vaccination for the current or preceding seasons	ICU admission	High dependence unit	Mechanical ventilation	Death while hospitalized	Aggregate severe symptoms
6B.1A.5a.2a6+HA_N27	88	0.77	1.09	1.15	1.13	1.08	1.09	0.97	0.88	1.13	1.13	0.99	0.94	0.95	0.86	1.19	0.99	1	1.02
6B.1A.5a.2a.1	11	1.94	0.92	0.78	0.81	0.79	0.71	0.99	1	0.73	0.86	0.92	0.87	0.86	0.87	1.06	0.97	0.97	0.95
6B.1A.5a.2a+HA_A65P	9	0.97	1.07	1.1	1.17	1.16	0.87	1.04	0.89	0.73	1.13	1.13	0.98	0.97	0.87	0.77	0.97	0.97	0.69
6B.1A.5a.2a+HA_A65P	7	0.97	1.05	0.79	0.74	0.79	1.13	1.23	0.94	1.16	0.67	0.92	1.28	1.26	1.26	1.23	0.97	0.97	1.41
6B.1A.5a.2a.1+HA_I23	5	1.24	0.56	0.74	0.89	0.79	0.56	0.93	1.17	0.73	0.67	0.92	0.8	0.79	0.87	0.93	0.97	0.98	0.83
6B.1A.5a.2a+HA_A65P	4	0.51	1.13	1.08	0.74	1.2	0.99	0.78	0.73	0.73	1.19	0.92	0.8	0.79	0.87	0.77	0.97	0.98	0.69
6B.1A.5a.2a	4	1.33	0.84	0.77	1.31	0.8	0.99	1.17	1.1	0.73	0.84	0.92	1.01	0.99	1.55	0.77	0.97	0.98	1.22
6B.1A.5a.2a.1+HA_D2	2	1.38	0.56	0.62	0.74	0.8	0.56	0.78	1.1	0.74	0.68	0.92	0.8	0.79	1.32	0.78	1.46	0.98	1.05
6B.1A.5a.2a.1+HA_K71	2	1.85	0.85	0.93	1.12	0.8	1.13	1.17	1.47	0.74	0.68	0.92	0.8	0.79	0.88	1.56	1.46	0.98	1.4
6B.1A.5a.2a+HA_D502	2	0.46	1.13	0.93	1.12	0.8	0.84	1.57	0.73	1.48	0.68	0.92	1.62	1.6	0.88	1.56	0.97	0.98	1.4

Step 2: Odds ratio analysis of clinical variables for enrichment or depletion association with the emerging variants

GIHSN test data – 2022-2023 – Clinical correlations - H1N1, H3N2, Bvic



Enrichment Analysis

Constellation	Count	Age	Fever	Malaise fatigue lethargy	Headache	Myalgia muscle ache body ache	Cough	Sore throat	Shortness of breath difficult breathing	Wheezing	Nasal congestion runny nose	Vaccination for the current season	Vaccination in the preceding season	Vaccination for the current or preceding seasons	ICU admission	High dependence unit	Mechanical ventilation	Death while hospitalized	Aggregate severe symptoms
H1N1_6B.1A.5a.2a6+HA_N277D+HA_S	88	0.95	1.08	1.18	1.16	1.12	1.07	1	0.93	1.28	1.19	1.01	1.04	1.05	0.94	1.08	0.99	1.01	1.01
H3N2_3C.2a1b.2a.2a.3a.1	39	1.1	1	0.84	0.82	0.99	1.06	0.84	1	0.96	0.83	0.98	0.91	0.9	0.91	1.28	0.97	0.98	1.19
H3N2_3C.2a1b.2a.2a.1b+HA_T26M	31	0.6	1.14	1.24	1.1	0.86	1.14	1.27	0.89	0.83	1.03	0.93	0.86	0.85	0.91	0.73	0.97	0.98	0.68
H3N2_3C.2a1b.2a.2b	28	0.86	0.87	0.86	0.87	0.83	0.78	0.93	0.88	0.89	0.96	0.93	0.89	0.89	1.01	0.73	1.04	0.98	0.76
H3N2_3C.2a1b.2a.2a.1b3+HA_D120G+	23	1.23	0.99	1.17	0.99	0.94	1.08	1.1	1.08	0.83	0.88	1.15	1.02	1.05	0.95	1	1.01	1.07	0.93
H3N2_3C.2a1b.2a.2b+HA_R49Q	22	2.3	1.01	0.98	1.19	0.99	1.08	1.16	1.09	0.83	0.85	1.02	1.03	1.02	0.91	1.3	1.06	0.98	1.21
H1N1_6B.1A.5a.2a.1	11	2.21	0.93	0.83	0.86	0.83	0.72	1.01	1.02	0.83	0.92	0.94	0.95	0.94	0.91	1.01	0.97	0.98	0.95
H3N2_3C.2a1b.2a.2b+HA_I258M	11	0.23	0.93	0.65	0.78	0.83	1.13	0.79	1.09	0.99	0.86	0.94	0.87	0.86	0.91	1.5	1.24	0.98	1.4
Bvic_V1A.3a.2	9	1.55	0.94	1.02	0.96	1.12	0.81	1.23	0.83	0.83	0.97	0.94	0.87	0.86	1.22	0.74	1.08	0.98	0.93
H1N1_6B.1A.5a.2a+HA_A65P+HA_E25	9	1.14	1.07	1.16	1.23	1.21	0.88	1.05	0.91	0.83	1.21	1.15	1.06	1.05	0.91	0.74	0.97	0.98	0.69

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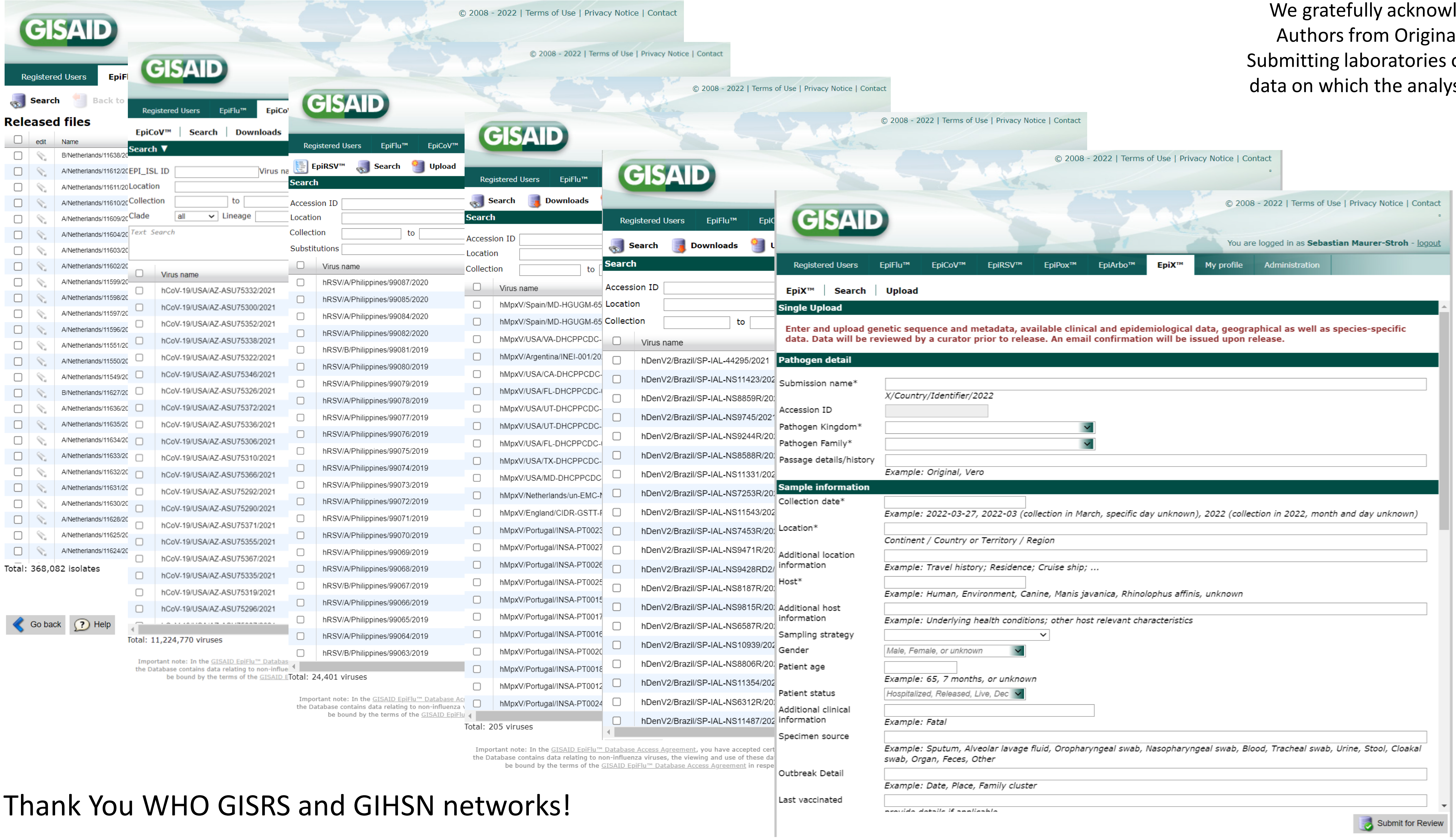
Extension to other priority pathogens

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



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☐		A/Netherlands/11611/20
☐		A/Netherlands/11610/20
☐		A/Netherlands/11609/20
☐		A/Netherlands/11604/20
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Total: 368,082 isolates

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EPI_ISL ID | Virus na
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☐	Virus name
☐	hCoV-19/USA/AZ-ASU75332/2021
☐	hCoV-19/USA/AZ-ASU75300/2021
☐	hCoV-19/USA/AZ-ASU75352/2021
☐	hCoV-19/USA/AZ-ASU75338/2021
☐	hCoV-19/USA/AZ-ASU75322/2021
☐	hCoV-19/USA/AZ-ASU75346/2021
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☐	hCoV-19/USA/AZ-ASU75371/2021
☐	hCoV-19/USA/AZ-ASU75355/2021
☐	hCoV-19/USA/AZ-ASU75367/2021
☐	hCoV-19/USA/AZ-ASU75335/2021
☐	hCoV-19/USA/AZ-ASU75319/2021
☐	hCoV-19/USA/AZ-ASU75296/2021

Total: 11,224,770 viruses

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☐	Virus name
☐	hRSV/A/Philippines/99087/2020
☐	hRSV/A/Philippines/99085/2020
☐	hRSV/A/Philippines/99084/2020
☐	hRSV/A/Philippines/99082/2020
☐	hRSV/B/Philippines/99081/2019
☐	hRSV/A/Philippines/99080/2019
☐	hRSV/A/Philippines/99079/2019
☐	hRSV/A/Philippines/99078/2019
☐	hRSV/A/Philippines/99077/2019
☐	hRSV/A/Philippines/99076/2019
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☐	hRSV/A/Philippines/99068/2019
☐	hRSV/B/Philippines/99067/2019
☐	hRSV/A/Philippines/99066/2019
☐	hRSV/A/Philippines/99065/2019
☐	hRSV/A/Philippines/99064/2019
☐	hRSV/B/Philippines/99063/2019

Total: 24,401 viruses

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Accession ID
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Collection to

☐	Virus name
☐	hMpxV/Spain/MD-HGUGM-65
☐	hMpxV/Spain/MD-HGUGM-65
☐	hMpxV/USA/VA-DHCPPCDC-
☐	hMpxV/Argentina/INEI-001/20
☐	hMpxV/USA/CA-DHCPPCDC-
☐	hMpxV/USA/FL-DHCPPCDC-
☐	hMpxV/USA/UT-DHCPPCDC-
☐	hMpxV/USA/UT-DHCPPCDC-
☐	hMpxV/USA/FL-DHCPPCDC-
☐	hMpxV/USA/TX-DHCPPCDC-
☐	hMpxV/USA/MD-DHCPPCDC
☐	hMpxV/Netherlands/un-EMC-
☐	hMpxV/England/CIDR-GSTT-
☐	hMpxV/Portugal/INSA-PT0023
☐	hMpxV/Portugal/INSA-PT0027
☐	hMpxV/Portugal/INSA-PT0026
☐	hMpxV/Portugal/INSA-PT0025
☐	hMpxV/Portugal/INSA-PT0015
☐	hMpxV/Portugal/INSA-PT0017
☐	hMpxV/Portugal/INSA-PT0016
☐	hMpxV/Portugal/INSA-PT0020
☐	hMpxV/Portugal/INSA-PT0018
☐	hMpxV/Portugal/INSA-PT0012
☐	hMpxV/Portugal/INSA-PT0024

Total: 205 viruses

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Accession ID
Location
Collection to

☐	Virus name
☐	hDenV2/Brazil/SP-IAL-44295/2021
☐	hDenV2/Brazil/SP-IAL-NS11423/202
☐	hDenV2/Brazil/SP-IAL-NS8859R/20
☐	hDenV2/Brazil/SP-IAL-NS9745/202
☐	hDenV2/Brazil/SP-IAL-NS9244R/20
☐	hDenV2/Brazil/SP-IAL-NS8588R/20
☐	hDenV2/Brazil/SP-IAL-NS11331/202
☐	hDenV2/Brazil/SP-IAL-NS7253R/20
☐	hDenV2/Brazil/SP-IAL-NS11543/202
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☐	hDenV2/Brazil/SP-IAL-NS8187R/20
☐	hDenV2/Brazil/SP-IAL-NS9815R/20
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☐	hDenV2/Brazil/SP-IAL-NS10939/202
☐	hDenV2/Brazil/SP-IAL-NS8806R/20
☐	hDenV2/Brazil/SP-IAL-NS11354/202
☐	hDenV2/Brazil/SP-IAL-NS6312R/20
☐	hDenV2/Brazil/SP-IAL-NS11487/202

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Single Upload

Enter and upload genetic sequence and metadata, available clinical and epidemiological data, geographical as well as species-specific data. Data will be reviewed by a curator prior to release. An email confirmation will be issued upon release.

Pathogen detail

Submission name*	*X/Country/Identifier/2022*
Accession ID	
Pathogen Kingdom*	
Pathogen Family*	
Passage details/history	*Example: Original, Vero*

Sample information

Collection date*	*Example: 2022-03-27, 2022-03 (collection in March, specific day unknown), 2022 (collection in 2022, month and day unknown)*
Location*	*Continent / Country or Territory / Region*
Additional location information	*Example: Travel history; Residence; Cruise ship; ...*
Host*	*Example: Human, Environment, Canine, Manis javanica, Rhinolophus affinis, unknown*
Additional host information	*Example: Underlying health conditions; other host relevant characteristics*
Sampling strategy	
Gender	*Male, Female, or unknown*
Patient age	*Example: 65, 7 months, or unknown*
Patient status	*Hospitalized, Released, Live, Dec*
Additional clinical information	*Example: Fatal*
Specimen source	*Example: Sputum, Alveolar lavage fluid, Oropharyngeal swab, Nasopharyngeal swab, Blood, Tracheal swab, Urine, Stool, Cloakal swab, Organ, Feces, Other*
Outbreak Detail	*Example: Date, Place, Family cluster*
Last vaccinated	

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Thank You WHO GISRS and GIHSN networks!

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GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

LEVERAGING ON THE GIHSN DATABASE & NETWORK

Moderator: Sandra S CHAVES, Foundation for Influenza Epidemiology

Foundation for
Influenza
Epidemiology

-Miranda DELAHOY, CDC, Atlanta, USA
-Cécile VIBOUD & Chelsea HANSEN, NIH, USA
-Bronke BOUDEWIJNS, Nivel, The Netherlands

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ANNUAL MEETING, 16 NOVEMBER 2023

RESEARCH UPDATE

Sandra CHAVES, Foundation for Influenza Epidemiology

Foundation for
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Sous l'égide de

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de
France

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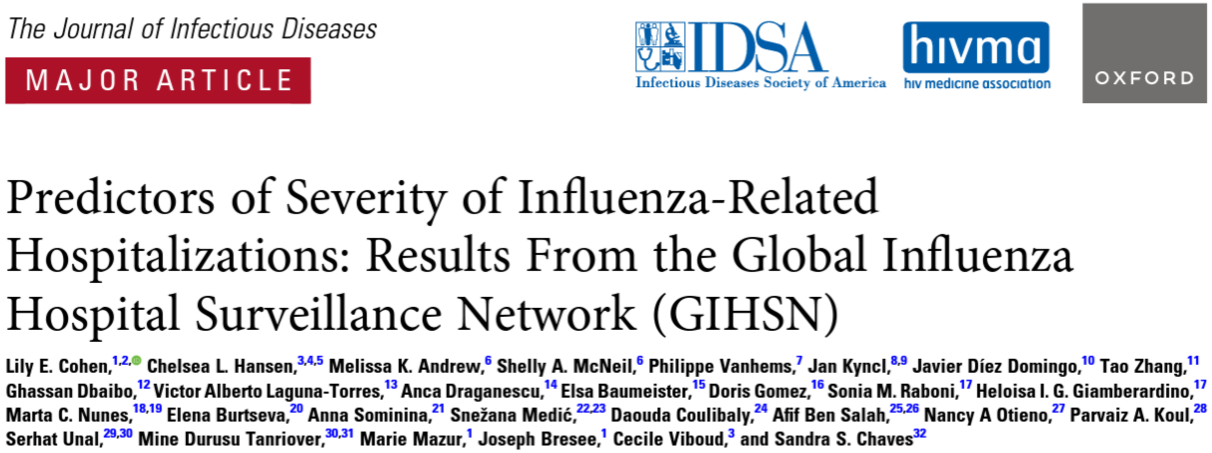
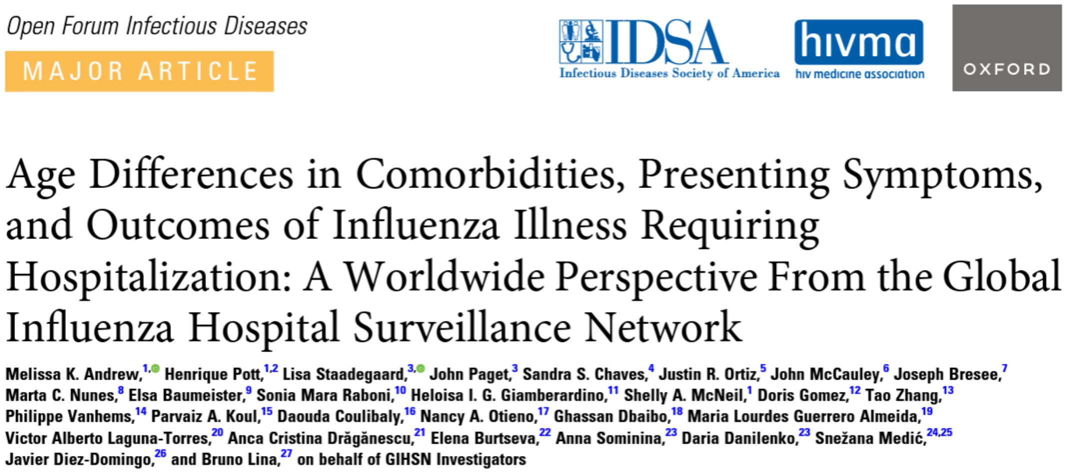


The Journal of Infectious Diseases

MAJOR ARTICLE

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

Lily E. Cohen,[1,2] Chelsea L. Hansen,[3,4,5] Melissa K. Andrew,[6] Shelly A. McNeil,[6] Philippe Vanhems,[7] Jan Kyncl,[8,9] Javier Díez Domingo,[10] Tao Zhang,[11] Ghassan Dbaibo,[12] Victor Alberto Laguna-Torres,[13] Anca Draganescu,[14] Elsa Baumeister,[15] Doris Gomez,[16] Sonia M. Raboni,[17] Heloisa I. G. Giamberardino,[17] Marta C. Nunes,[18,19] Elena Burtseva,[20] Anna Sominina,[21] Snežana Medić,[22,23] Daouda Coulibaly,[24] Afif Ben Salah,[25,26] Nancy A Otieno,[27] Parvaiz A. Koul,[28] Serhat Unal,[29,30] Mine Durusu Tanriover,[30,31] Marie Mazur,[1] Joseph Bresee,[1] Cecile Viboud,[3] and Sandra S. Chaves[32]

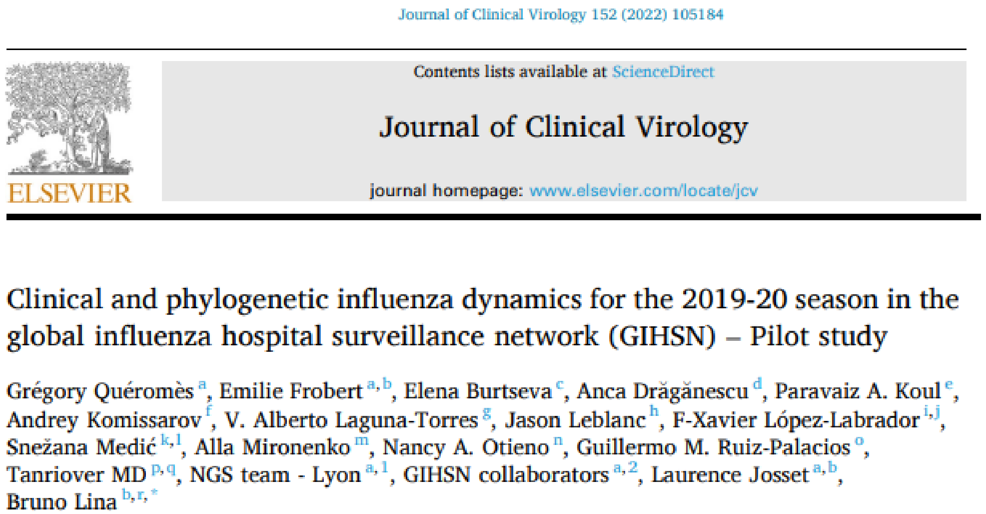


Open Forum Infectious Diseases

MAJOR ARTICLE

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,[1] Henrique Pott,[1,2] Lisa Staadegaard,[3] John Paget,[3] Sandra S. Chaves,[4] Justin R. Ortiz,[5] John McCauley,[6] Joseph Bresee,[7] Marta C. Nunes,[8] Elsa Baumeister,[9] Sonia Mara Raboni,[10] Heloisa I. G. Giamberardino,[11] Shelly A. McNeil,[1] Doris Gomez,[12] Tao Zhang,[13] Philippe Vanhems,[14] Parvaiz A. Koul,[15] Daouda Coulibaly,[16] Nancy A. Otieno,[17] Ghassan Dbaibo,[18] Maria Lourdes Guerrero Almeida,[19] Victor Alberto Laguna-Torres,[20] Anca Cristina Drăgănescu,[21] Elena Burtseva,[22] Anna Sominina,[23] Daria Danilenko,[23] Snežana Medić,[24,25] Javier Diez-Domingo,[26] and Bruno Lina,[27] on behalf of GIHSN Investigators



Journal of Clinical Virology 152 (2022) 105184

Contents lists available at ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

Clinical and phylogenetic influenza dynamics for the 2019-20 season in the global influenza hospital surveillance network (GIHSN) – Pilot study

Grégory Quéromès [a], Emilie Frobert [a,b], Elena Burtseva [c], Anca Drăgănescu [d], Paravaiz A. Koul [e], Andrey Komissarov [f], V. Alberto Laguna-Torres [g], Jason Leblanc [h], F-Xavier López-Labrador [i,j], Snežana Medić [k,l], Alla Mironenko [m], Nancy A. Otieno [n], Guillermo M. Ruiz-Palacios [o], Tanriover MD [p,q], NGS team - Lyon [a,1], GIHSN collaborators [a,2], Laurence Josset [a,b], Bruno Lina [b,r,*]

Microbiology and Immunology

ORIGINAL ARTICLE | Free Access

The association of breastfeeding and other factors on respiratory virus positivity and severity in hospitalized children

Laura Holtman Ferreira, Breno Gonçalves da Silva, Heloísa Ihle Giamberardino, Ana Paula Pacheco, Luciane Aparecida Pereira, Gustavo Genelhoud, Ricardo Rasmussen Petterle, Sonia Mara Raboni

First published: 15 February 2022 | https://doi.org/10.1111/1348-0421.12969

More information on
www.gihsn.org

RESEARCH GRANT

In 2021 the FIE started to support analytical and research projects leveraging the GIHSN platform

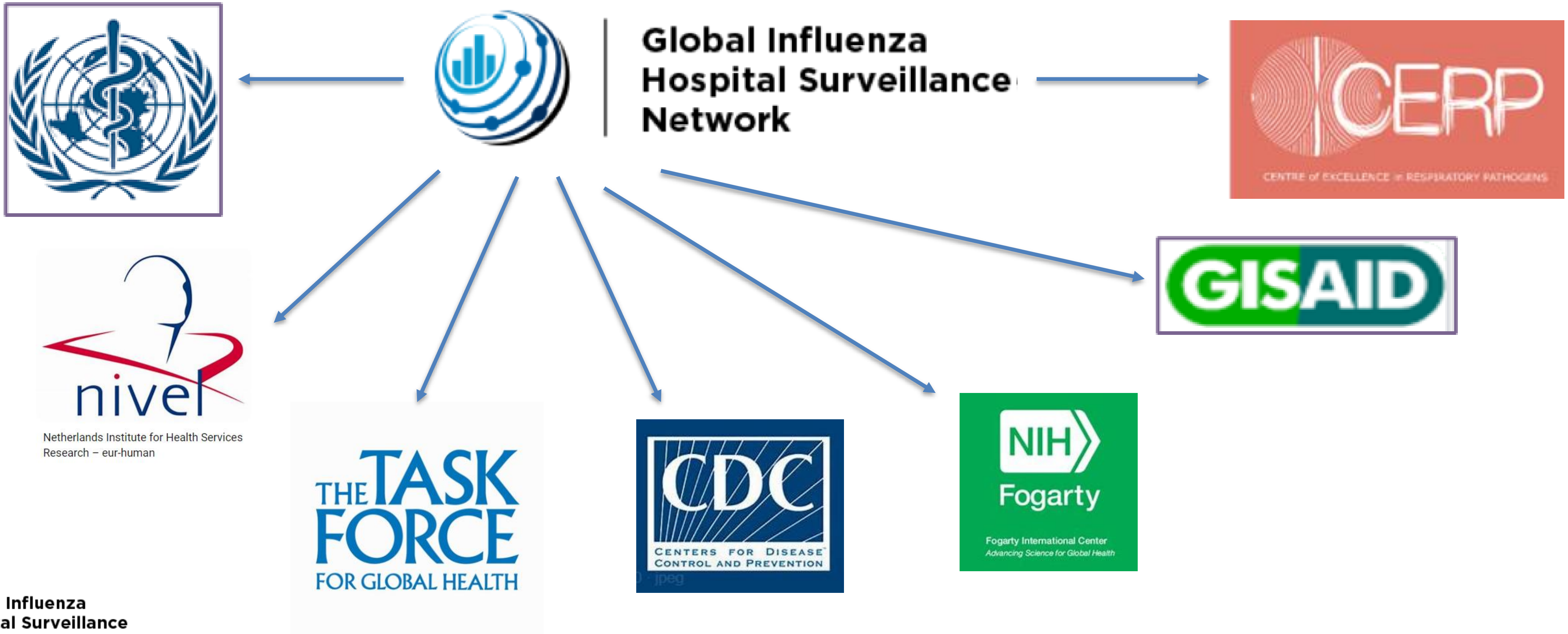
- Categories: Novel analysis of existing data, use of stored respiratory specimens for pathogen discovery or other relevant studies, others
- Support: Grants
- Process: Proposals to be technically approved by ISC and sites and endorsed by the EC

RESEARCH PROJECTS SUPPORTED BY FIE

Research projects validated by the EC (in March 2022)

Title	Leading author	Status
Experience of older adults hospitalized with influenza and acute respiratory illness in relation to function in Activities of Daily Living: a report from the GIHSN	M K Andrew	Awaiting request for data
GIHSN Severity Scale (GIHSN SevScale) to categorize hospitalizations across the network based on broad severity parameters to be linked with WGS data	J Paget B Boudewijns (Nivel)	Finalized results and manuscript in progress Follow up analyses under discussion

EXPANDING COLLABORATIONS BEYOND GIHSN STAKEHOLDERS



PRESENTATIONS + DISCUSSIONS

Enterovirus surveillance and proposed collaboration with the GIHSN

Miranda Delahoy is senior epidemiologist on the Acute Flaccid Myelitis and Domestic Polio Team in the NCIRD/CDC. She earned a PhD in Environmental Health Sciences from Emory University and completed CDC's Epidemic Intelligence Service fellowship in 2022. She currently works on EV-D68 surveillance initiatives at CDC

The importance of denominator for burden of disease estimates and how it could be implemented in the GIHSN

Cecile Viboud had her PhD in mathematical epidemiological. She joined the Division of International Epidemiology and Population Studies of the Fogarty International Center, NIH, in 2003. She has published extensively in the field of respiratory virus modelling

The SevScale project

Bronke Boudewijns is a junior researcher at the Netherlands Institute for Health Services Research (Nivel), where she works in the Infectious Diseases program since September 2022. Her main focus is on influenza and SARS-CoV-2 related projects, one of which is the SevScale project. Bronke's background is in biomedical sciences and epidemiology, and before joining Nivel she worked at RIVM

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ANNUAL MEETING, 16 NOVEMBER 2023

EV-D68 SURVEILLANCE & PROPOSED COLLABORATION WITH GIHSN

Miranda DELAHOY, US CDC

Foundation for
Influenza
Epidemiology

Sous l'égide de
Fondation
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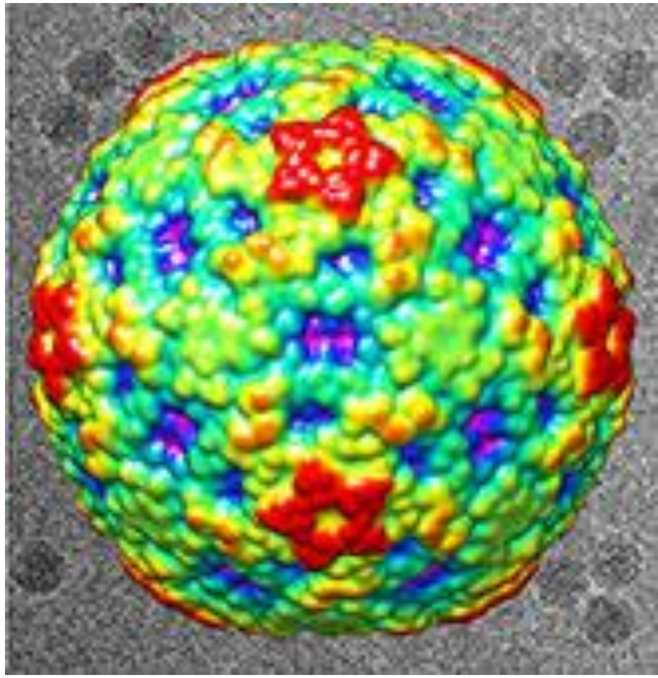
France

EV-D68 surveillance: Proposed global partnership between GIHSN, CDC, and the Abbott Pandemic Defense Coalition



Miranda Delahoy, PhD, MSPH
Acute Flaccid Myelitis and Domestic Polio Team
Centers for Disease Control and Prevention

GIHSN annual meeting
November 16, 2023
WHO HQ, Geneva, Switzerland

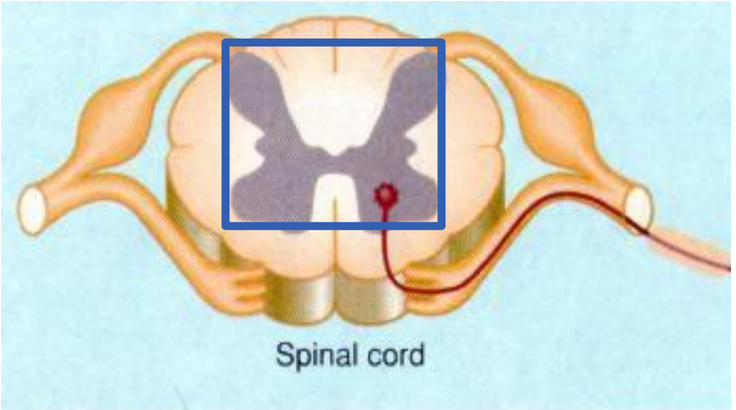
Background: EV-D68 epidemiology

EV-D68 causes mild and severe acute respiratory illness.

- First isolated in 1962
- Associated with mild to severe respiratory illness
- Symptoms include shortness of breath, cough, and wheezing
- Likely spreads from person to person when an infected person coughs, sneezes, or touches a surface that is then touched by others
- No approved specific therapies or vaccines

EV-D68 can also cause acute flaccid myelitis (AFM).

- Uncommon but serious neurologic condition
- Signs and symptoms are similar to poliomyelitis
  - Sudden limb weakness +/- cranial nerve weakness
  - Inflammatory lesions in spinal cord gray matter
- Most reported cases (>90%) are in children
- Most cases have preceding mild viral illness
- Viral testing in AFM patients has been low yield

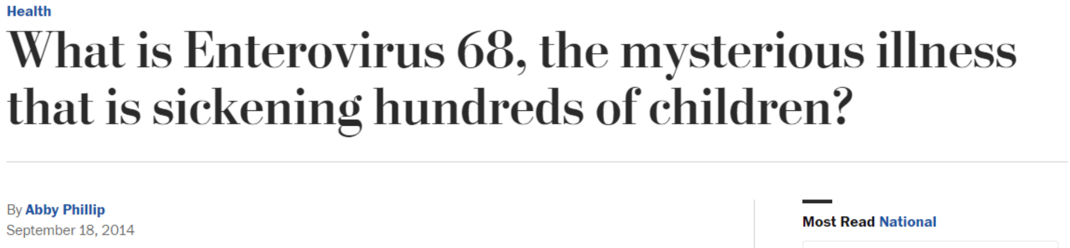


Blue box surrounds gray matter

EV-D68 caused a nationwide outbreak of respiratory illness in the US in 2014.

What is Enterovirus EV-D68, the disease causing alarm in the Midwest?

By **Jethro Mullen**, CNN
updated 3:33 PM EDT, Tue September 9, 2014



What is Enterovirus 68, the mysterious illness that is sickening hundreds of children?

By Abby Phillip
September 18, 2014

4 Things We've Learned About Enterovirus D68, And 1 Mystery

October 9, 2014 · 12:16 PM ET

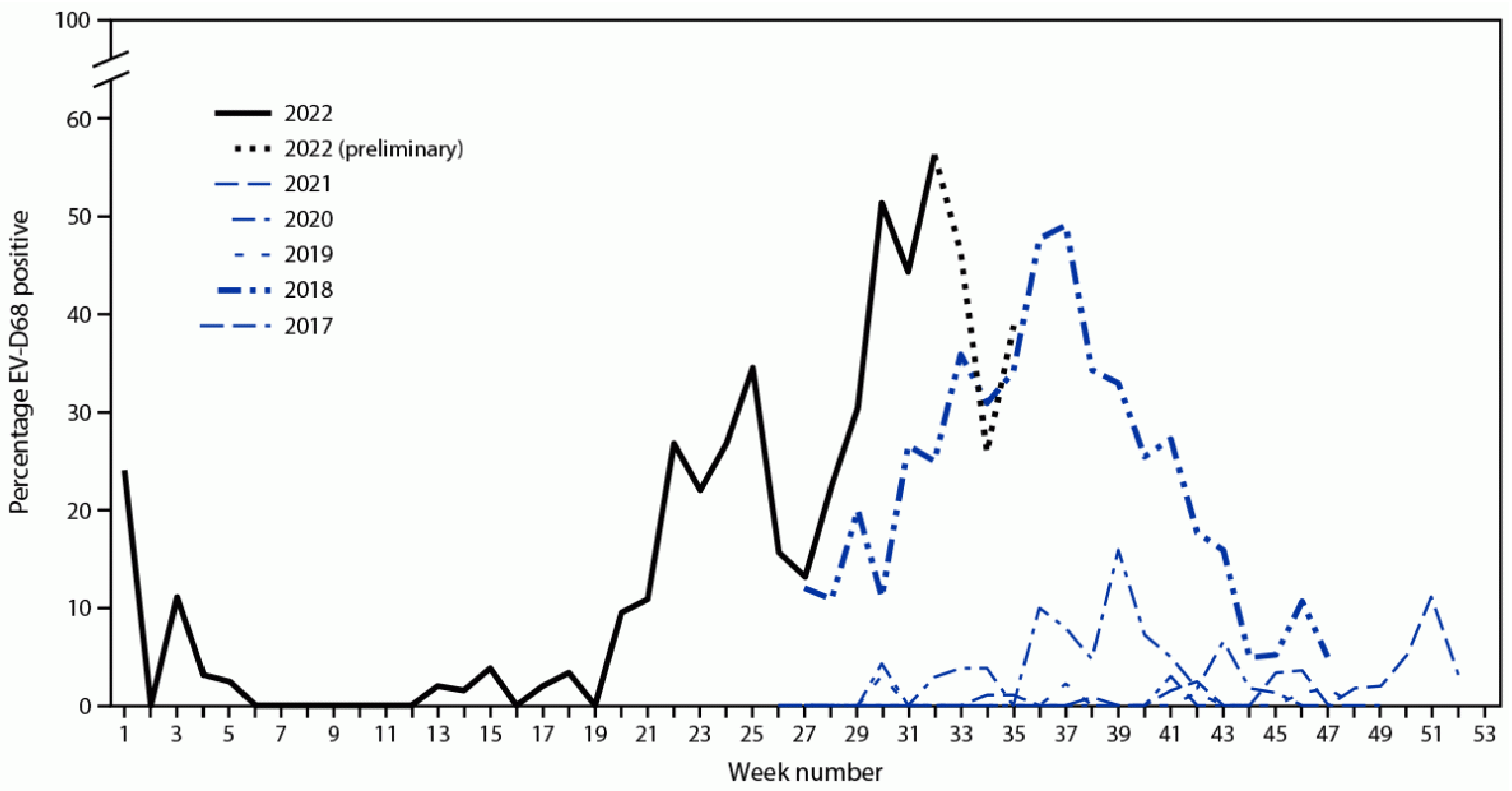
By Nancy Shute

"By Aug. 20, we were beyond our bed capacity," Dr. Mary Anne Jackson, chief of the infectious diseases section at Children's Mercy, said at the IDWeek meeting in Philadelphia.

Enterovirus D68 is spreading across the US — what we know and don't know

By Julia Belluz | @juliaoftoronto | julia.belluz@voxmedia.com | Updated Oct 7, 2014, 4:14pm EDT

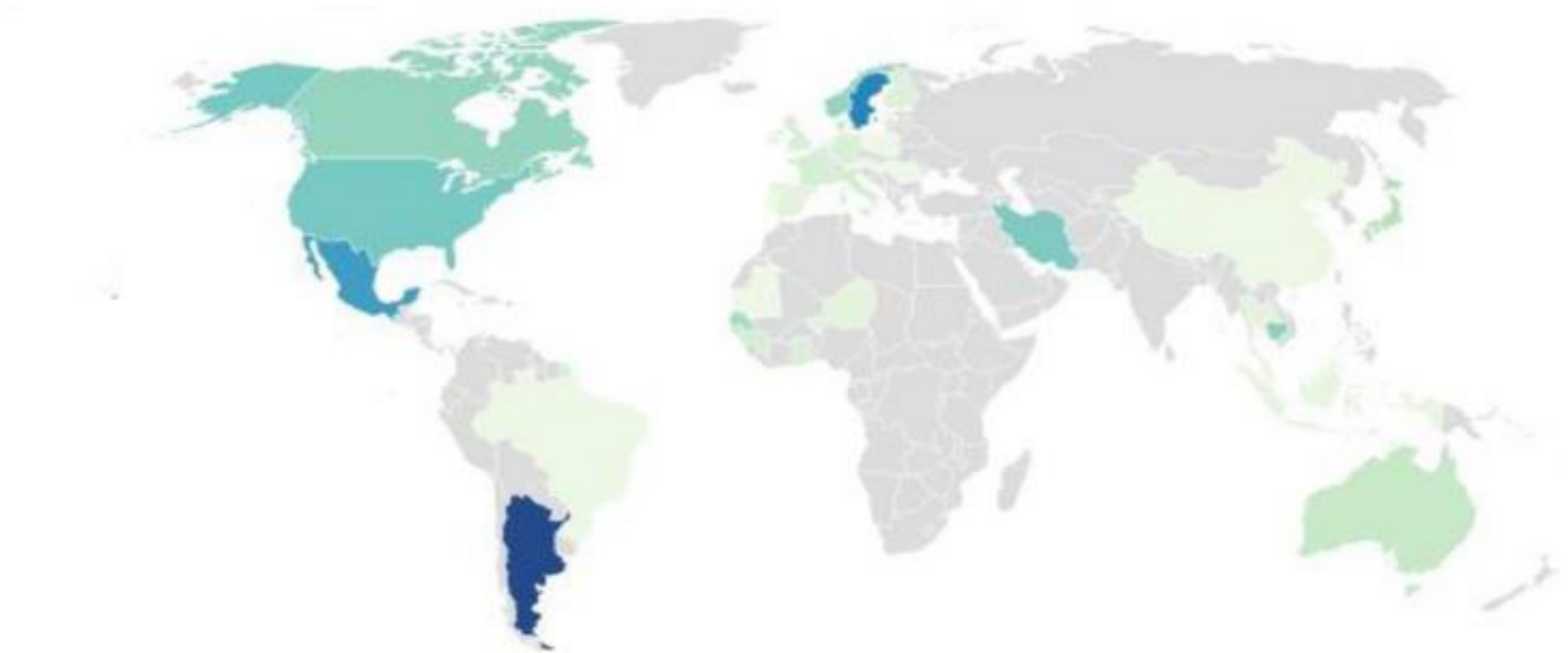
EV-D68 surveillance data have been collected by the New Vaccine Surveillance Network since 2017.



Positive EV-D68 test results among children and adolescents aged <18 years with ARI and positive RV/EV test results — emergency department or inpatient units — NVSN, United States, 2017–2022

Source: Ma et al. MMWR October 7 2022. DOI: http://dx.doi.org/10.15585/mmwr.mm7140e1.

Since 2014, EV-D68 outbreaks have been reported globally. However, there is a need for systematized global surveillance.



Countries from which a study of EV-D68 infections was identified in a systematic review and meta-analysis

Fall et al. Global Prevalence and case fatality rate of Enterovirus D68 infections, a systematic review and meta-analysis. Feb 8 2022.

Global EV-D68 surveillance is of public health importance.

Geographic patterns

Temporal trends

Inform preparedness

Impact of COVID-19 pandemic on transmission

Proposed global EV-D68 surveillance partnership

Three partners bring epidemiologic and laboratory expertise to a proposed global EV-D68 surveillance network.

Global Influenza
Hospital Surveillance
Network

Abbott

Abbott Pandemic Defense Coalition (APDC)

- Global network of sites collecting specimens for early detection & response to pandemic threats
- Laboratory expertise and resources (EV-D68 assay)

CDC
Centers for Disease Control and Prevention

US Centers for Disease Control and Prevention (CDC)

- EV-D68 surveillance expertise
- Validated EV-D68 assay
- Capacity for limited retrospective respiratory specimen testing for EV-D68 and providing technical assistance

20 SITES MONITORING INFECTIOUS DISEASESE ON 5 CONTINENTS

Abbott Pandemic Defense Coalition, 2023

USA – Rush University
UCSF
Stanford University
SUNY-Buffalo

Georgia – National Center for Disease Control (NCDC)
Pakistan – Aga Khan University (AKU)
Egypt – Ain Shams University (ASU)

Senegal – IRESSEF
Sierra Leone – OneHealth/University of Sierra Leone
Cameroon – University of Yaoundé I

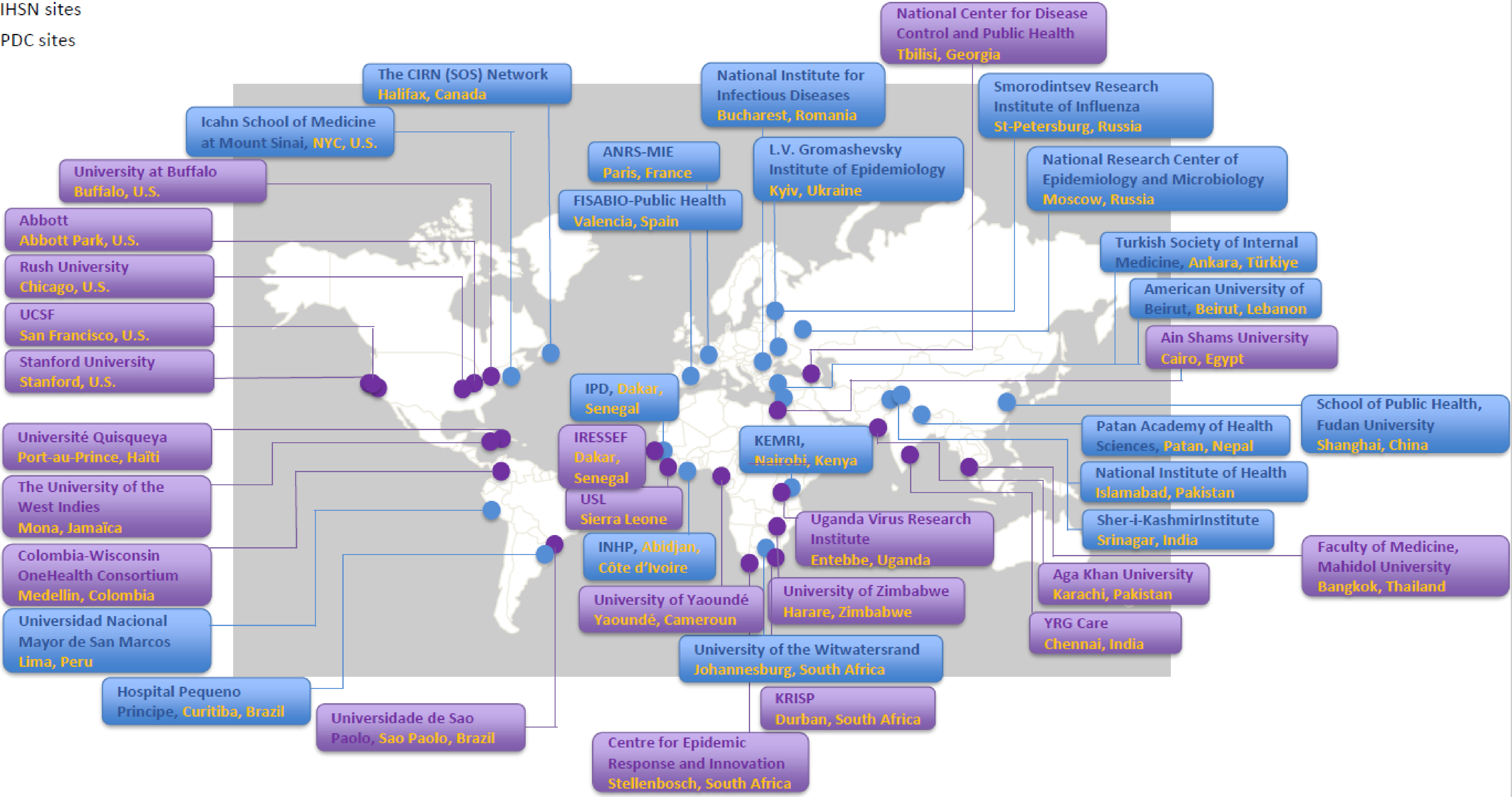
India – YRG Care
Thailand – Mahidol University

Haiti – Quisqueya University
Jamaica – University of the West Indies (UWI)

Colombia – OneHealth/Universidad Nacional Colombia
Peru – Universidad Peruana Cayetano Heredia (UPCH)
Brazil – University of São Paulo (USP)

Uganda – Uganda Viral Research Institute (UVRI)
Zimbabwe – University of Zimbabwe
South Africa – Centre for Epidemic Response and Innovation (CERI)

- ● GIHSN sites
- ● APDC sites



The CIRN (SOS) Network
Halifax, Canada

Icahn School of Medicine at Mount Sinai, NYC, U.S.

University at Buffalo
Buffalo, U.S.

Abbott
Abbott Park, U.S.

Rush University
Chicago, U.S.

UCSF
San Francisco, U.S.

Stanford University
Stanford, U.S.

Université Quisqueya
Port-au-Prince, Haïti

The University of the West Indies
Mona, Jamaïca

Colombia-Wisconsin OneHealth Consortium
Medellin, Colombia

Universidad Nacional Mayor de San Marcos
Lima, Peru

Hospital Pequeno Principe, Curitiba, Brazil

Universidade de Sao Paolo, Sao Paolo, Brazil

ANRS-MIE
Paris, France

FISABIO-Public Health
Valencia, Spain

IPD, Dakar, Senegal

IRESSEF
Dakar, Senegal

USL
Sierra Leone

INHP, Abidjan, Côte d'Ivoire

University of Yaoundé
Yaoundé, Cameroun

Centre for Epidemic Response and Innovation
Stellenbosch, South Africa

National Institute for Infectious Diseases
Bucharest, Romania

L.V. Gromashevsky Institute of Epidemiology
Kyiv, Ukraine

KEMRI,
Nairobi, Kenya

Uganda Virus Research Institute
Entebbe, Uganda

University of Zimbabwe
Harare, Zimbabwe

University of the Witwatersrand
Johannesburg, South Africa

KRISP
Durban, South Africa

National Center for Disease Control and Public Health
Tbilisi, Georgia

Smorodintsev Research Institute of Influenza
St-Petersburg, Russia

National Research Center of Epidemiology and Microbiology
Moscow, Russia

Turkish Society of Internal Medicine, Ankara, Türkiye

American University of Beirut, Beirut, Lebanon

Ain Shams University
Cairo, Egypt

School of Public Health, Fudan University
Shanghai, China

Patan Academy of Health Sciences, Patan, Nepal

National Institute of Health
Islamabad, Pakistan

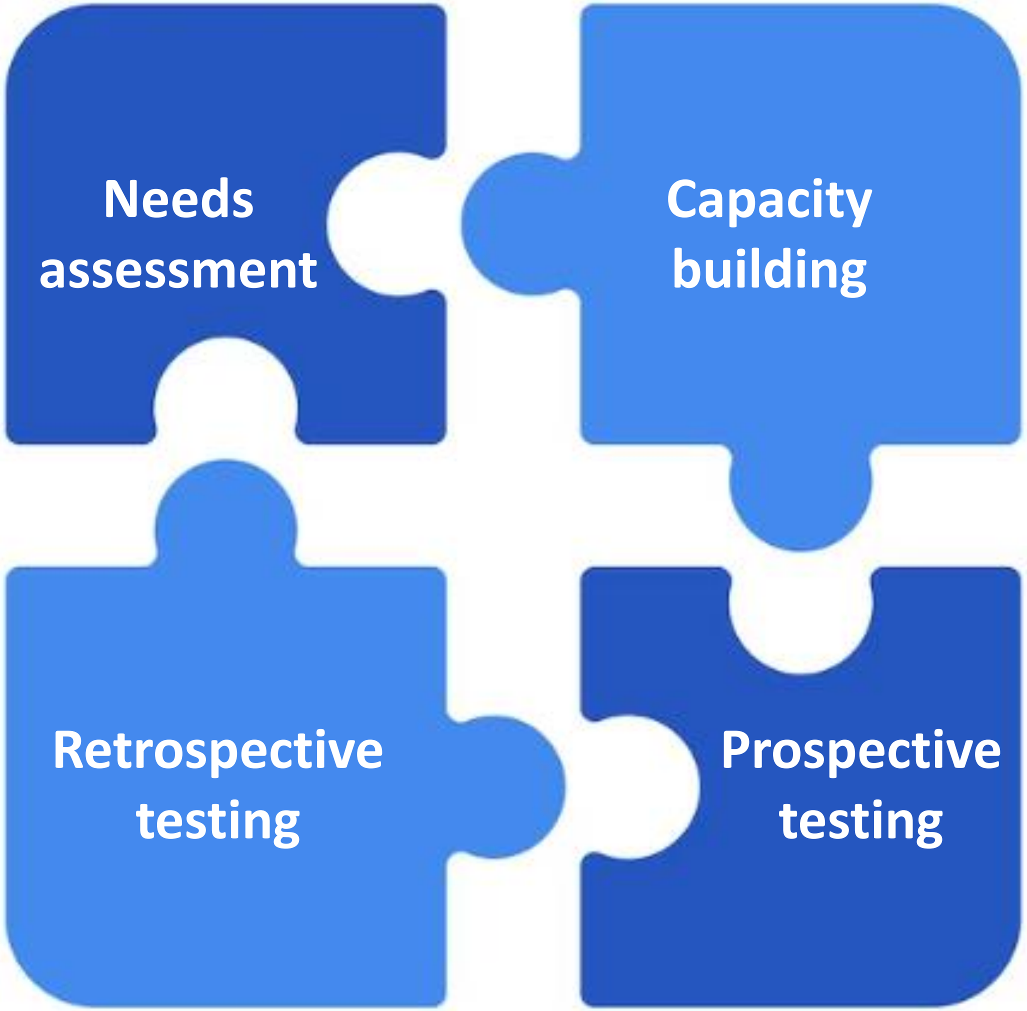
Sher-i-KashmirInstitute
Srinagar, India

Faculty of Medicine, Mahidol University
Bangkok, Thailand

Aga Khan University
Karachi, Pakistan

YRG Care
Chennai, India

EV-D68 global surveillance vision



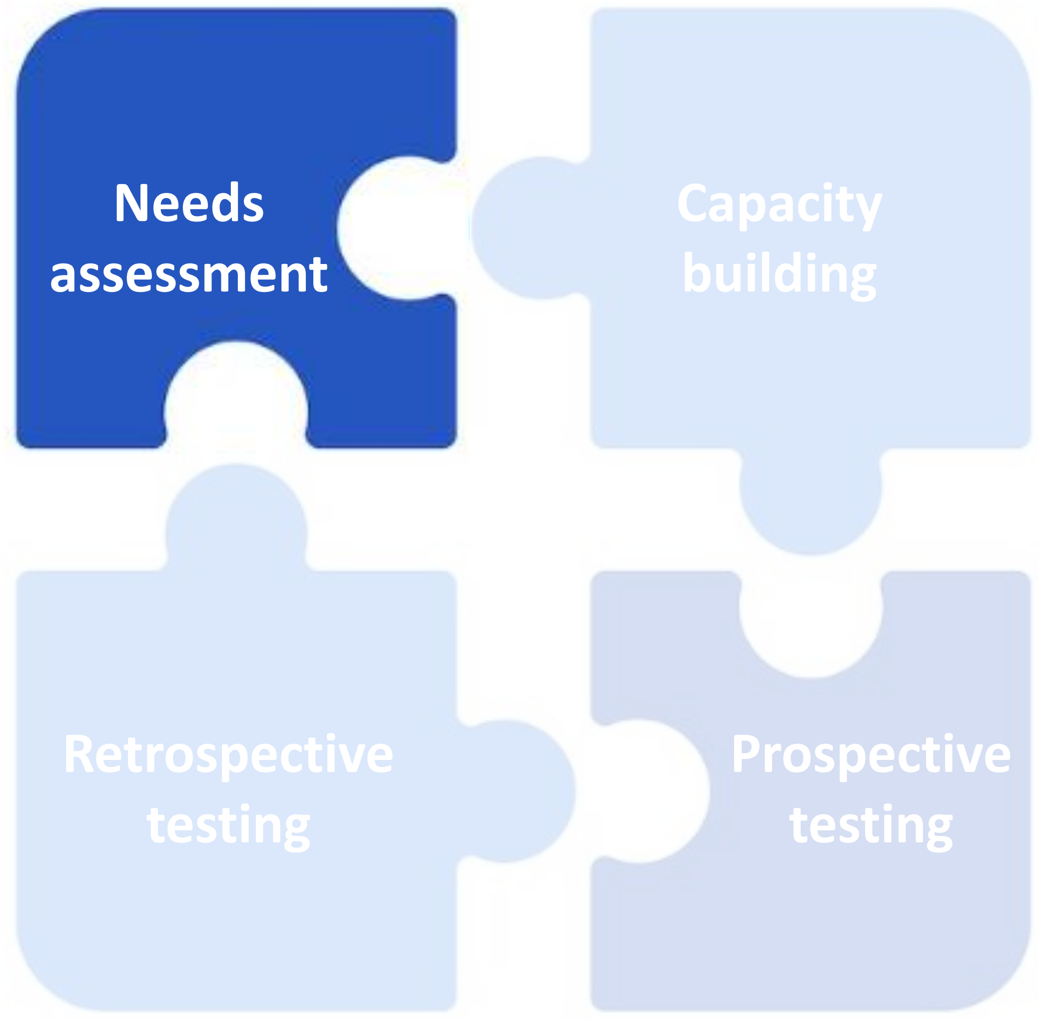
Needs assessment

Capacity building

Retrospective testing

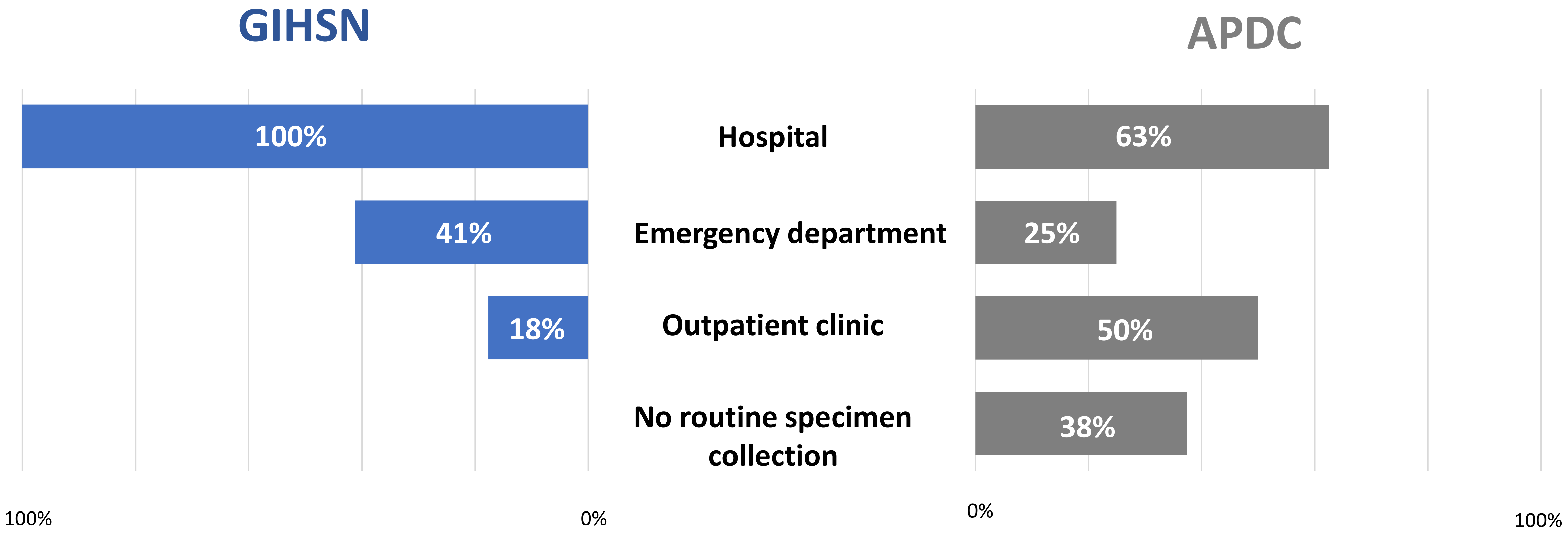
Prospective testing

EV-D68 global surveillance needs assessment



- Characterize **enrollment criteria** to understand **comparability of epidemiologic data** between sites & networks
- Understand **current testing capacity**
- **Quantify and characterize stored respiratory specimens** available for EV-D68 testing
- Understand **barriers to testing for EV-D68** to find potential solutions

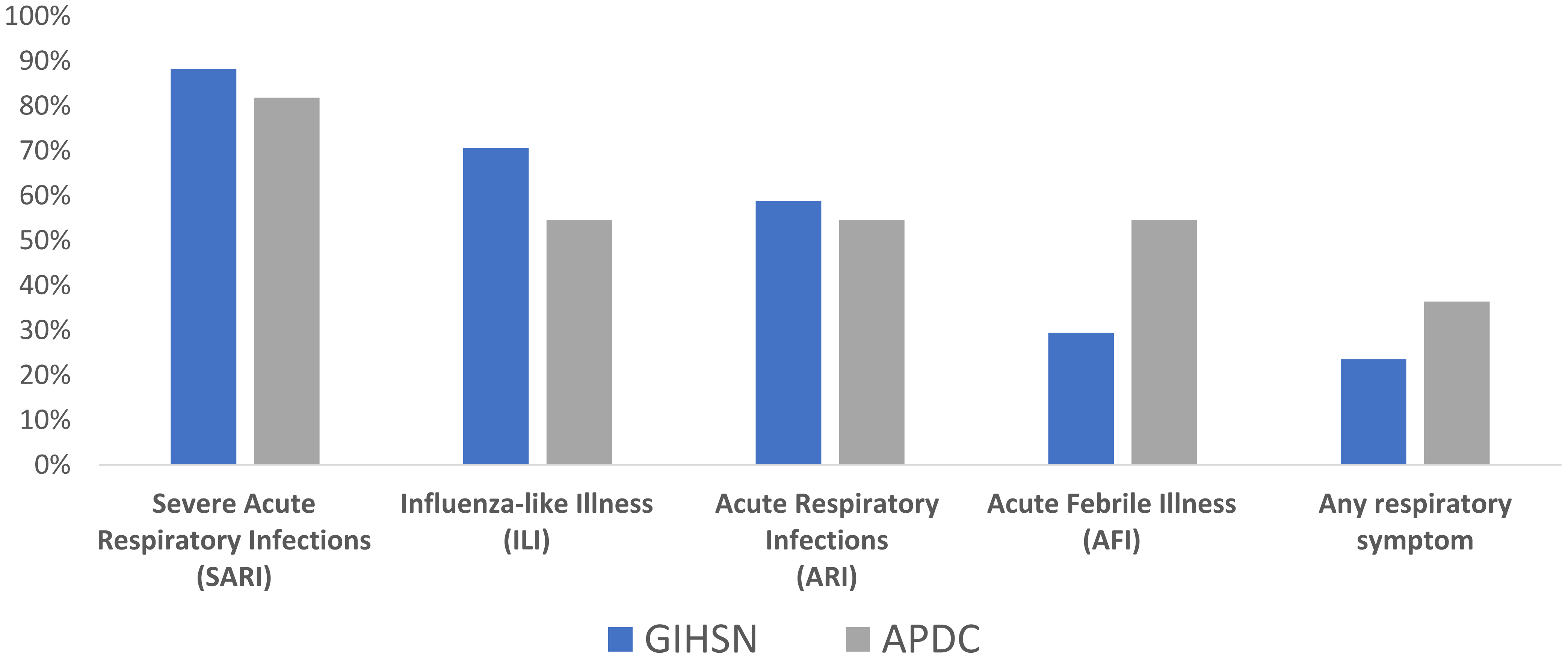
All GIHSN sites collect respiratory specimens from hospitalized patients. APDC sites collect specimens from hospitalized patients and outpatients.



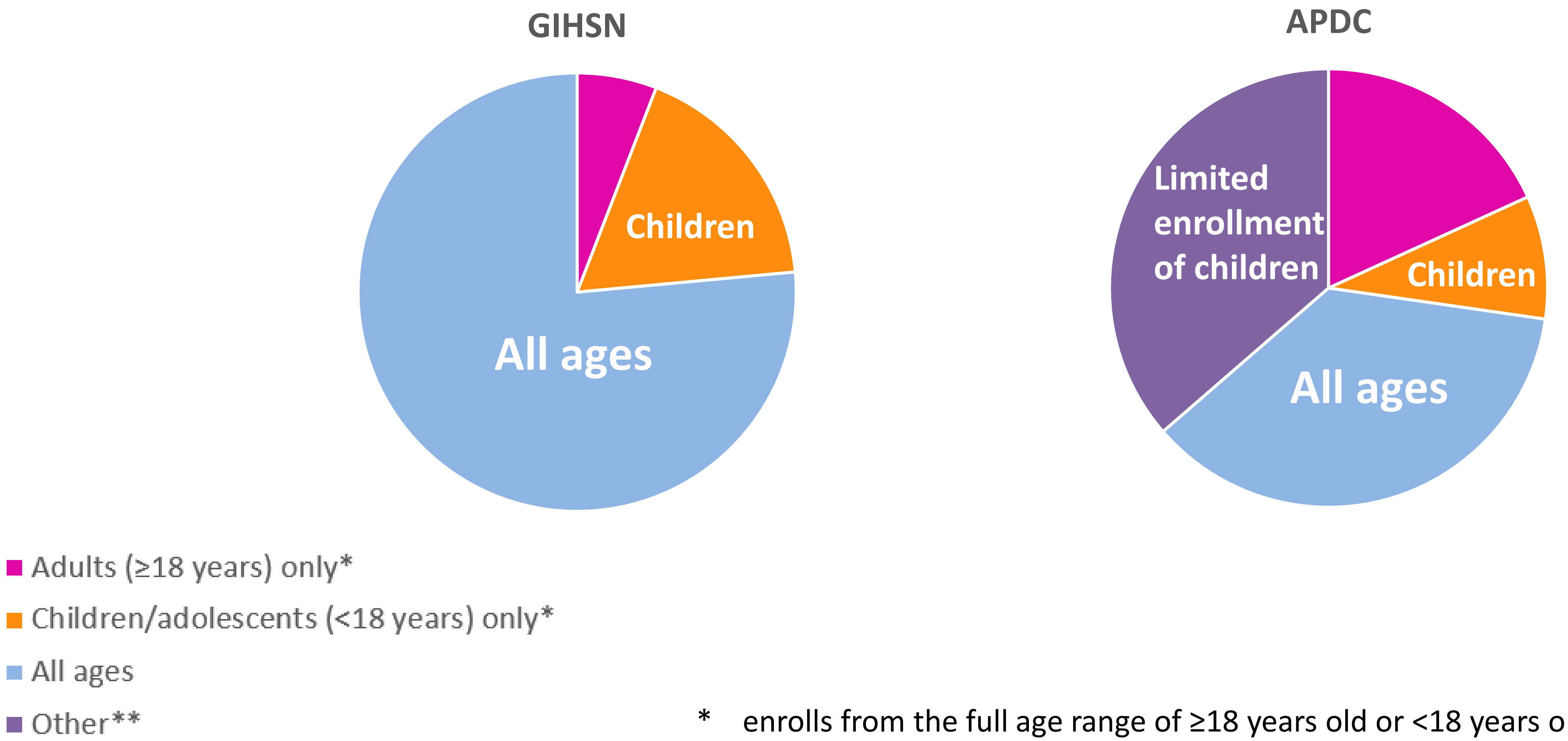
17 sites responded

16 sites responded

Most GIHSN & APDC sites employ systematic SARI specimen collection.



Nearly all GIHSN sites and most APDC sites collect specimens from children.



* enrolls from the full age range of ≥18 years old or <18 years old

** enrolls from a limited age range of children and/or adults (e.g., only ages 5–17 years old)

GIHSN sites test for several viruses.

Virus testing at GIHSN sites — as reported on needs assessment

	Influenza	SARS-CoV-2	RSV	HMPV	HCOV	PIV	Adenovirus	RV/EV	EV-D68
Brazil	×	×	×	×	×	×	×	×	×
China	×		×	×		×	×	×	
Cote d'Ivoire	×	×	×	×	×	×	×	×	×
France	×	×	×					×	
Kenya	×	×	×				×		
Lebanon	×	×	×	×	×	×	×	×	
Nepal	×								
Pakistan	×	×	×	×	×	×	×	×	
Peru	×	×	×	×		×	×		
Romania	×	×	×	×	×	×	×	×	
Russia–St. Petersburg	×	×	×	×	×	×	×	×	*
Senegal	×	×	×	×	×	×	×	×	×
South Africa	×	×	×	×			×	×	
Spain	×	×	×	×	×	×	×	×	×
Türkiye	×	×	×	×	×	×	×	×	
Ukraine	×	×							
USA–New York	×	×	×	×	×	×	×	×	

*in progress

RV/EV = rhinovirus/enterovirus

13 GIHSN sites conduct RV/EV testing.
3 APDC sites (not pictured) conduct RV/EV testing.

Virus testing at GIHSN sites — as reported on needs assessment

	Influenza	SARS-CoV-2	RSV	HMPV	HCOV	PIV	Adenovirus	RV/EV	EV-D68
Brazil	×	×	×	×	×	×	×	×	×
China	×		×	×		×	×	×	
Cote d'Ivoire	×	×	×	×	×	×	×	×	×
France	×	×	×					×	
Kenya	×	×	×				×		
Lebanon	×	×	×	×	×	×	×	×	
Nepal	×								
Pakistan	×	×	×	×	×	×	×	×	
Peru	×	×	×	×		×	×		
Romania	×	×	×	×	×	×	×	×	
Russia–St. Petersburg	×	×	×	×	×	×	×	×	*
Senegal	×	×	×	×	×	×	×	×	×
South Africa	×	×	×	×			×	×	
Spain	×	×	×	×	×	×	×	×	×
Türkiye	×	×	×	×	×	×	×	×	
Ukraine	×	×							
USA–New York	×	×	×	×	×	×	×	×	

*in progress

RV/EV = rhinovirus/enterovirus

4 GIHSN sites conduct EV-D68 testing.
2 APDC sites (not pictured) conduct EV-D68 testing.

Virus testing at GIHSN sites — as reported on needs assessment

	Influenza	SARS-CoV-2	RSV	HMPV	HCOV	PIV	Adenovirus	RV/EV	EV-D68
Brazil	×	×	×	×	×	×	×	×	×
China	×		×	×		×	×	×	
Cote d'Ivoire	×	×	×	×	×	×	×	×	×
France	×	×	×					×	
Kenya	×	×	×				×		
Lebanon	×	×	×	×	×	×	×	×	
Nepal	×								
Pakistan	×	×	×	×	×	×	×	×	
Peru	×	×	×	×		×	×		
Romania	×	×	×	×	×	×	×	×	
Russia–St. Petersburg	×	×	×	×	×	×	×	×	*
Senegal	×	×	×	×	×	×	×	×	×
South Africa	×	×	×	×			×	×	
Spain	×	×	×	×	×	×	×	×	×
Türkiye	×	×	×	×	×	×	×	×	
Ukraine	×	×							
USA–New York	×	×	×	×	×	×	×	×	

*in progress

RV/EV = rhinovirus/enterovirus

Across the two networks, there are many stored respiratory specimens that may be available for further testing.

>60,000

Stored respiratory specimens

>600

Respiratory specimens known to be EV/RV+

GIHSN and APDC sites reported similar barriers to EV-D68 testing and sequencing.

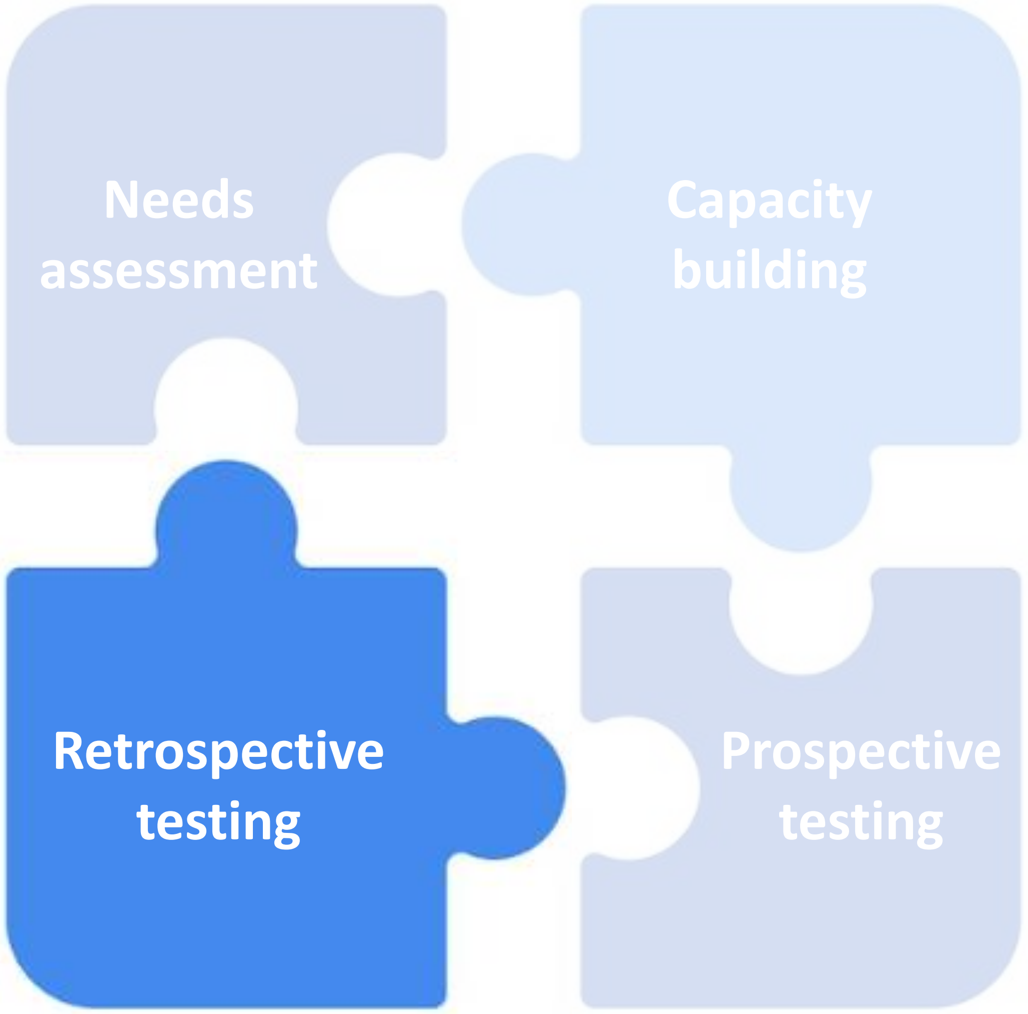
Lab resources

Personnel and staff training

Reagents

Equipment

EV-D68 global surveillance: retrospective testing



There is a need for a specimen prioritization plan for retrospective testing.

RV/EV+

from children

collected during
certain years

There will be trade-offs to consider when choosing which stored specimens to test.

Representation of different:

- **Geographic regions**
- **Age groups**
- **Years**

Testing capacity

Timeline

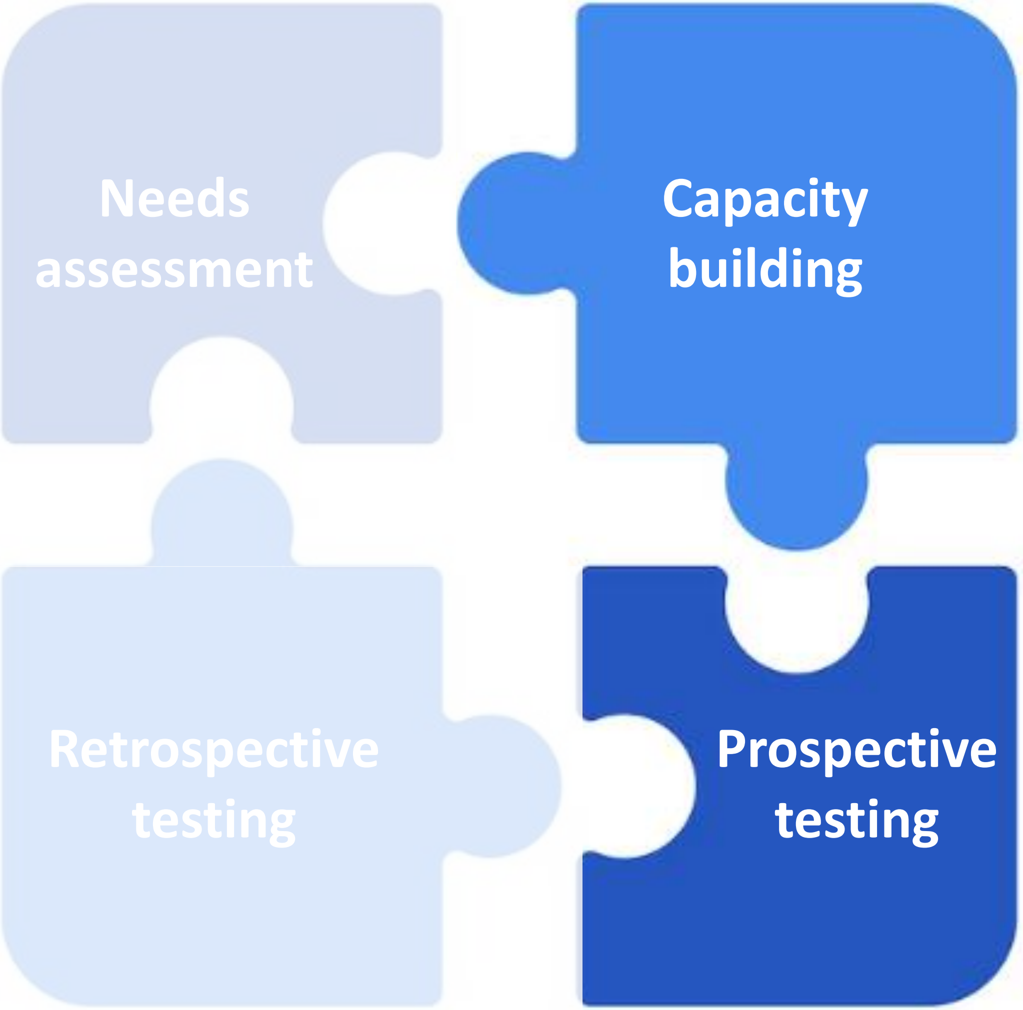
Retrospective testing at CDC will likely be limited to a subset of GIHSN “pilot” sites.

- CDC can test a subset of stored respiratory specimens.

- **We are looking to identify sites:**
  - With an interest in prospective EV-D68 testing
  - With the ability to ship respiratory specimens to CDC
  - Currently conducting RV/EV testing
    - There may also be an opportunity for retrospective testing of samples collected from pilot sites that do not yet have RV/EV testing capacity, but are interested in such testing.

- We are also interested in connecting with sites already testing for EV-D68.

EV-D68 global surveillance: prospective testing

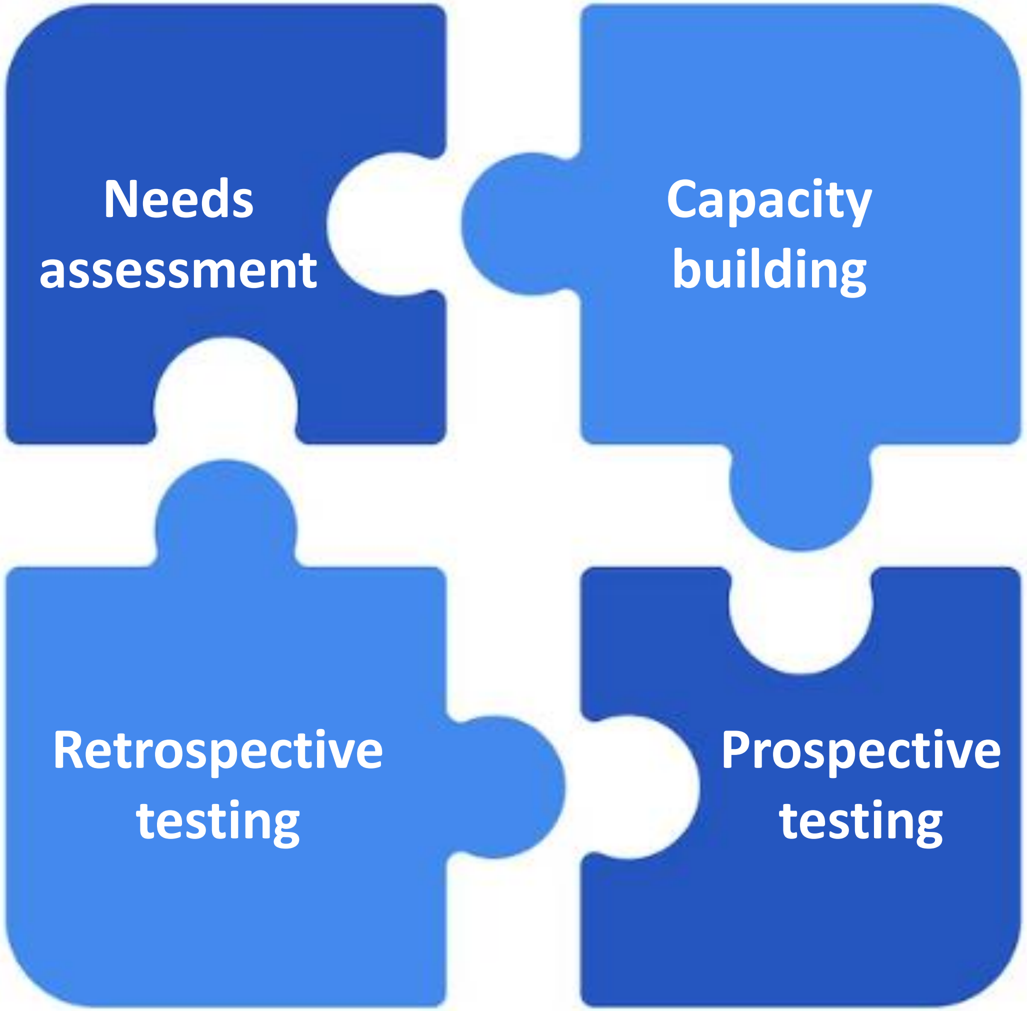

Needs assessment

Capacity building

Retrospective testing

Prospective testing

EV-D68 global surveillance vision



Needs assessment

Capacity building

Retrospective testing

Prospective testing

Thank you

GIHSN/Impact Healthcare:
Sandra Chaves, Catherine Commaille-Chapus

APDC:
Francisco Averhoff, Mary Rodgers

Division of Viral Diseases, CDC:
Adriana Lopez, Terry Ng, Sarah Kidd, Janell Routh

Coronavirus and Other Respiratory Viruses Division (CORVD), CDC:
Claire Midgley, Melisa M. Shah

GIHSN & APDC PIs and site personnel

WHO hosts

For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 www.cdc.gov

Geneva presentation outline

- EV-D68 background (3’)
- Outstanding questions in EV-D68 epidemiology/need for global surveillance (1’)
- Collaborators for proposed global network (CDC, GIHSN, APDC) (2’)
- Surveillance vision: needs assessment, capacity building, retrospective pilot testing, prospective testing (2’)
- Needs assessment high-level results (4’)
- Open questions & next steps, informed by needs assessment (3’)
- Discussion (10’)

All GIHSN sites enroll from the hospital setting.

GIHSN	Hospital	ED	Outpatient
Brazil	×		
China	×		
Cote d'Ivoire	×	×	
France	×	×	
Kenya	×	×	×
Lebanon	×		
Nepal	×		
Pakistan	×	×	×
Peru	×		
Romania	×		
Russia–St. Petersburg	×	×	
Senegal	×	×	×
South Africa	×		
Spain	×		
Türkiye	×	×	
Ukraine	×		
USA–New York	×		

APDC sites enroll primarily from the hospital.

GIHSN	Hospital	ED	Outpatient
Brazil	×		
China	×		
Cote d'Ivoire	×	×	
France	×	×	
Kenya	×	×	×
Lebanon	×		
Nepal	×		
Pakistan	×	×	×
Peru	×		
Romania	×		
Russia–St. Petersburg	×	×	
Senegal	×	×	×
South Africa	×		
Spain	×		
Türkiye	×	×	
Ukraine	×		
USA–New York	×		

APDC Sites	Hospital	ED	Outpatient
Brazil	×	×	▨
Cameroon	×	▨	×
Colombia	▨	▨	▨
Georgia	×	▨	×
Haiti	×	▨	×
India	×	▨	×
Jamaica	×	×	▨
Pakistan	×	▨	×
Peru	×	×	×
Senegal	▨	▨	▨
Sierra Leone	▨	▨	▨
South Africa	▨	▨	▨
Thailand	▨	▨	▨
Uganda	×		×
USA–San Francisco	×	×	×
Zimbabwe	▨	▨	▨

*Zimbabwe enrolls in outbreaks or sporadic cases

**Colombia and Thailand not collecting respiratory specimens.

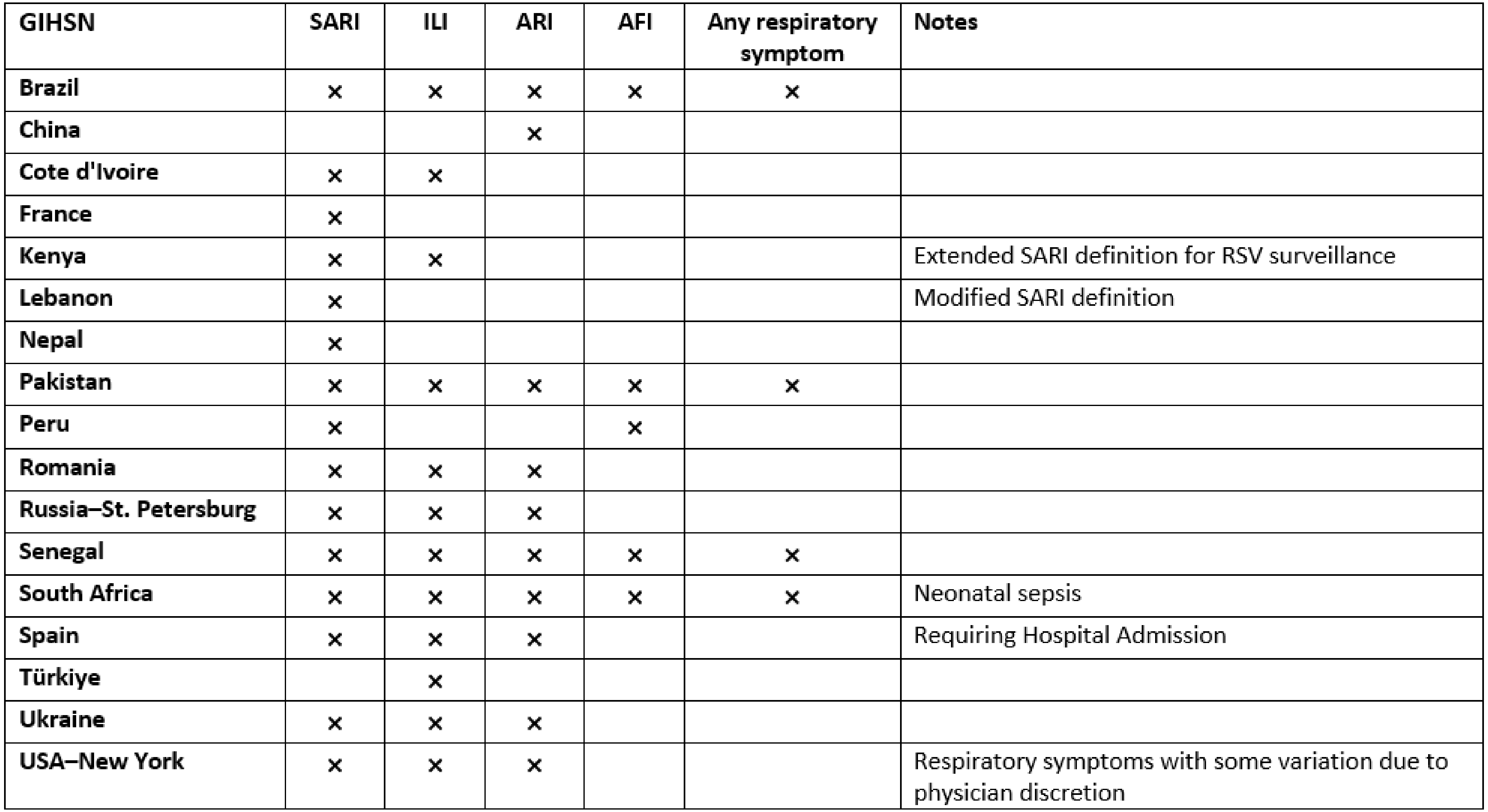
***Senegal, Sierra Leone, South Africa plan to collect respiratory specimens in the future.

APDC has less focus on children < 5yo.

	<1 year	1-4	5-17	18-64	65+
Brazil	×	×	×		
China	×	×	×		
Cote d'Ivoire	×	×	×	×	×
France				×	×
Kenya	×	×	×	×	×
Lebanon	×	×	×	×	×
Nepal	×	×	×	×	×
Pakistan	×	×	×	×	×
Peru	×	×	×	×	×
Romania	×	×	×	×	×
Russia–St. Petersburg	×	×	×	×	×
Senegal	×	×	×	×	×
South Africa	×	×	×		
Spain	×	×	×	×	×
Türkiye	×	×	×	×	×
Ukraine	×	×	×	×	×
USA–New York	×	×	×	×	×

APDC Sites	<1 year	1-4	5-17	18-64	65+
Brazil	×	×	×		
Cameroon				×	×
Georgia	×	×	×	×	×
Haiti		×	×	×	
India			×	×	×
Jamaica	×	×	×	×	×
Pakistan				×	
Peru			×	×	×
Uganda	×	×	×	×	×
USA–San Francisco	×	×	×	×	×
Zimbabwe		×	×	×	

Most GIHSN sites employ systematic SARI sample collection.



GIHSN	SARI	ILI	ARI	AFI	Any respiratory symptom	Notes
Brazil	×	×	×	×	×	
China			×			
Cote d'Ivoire	×	×				
France	×					
Kenya	×	×				Extended SARI definition for RSV surveillance
Lebanon	×					Modified SARI definition
Nepal	×					
Pakistan	×	×	×	×	×	
Peru	×			×		
Romania	×	×	×			
Russia–St. Petersburg	×	×	×			
Senegal	×	×	×	×	×	
South Africa	×	×	×	×	×	Neonatal sepsis
Spain	×	×	×			Requiring Hospital Admission
Türkiye		×				
Ukraine	×	×	×			
USA–New York	×	×	×			Respiratory symptoms with some variation due to physician discretion

Most APDC sites employ systematic SARI sample collection.

GIHSN	SARI	ILI	ARI	AFI	Any respiratory symptom
Brazil	×	×	×	×	×
China			×		
Cote d'Ivoire	×	×			
France	×				
Kenya	×	×			
Lebanon	×				
Nepal	×				
Pakistan	×	×	×	×	×
Peru	×			×	
Romania	×	×	×		
Russia–St. Petersburg	×	×	×		
Senegal	×	×	×	×	×
South Africa	×	×	×	×	×
Spain	×	×	×		
Türkiye		×			
Ukraine	×	×	×		
USA–New York	×	×	×		

APDC Sites	SARI	ILI	ARI	AFI	Any respiratory symptom
Brazil	×		×		
Cameroon					×
Georgia	×	×		×	
Haiti	×	×	×	×	
India	×	×	×	×	
Jamaica	×				
Pakistan				×	×
Peru	×	×	×	×	×
Uganda	×	×			×
USA–San Francisco	×		×	×	
Zimbabwe	×	×	×		

Global Influenza
Hospital Surveillance
Network

www.gihsn.org

coordination

IMPACT
Healthcare

ANNUAL MEETING, 16 NOVEMBER 2023

LEVERAGING THE GIHSN TO SUPPORT DISEASE BURDEN ESTIMATION

Cécile VIBOUD, Fogarty International Center

Foundation for
Influenza
Epidemiology

Sous l'égide de

Fondation
de
France

Fogarty International Center

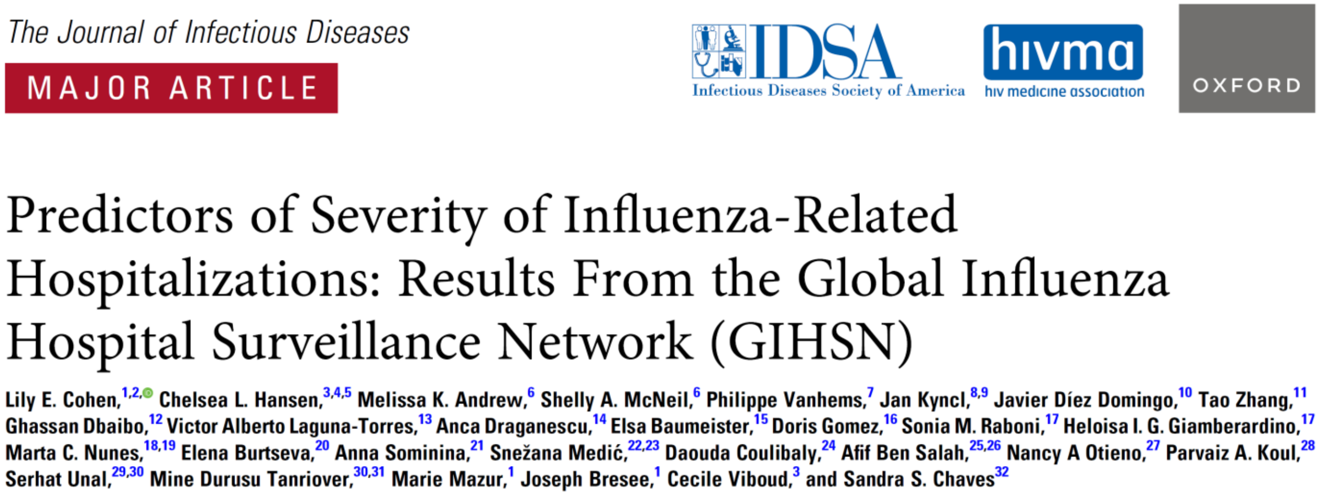
Leveraging the GIHSN network to support disease burden estimation

Chelsea Hansen[1], Sandra Chaves[2], Marta Nunes[3], Cécile Viboud[1]

[1] *Fogarty International Center, National Institutes of Health, USA*
[2] *Foundation for Influenza Epidemiology, Fondation de France, Paris, France.*
[3] *Center of Excellence in Respiratory Pathogens, Universite Claude Bernard, Lyon I, France*

Annual GIHSN Meeting, Geneva, Nov 16-17, 2023

Previous work: Comparing influenza severity across settings

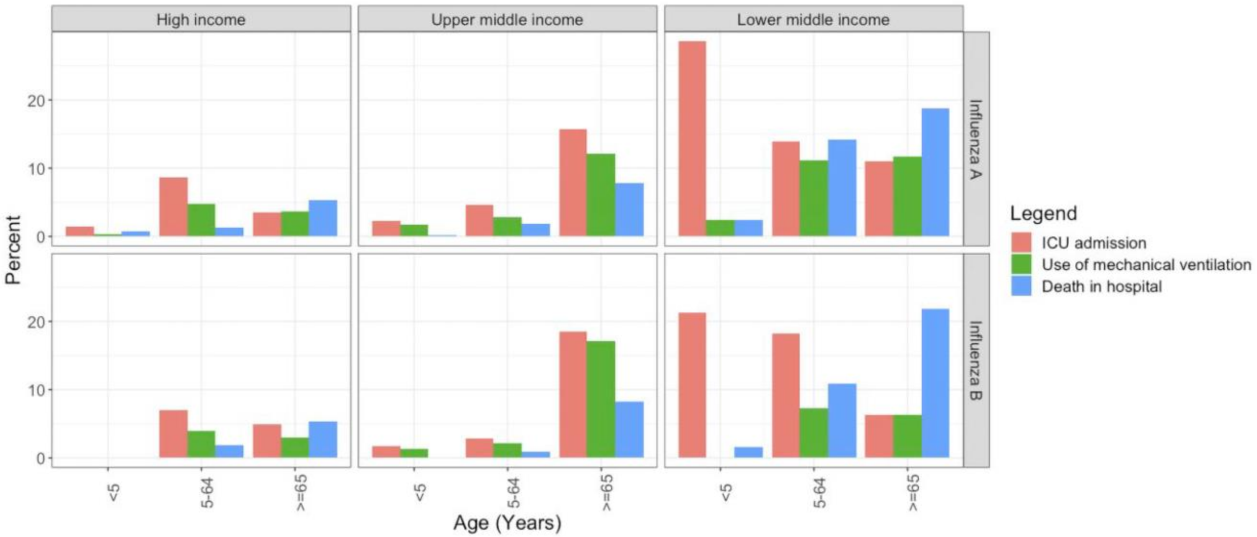


The Journal of Infectious Diseases

MAJOR ARTICLE

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

Lily E. Cohen,[1,2] Chelsea L. Hansen,[3,4,5] Melissa K. Andrew,[6] Shelly A. McNeil,[6] Philippe Vanhems,[7] Jan Kyncl,[8,9] Javier Díez Domingo,[10] Tao Zhang,[11] Ghassan Dbaibo,[12] Victor Alberto Laguna-Torres,[13] Anca Draganescu,[14] Elsa Baumeister,[15] Doris Gomez,[16] Sonia M. Raboni,[17] Heloisa I. G. Giamberardino,[17] Marta C. Nunes,[18,19] Elena Burtseva,[20] Anna Sominina,[21] Snežana Medić,[22,23] Daouda Coulibaly,[24] Afif Ben Salah,[25,26] Nancy A Otieno,[27] Parvaiz A. Koul,[28] Serhat Unal,[29,30] Mine Durusu Tanriover,[30,31] Marie Mazur,[1] Joseph Bresee,[1] Cecile Viboud,[3] and Sandra S. Chaves[32]

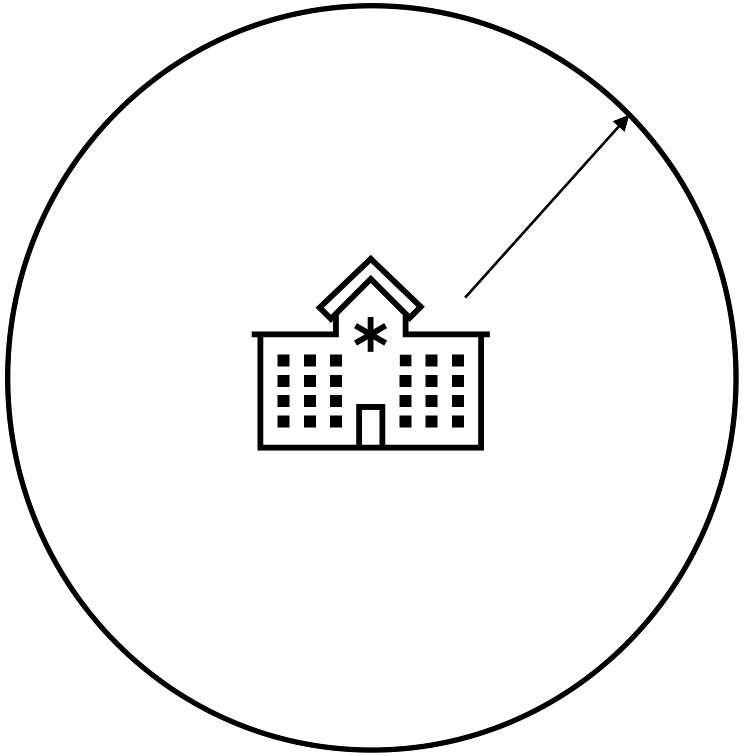


- Previous work from GIHSN demonstrated an increased risk of ICU admission (OR=6.95), mechanical ventilation (OR=3.52), and death (OR=4.02) among patients hospitalized in LMICs compared to high income settings

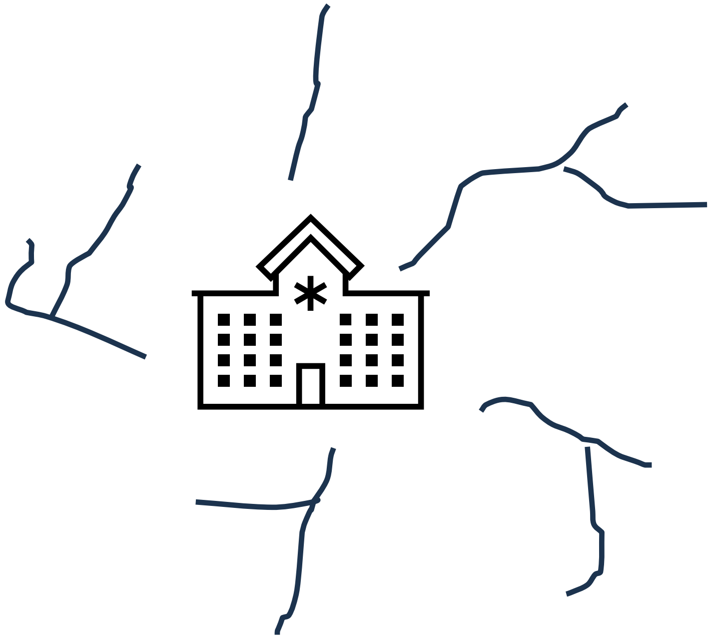
- These data cannot be used to compare disease rates across settings without population denominators

Methods for defining hospital catchment areas

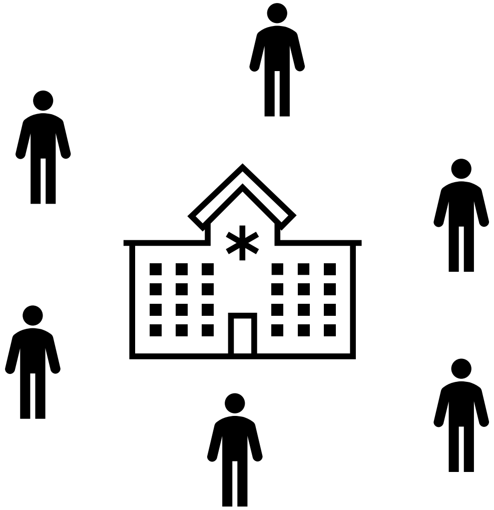
Straight-line distance



Road network distance/travel time



Geo-coded patient residence information



Preferred method!

Theoretical example

Legend

GIHSN Hospital

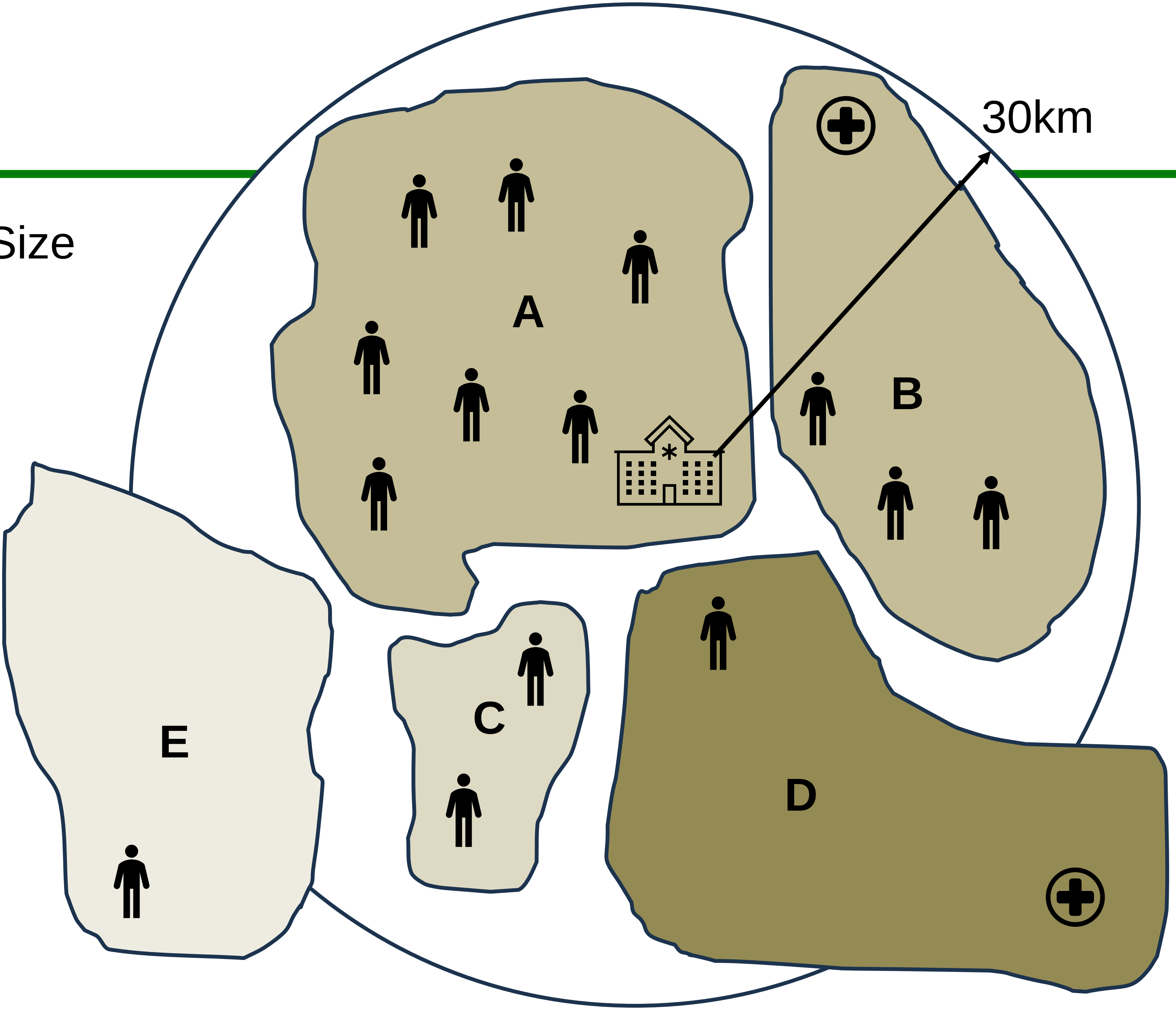
Flu patient seeking care at GIHSN Hospital

Other healthcare facility

Population Size

■	700
▩	500
▨	200
□	100

Overall population: 2000
Observed cases: 14
Crude cumulative case rate: 7 per 1000



Theoretical example: cumulative case ratio method

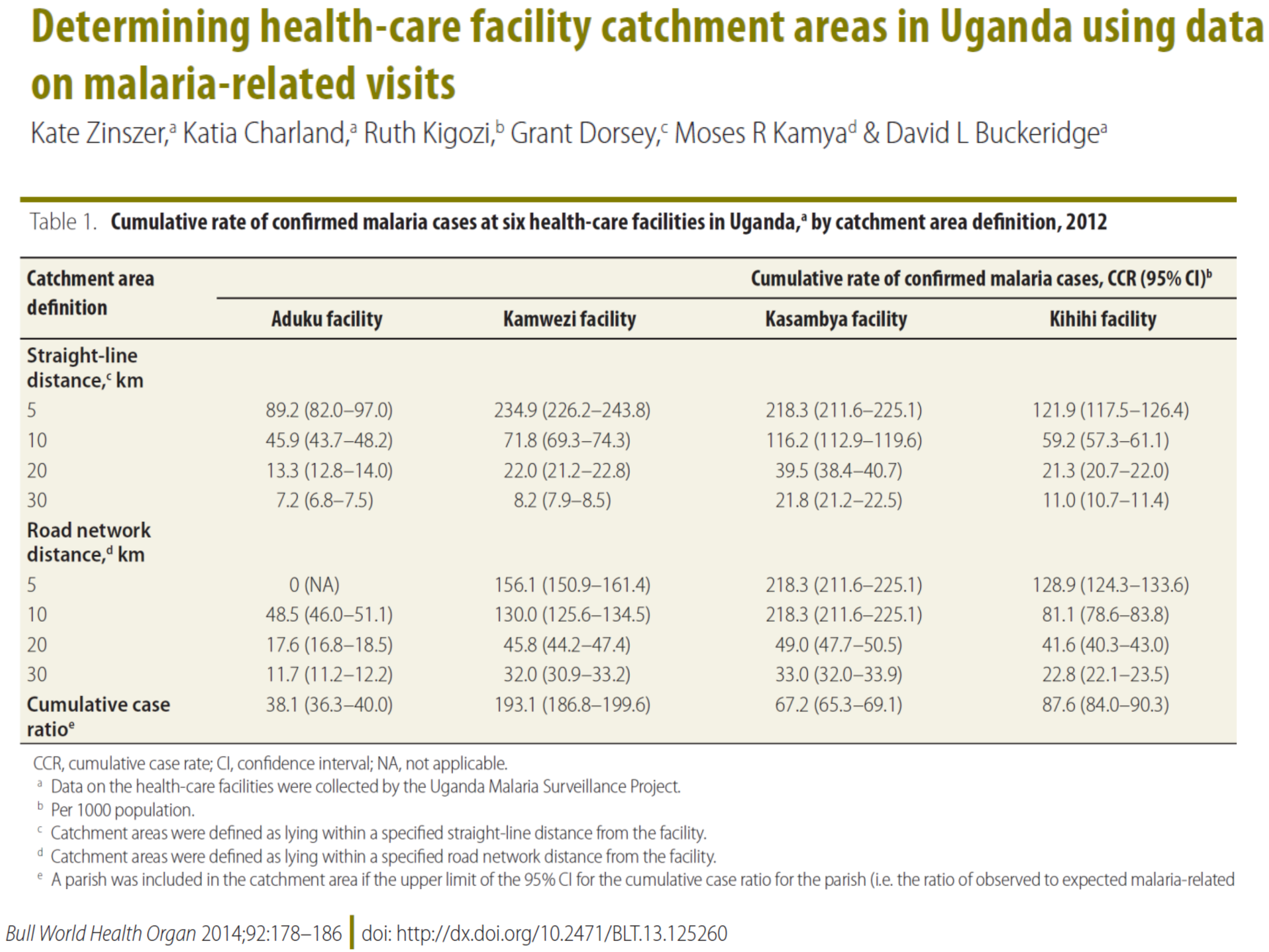
Neighborhood	Population	Observed patients	Expected patients*	Cumulative case ratio (Observed/Expected)	Include in denominator **
A	500	7	3.5	2 (0.8-3.8)	Yes
B	500	3	3.5	0.9 (0.2-2.1)	Yes
C	200	2	1.4	1.4 (0.1-4.1)	Yes
D	700	1	4.9	0.2 (0.0-0.8)	No
E	100	1	0.7	1.7 (0.0-6.5)	Yes

*Based on cumulative case rate for all neighborhoods in 30km radius (7 per 1000)

**Neighborhood is either contributing 0 or 100% of their population to the denominator

Adjusted influenza hospitalization rate = 10 per 1000 population (13/1300)

Catchment area sensitivity to methodology: case study from Uganda



Determining health-care facility catchment areas in Uganda using data on malaria-related visits

Kate Zinszer,[a] Katia Charland,[a] Ruth Kigozi,[b] Grant Dorsey,[c] Moses R Kamya[d] & David L Buckeridge[a]

Table 1. **Cumulative rate of confirmed malaria cases at six health-care facilities in Uganda,[a] by catchment area definition, 2012**

Catchment area definition	Cumulative rate of confirmed malaria cases, CCR (95% CI)[b]			
	Aduku facility	**Kamwezi facility**	**Kasambya facility**	**Kihihi facility**
Straight-line distance,[c] km				
5	89.2 (82.0–97.0)	234.9 (226.2–243.8)	218.3 (211.6–225.1)	121.9 (117.5–126.4)
10	45.9 (43.7–48.2)	71.8 (69.3–74.3)	116.2 (112.9–119.6)	59.2 (57.3–61.1)
20	13.3 (12.8–14.0)	22.0 (21.2–22.8)	39.5 (38.4–40.7)	21.3 (20.7–22.0)
30	7.2 (6.8–7.5)	8.2 (7.9–8.5)	21.8 (21.2–22.5)	11.0 (10.7–11.4)
Road network distance,[d] km				
5	0 (NA)	156.1 (150.9–161.4)	218.3 (211.6–225.1)	128.9 (124.3–133.6)
10	48.5 (46.0–51.1)	130.0 (125.6–134.5)	218.3 (211.6–225.1)	81.1 (78.6–83.8)
20	17.6 (16.8–18.5)	45.8 (44.2–47.4)	49.0 (47.7–50.5)	41.6 (40.3–43.0)
30	11.7 (11.2–12.2)	32.0 (30.9–33.2)	33.0 (32.0–33.9)	22.8 (22.1–23.5)
Cumulative case ratio[e]	38.1 (36.3–40.0)	193.1 (186.8–199.6)	67.2 (65.3–69.1)	87.6 (84.0–90.3)

CCR, cumulative case rate; CI, confidence interval; NA, not applicable.

[a] Data on the health-care facilities were collected by the Uganda Malaria Surveillance Project.

[b] Per 1000 population.

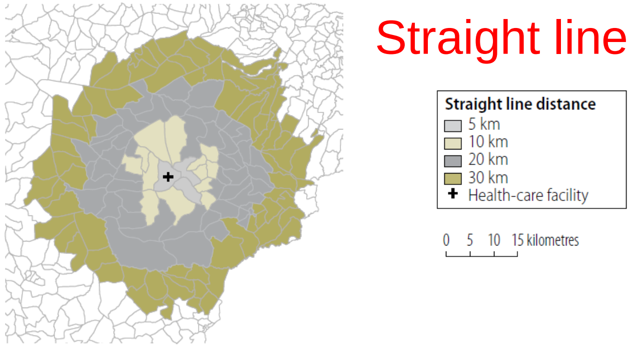
[c] Catchment areas were defined as lying within a specified straight-line distance from the facility.

[d] Catchment areas were defined as lying within a specified road network distance from the facility.

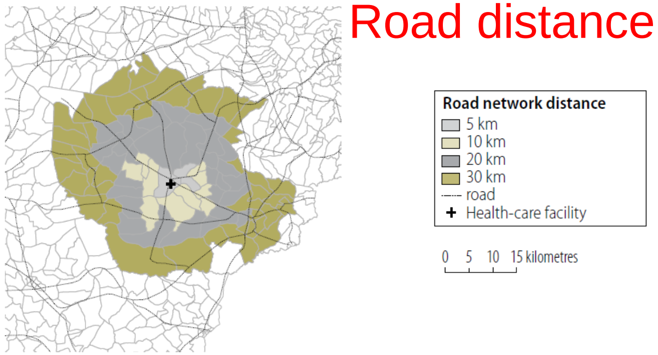
[e] A parish was included in the catchment area if the upper limit of the 95% CI for the cumulative case ratio for the parish (i.e. the ratio of observed to expected malaria-related

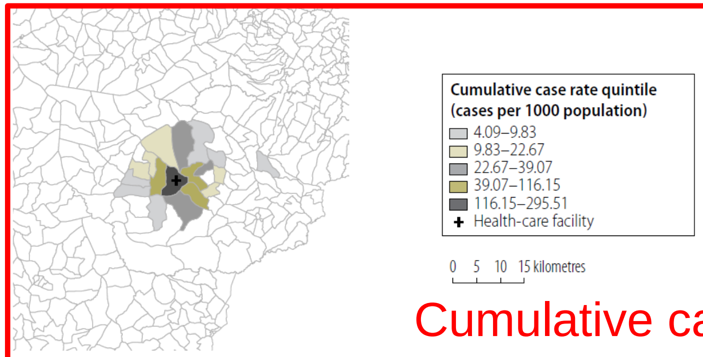
Bull World Health Organ 2014;92:178–186 | doi: http://dx.doi.org/10.2471/BLT.13.125260

Straight line method



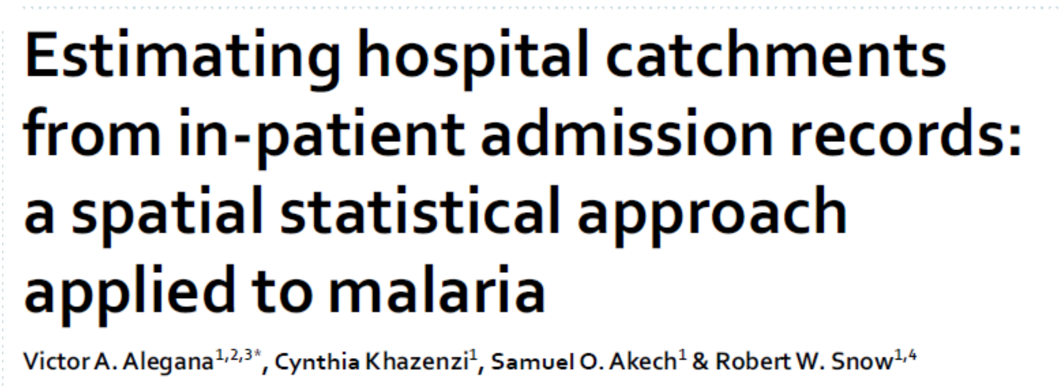
Road distance method





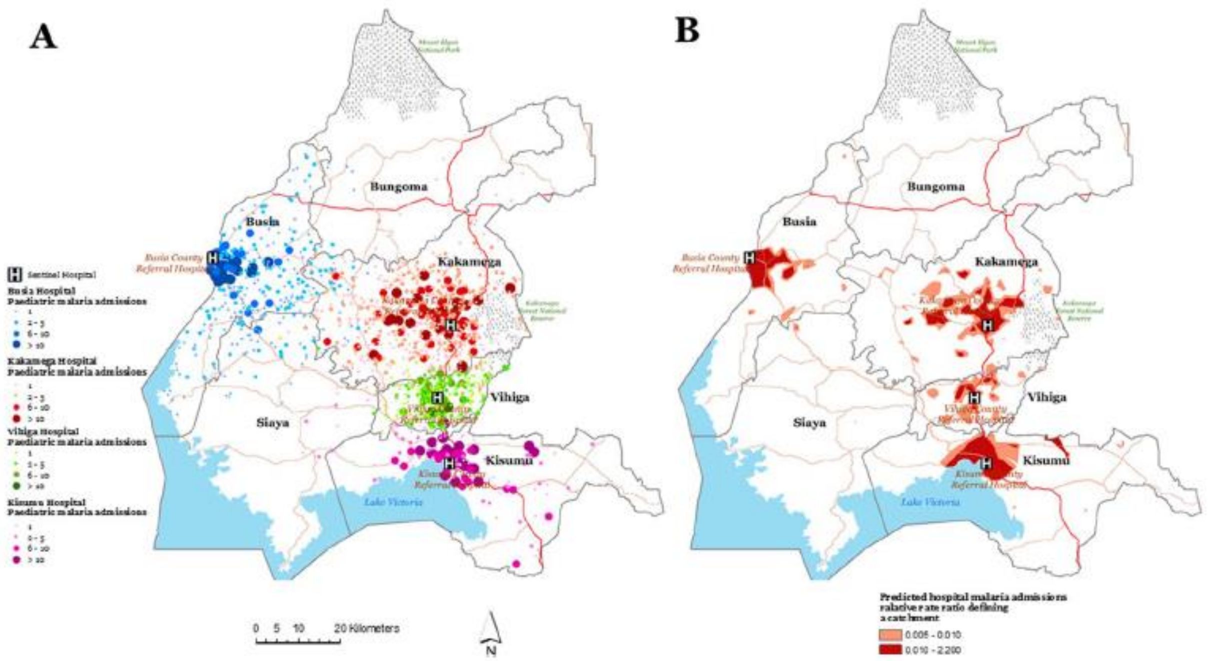
Cumulative case ratio method

Methodological refinements: A case study from Kenya



Estimating hospital catchments from in-patient admission records: a spatial statistical approach applied to malaria

Victor A. Alegana[1,2,3*], Cynthia Khazenzi[1], Samuel O. Akech[1] & Robert W. Snow[1,4]



Scientific Reports https://doi.org/10.1038/s41598-020-58284-0

Limitations in previous methods

- Distance and travel time methods do not consider competition from other hospitals
- Case ratio methods assume uniform care-seeking and disease burden

Methodological refinements

- Bayesian hierarchical zero-inflated Poisson regression implicitly considers hospital competition by including zero counts
- Includes covariate for distance to nearest road to account for accessibility (could include more variables)
- Considers severity of disease
- Highlights strong effect of distance to hospital for milder cases

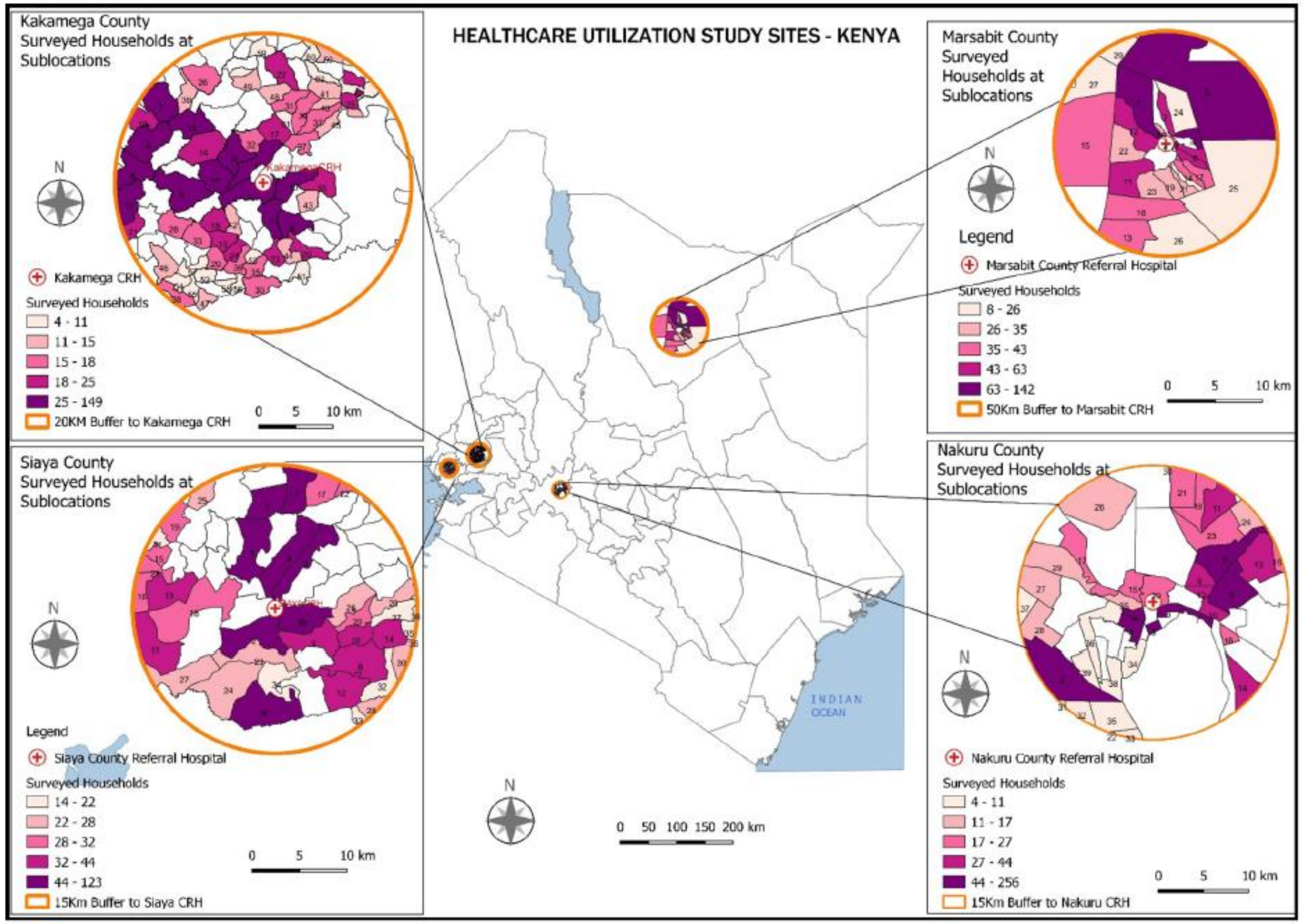
Complimentary Approaches: Healthcare provider surveys (theoretical example)

Ask healthcare providers: What proportion of your patients come from each neighborhood?

	Neighborhood A	Neighborhood B	Neighborhood C	Neighborhood D	Neighborhood E
HC provider 1	85%	10%	3%	0%	2%
HC provider 2	90%	5%	5%	0%	0%
HC provider 3	70%	10%	15%	4%	1%
HC provider 4	75%	13%	10%	2%	0%
Ensemble	80%	10%	7%	2%	1%

Compare this with population size to determine thresholds for inclusion

Complimentary approaches: Healthcare Utilization Surveys (case study)



Emukule *et al. BMC Public Health* (2023) 23:353
https://doi.org/10.1186/s12889-023-15252-3

BMC Public Health

RESEARCH **Open Access**

Healthcare-seeking behavior for respiratory illnesses in Kenya: implications for burden of disease estimation

Gideon O. Emukule[1*], Eric Osoro[2], Bryan O. Nyawanda[3], Isaac Ngere[2], Daniel Macharia[1], Godfrey Bigogo[3], Nancy A. Otieno[3], Sandra S. Chaves[1,4], M. Kariuki Njenga[2] and Marc-Alain Widdowson[1,5]

- 2018 survey of households
- Reported which hospital they went to, if any (competition)
- Hospital-based surveillance captures less than one quarter of severe pneumonia in the community

Planned activities: estimate catchment areas, and influenza disease rates, for select GISHN hospitals

- The current pilot project has 4 aims
    1. Build catchment areas around the GISHN sites in Kenya, South Africa, and Lebanon to estimate population denominators
    2. Estimate distance and travel-time to GIHSN sites for the catchment area populations
    3. Estimate influenza hospitalization rates and in-hospital mortality rates from 2017-2024
    4. Identify how care-seeking behavior and catchment areas may differ based on disease severity and patient age or have changed because of the COVID-19 pandemic

Data requirements

Data	Details	Source
Residence location* information for patients included in the GIHSN database	Individual-level; linked to GIHSN database	GIHSN sites
Residence location* information for all patients with respiratory symptoms	Aggregated by age, geographic unit, and season	GIHSN sites
Population estimates from all geographic units included in the catchment area	Smallest geographic unit available	Census data (where available); WorldPop

Ideally for all years for which the hospital has contributed surveillance data to GISHN

*exact address is not required, fine-scale administrative units (neighborhood, village, etc.) would be sufficient

Questions for sites and open discussion (1/2)

- Would other hospitals beyond Lebanon, Kenya and South Africa be interested in participating/have the necessary patient residence location? Could we do this in a few HIC and LMIC sites?

- How is patient residence location captured in your hospital?
- What is the proportion of missing patient locations?
- What is the smallest administrative unit in your country?
- Can patient location be connected to GISHN records?
- How would you be able to share the data for analysis?

Questions for sites and open discussion (2/2)

- Have other hospitals conducted healthcare utilization surveys?

- Would hospital physicians and nurses be amenable to a survey of patient locations?

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ANNUAL MEETING, 16 NOVEMBER 2023

THE SEVSCALE PROJECT

Bronke BOUDEWIJNS, Nivel

Foundation for
Influenza
Epidemiology

Sous l'égide de

Fondation
de
France

SevScale project

GIHSN Meeting, 16 November 2023

NIVEL
Kennis voor betere zorg

Bronke Boudewijns

In memory of dr. John Paget

Introduction

- Currently there is no classification of severity in hospitalized influenza patients
- Work led by prof. **Bruno Lina:** oxygen supplementation more common in certain lineages/clades

  → Severity clusters in these lineages/clades

- Need for a severity score that takes into account more aspects of severity
- Attaching a severity score to sequence information could help in strain selection

Fig 3: Phylogenetic tree of the H3N2 viruses analyzed between 1st of September 2022 and 1st of February 2023.
Cases requiring oxygen supplementation are in yellow. Red squares indicate increased cases with oxygen supplementation.

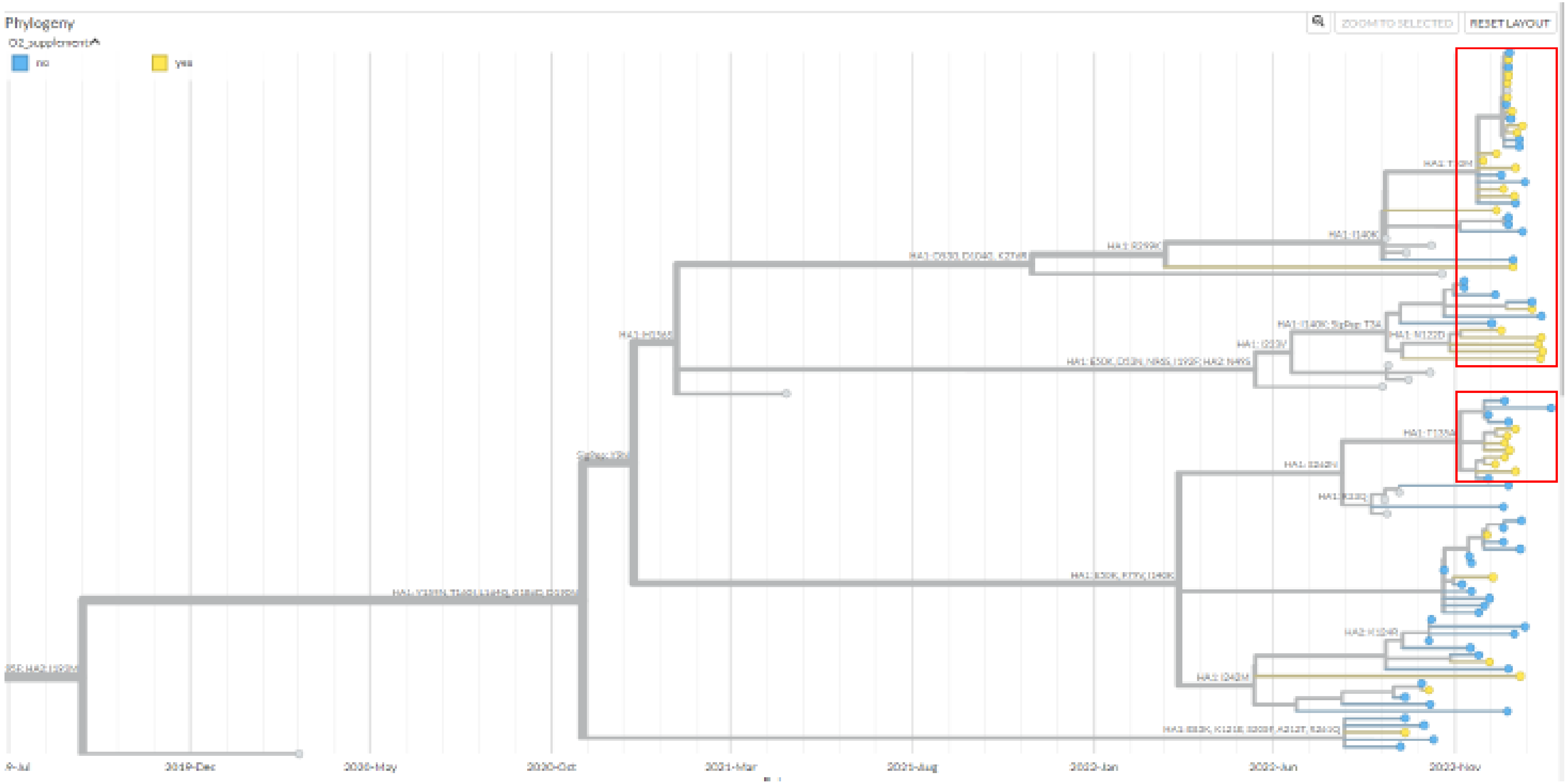
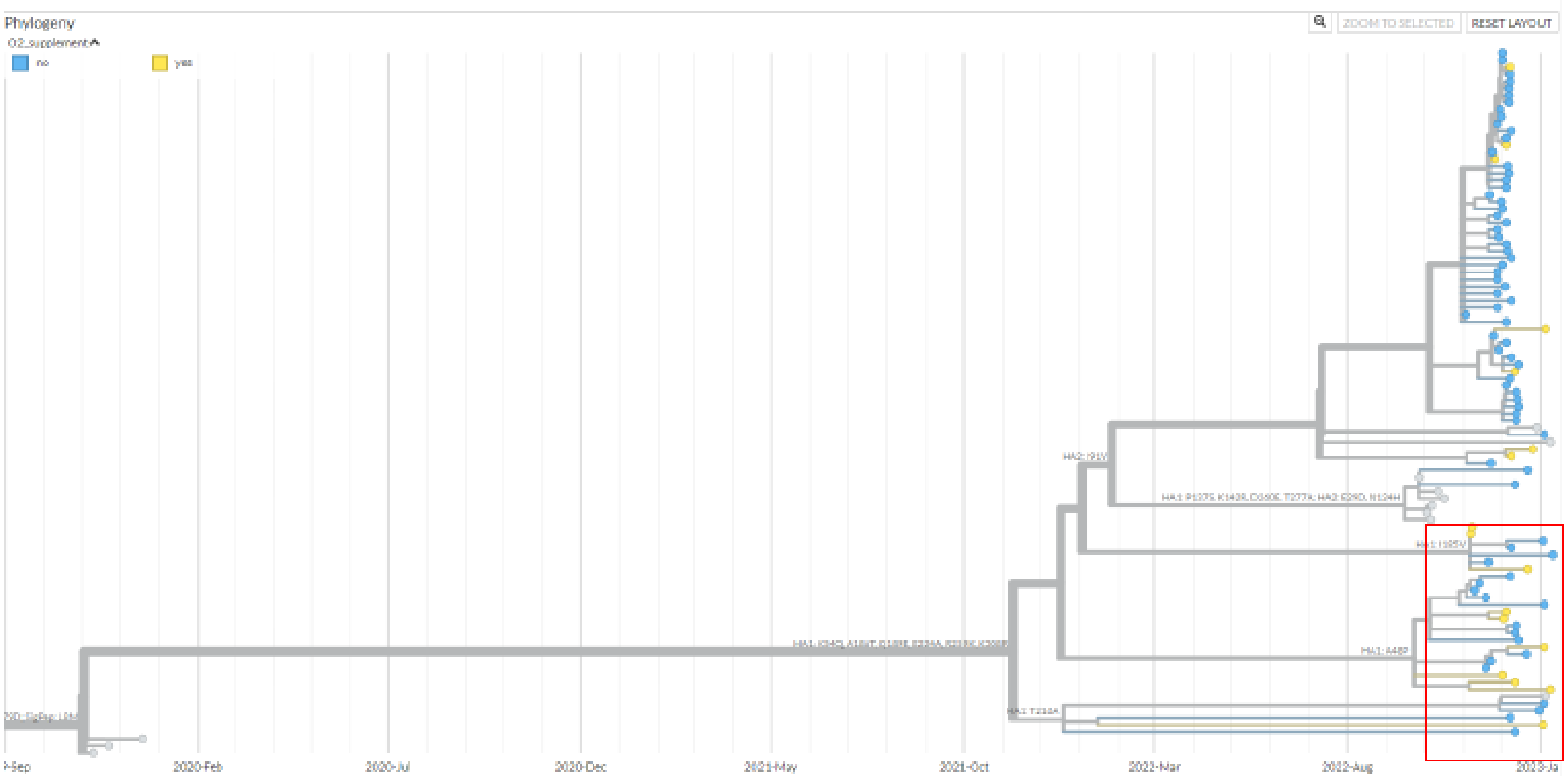


Fig 2: Phylogenetic tree of the H1N1pdm09 viruses analyzed between 1st of Sept 2022 and 1st of Feb 2023.

Cases requiring oxygen supplementation are in yellow. Red square indicates increased cases with oxygen supplementation



Research question

Retrospective analysis of the GIHSN database which uses advanced statistical methods to establish an age-specific **Severity Scale** for the **influenza-positive hospitalized patients** collected in the GIHSN project

Countries

Income group	Country	Number of seasons (seasons*)	WHO transmission zone
High income	Spain	11 (2012/13 – 2022/23)	South West Europe
	Canada	5 (2017/18 – 2021/22)	North America
Upper middle income	Russia	11 (2012/13 – 2022/23)	Eastern Europe
	Türkiye	9 (2012/13 – 2016/17 & 2019/20 – 2022/23)	Western Asia
	Brazil	5 (2018/19 – 2022/23)	Tropical South America
	South Africa	5 (2016/17 – 2021/22)	Southern Africa
Lower middle income	India	8 (2015/16 – 2022/23)	Southern Asia
	Kenya	6 (2017/18 – 2022/23)	Eastern Africa
	Côte d’Ivoire	6 (2017/18 – 2022/23)	Western Africa

* For season 2022/23 data until week 3-2023 are included

Severity indicators

- 16 indicators for severity included from GIHSN database
  - Measured at admission, during stay and at discharge

- High percentage of missing data
  - Varies between subgroups of cases

- Indicators measured during hospital stay were reported most frequently

- Change of methods → **more general model** using **all cases** in the dataset and **all ages**

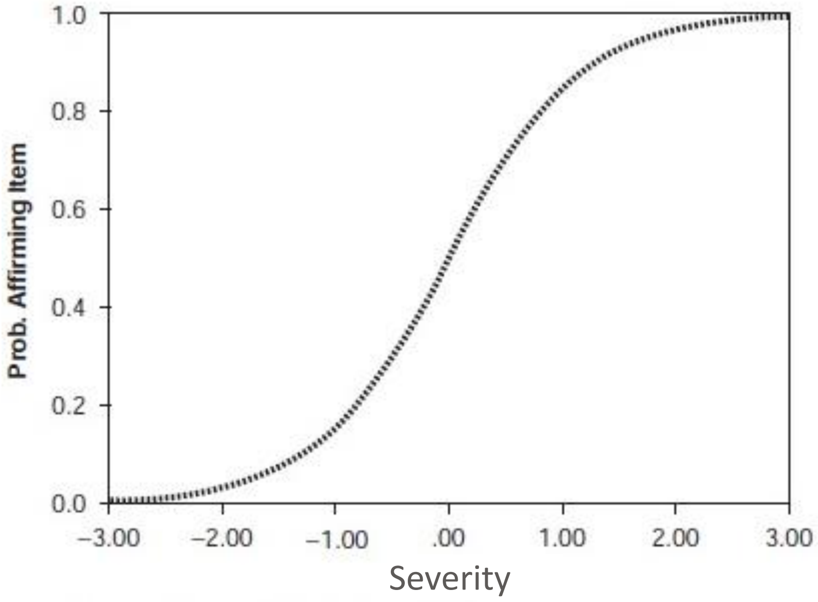
Severity indicator	% complete all cases	% complete influenza positive
ICU admission	71%	99%
Mechanical ventilation	62%	88%
Length of stay	69%	100%
Death while hospitalized	71%	99%

Chronic conditions

Condition	% complete all cases	% complete influenza positive
Cardiovascular disease	57%	84%
diabetes	57%	84%
COPD	55%	84%

Model development

- We used an Item Response Model
- 16 severity variables as items
- Probability model
- The model produces estimates for each item
- Rarer items are indicative of higher severity



Model application

- The systematic effects from the items are combined into one latent Severity Score
- Higher score = more severe
- Not all items have to be reported

→ Less information will result in a score closer to the mean

Distribution of model scores

N-cases	104,372
Mean	-1.974
Standard Deviation	0.634
Percentile 1%	-2.827
Percentile 5%	-2.668
Percentile 25%	-2.275
Percentile 50%	-2.254
Percentile 75%	-1.602
Percentile 95%	-0.690
Percentile 99%	0.313

Severity categories + comparison of subgroups

Low	50,420 (48.3%)
Medium	27,875 (26.7%)
High	26,077 (25.0%)

Flu positive			
	Low	Medium	High
No	14,344 (38.9%)	11,977 (32.5%)	10,531 (28.6%)
Yes	12,497 (58.8%)	5,033 (23.7%)	3,732 (**17.6%**)

Age group			
	Low	Medium	High
00-04	20,404 (52.4%)	11,799 (30.3%)	6,768 (17.4%)
05-17	4,462 (56.9%)	2,204 (28.1%)	1,173 (15.0%)
18-49	9,861 (52.5%)	5,319 (28.3%)	3,602 (19.2%)
50-64	3,981 (38.5%)	2,535 (24.5%)	3,832 (**37.0%**)
65+	11,701 (41.2%)	6,010 (21.2%)	10,677 (**37.6%**)

Comparing subgroups

Chronic conditions			
	Low	Medium	High
None	32,337 (54.3%)	17,882 (30.0%)	9,377 (15.7%)
One	8,902 (44.3%)	5,169 (25.7%)	6,023 (30.0%)
Two or more	9,181 (37.2%)	4,824 (19.5%)	10,677 (43.3%)

Income level country			
	Low	Medium	High
High income	17,990 (48.1%)	8,365 (22.3%)	11,085 (29.6%)
Upper middle income	28,204 (54.6%)	15,135 (29.3%)	8,328 (16.1%)
Lower middle income	4,226 (27.7%)	4,375 (28.7%)	6,664 (43.7%)

Were we too ambitious?

- We still think it is a good idea
- It certainly requires more work
- It could be applied to other databases
- The project will be handed over to Prof Marta Nunes’ group at the University of Lyon to take this forward

Expert group

- **Prof Marta Nunes**, University of Lyon, France [Chair of GISHN]
- **Prof Bruno Lina**, University of Lyon, France [Virologist responsible for the sequencing of GISHN specimens]
- **John McCauley**, Worldwide Influenza Centre, The Francis Crick Institute, London, UK [Virologist]
- **Prof Melissa Andrew,** Dalhousie University and Canadian Center for Vaccinology, Halifax, Canada [clinician who has developed a Severity Score for Canada]
- **Prof Henrique Pott**, Dalhousie University and Canadian Center for Vaccinology, Halifax, Canada & Department of Medicine, Universidade Federal de São Carlos, São Carlos, Brazil [clinician who has developed a Severity Score for Canada]
- **Prof Justin Ortiz**, University of Maryland, USA [clinician, epidemiologist and expert]
- **Prof Oana Sandalescu**, National Institute for Infectious Diseases "Prof. Dr. Matei Bals", Bucharest, Romania [clinician, epidemiologist and contact person for validation exercise]
- **Sandra Chaves**, Foundation for Influenza Epidemiology, Fondation de France, Paris, France [Epidemiologist, expert and funder of SevScale]

COFFEE BREAK

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GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

COLLABORATION WITH WHO

Moderators: Wenqing ZHANG, WHO & Cédric MAHE, FIE

Foundation for
Influenza
Epidemiology

- -Jean-Michel HERAUD, WHO
- -Magdi SAMAAN, WHO
- -Stefano TEMPIA, WHO

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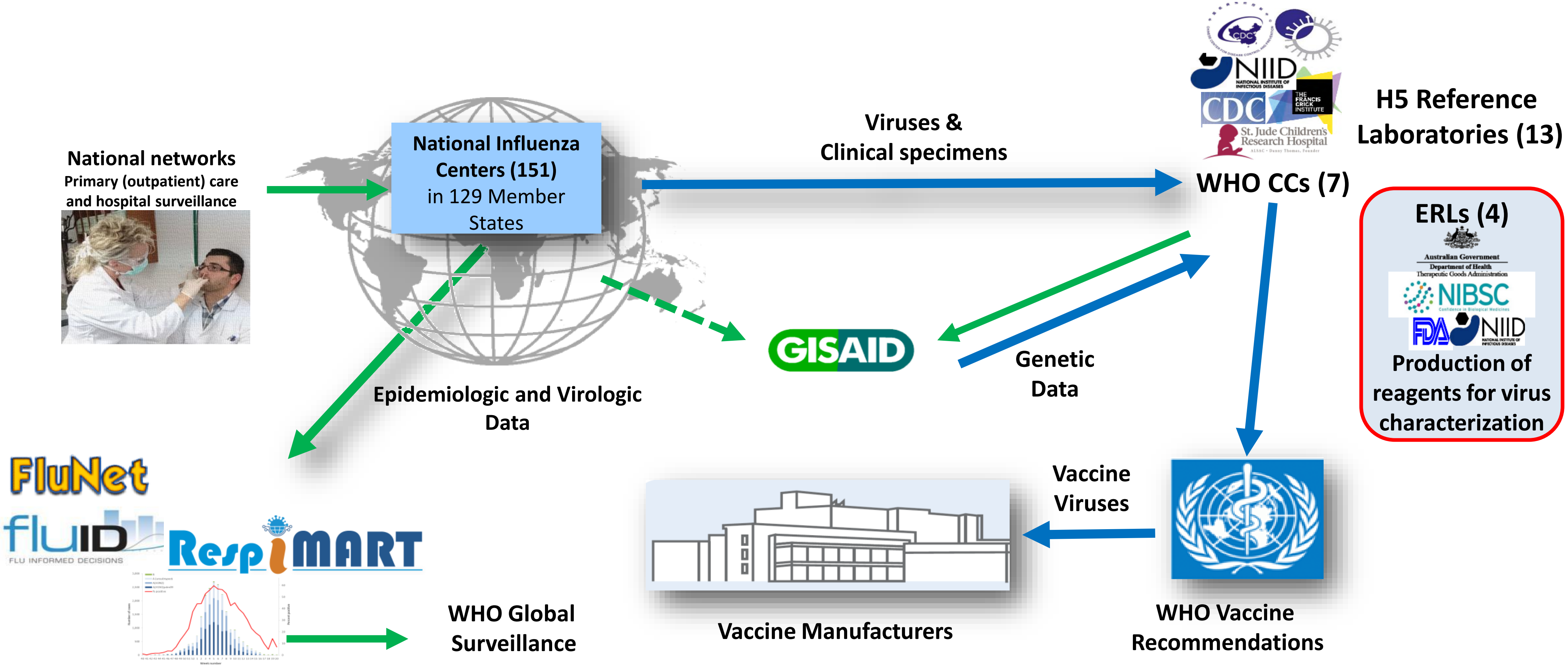
GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

VIRUS CO-CIRCULATION AND ALERT MECHANISMS

Jean Michel HERAUD, WHO, GIP

Foundation for
Influenza
Epidemiology

Influenza surveillance within GISRS (and e-GISRS)



National networks
Primary (outpatient) care
and hospital surveillance

National Influenza Centers (151)
in 129 Member States

Viruses & Clinical specimens

WHO CCs (7)

H5 Reference Laboratories (13)

ERLs (4)

Production of reagents for virus characterization

Epidemiologic and Virologic Data

Genetic Data

Vaccine Viruses

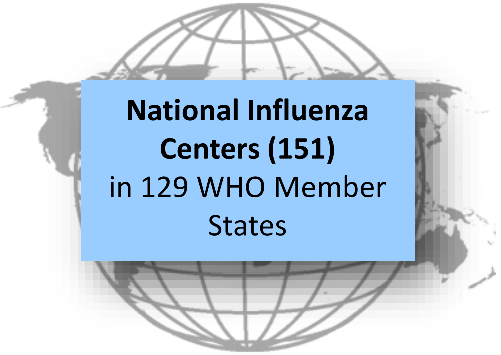
WHO Global Surveillance

Vaccine Manufacturers

WHO Vaccine Recommendations

[Adapted from Belinda Herring and WHO Collaborating Centre for Surveillance, Epidemiology and Control of Influenza at the US CDC, courtesy of Jacqueline Katz]

GISRS in Numbers



National Influenza Centers (151)
in 129 WHO Member States

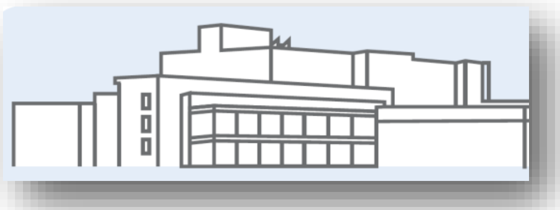
Viruses &
Clinical specimens

WHO CCs

- Monitoring of emerging strains, antiviral assessment
- Risk Assessment
- Management
- WHO CVV recommendations for vaccine composition
- NIC's have access to many GISRS benefits

WHO Vaccine Recommendations

Vaccine Viruses



Vaccine Manufacturers

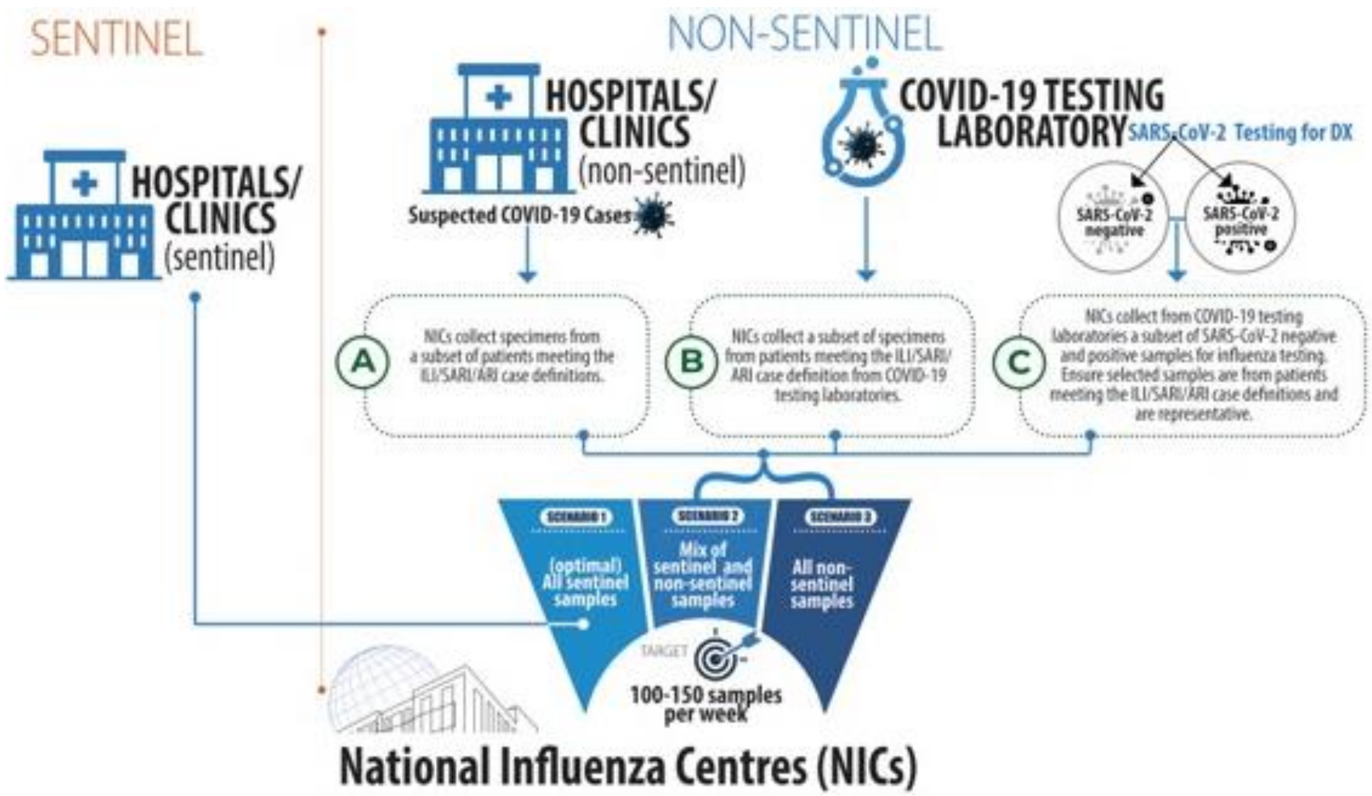
Globally NICs processed between 16 to 19 million specimens per year for influenza from sentinel sites. (2015 to 2019)

An average of 400,000 to 800,000 specimens are reported as positive for influenza each year

In 2022, influenza labs shared approximately 40,000 influenza virus isolates and/or influenza virus-positive clinical specimens with WHO CCs.

[Adapted from Belinda Herring and WHO Collaborating Centre for Surveillance, Epidemiology and Control of Influenza at the US CDC, courtesy of Jacqueline Katz]

GISRS and SARS-CoV-2 integration



A NICs collect specimens from a subset of patients meeting the ILI/SARI/ARI case definitions.

B NICs collect a subset of specimens from patients meeting the ILI/SARI/ARI case definition from COVID-19 testing laboratories.

C NICs collect from COVID-19 testing laboratories a subset of SARS-CoV-2 negative and positive samples for influenza testing. Ensure selected samples are from patients meeting the ILI/SARI/ARI case definitions and are representative.

178 MS implemented integrated surveillance

- 129 MS with NICs (as of November 2023)
- 49 MS with NICs-to-be

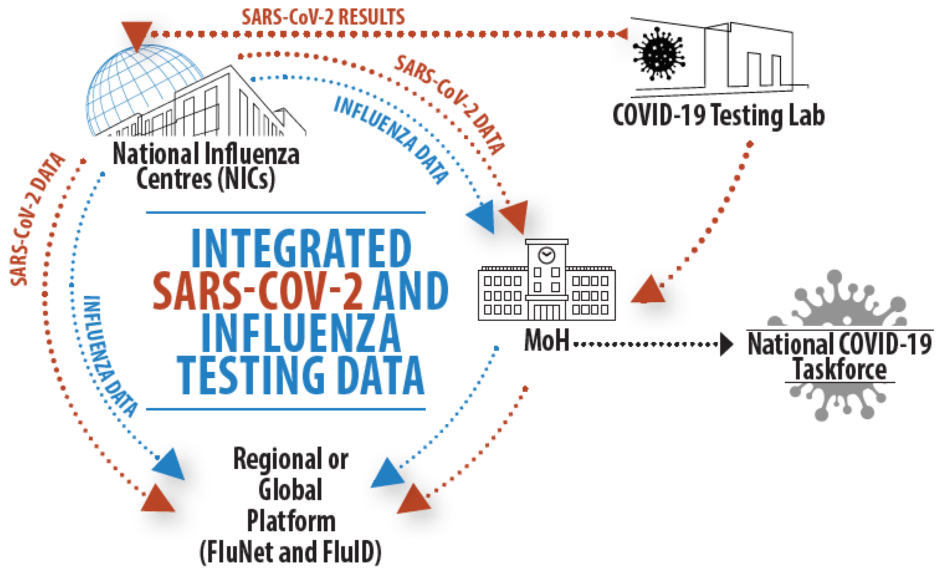
Challenges

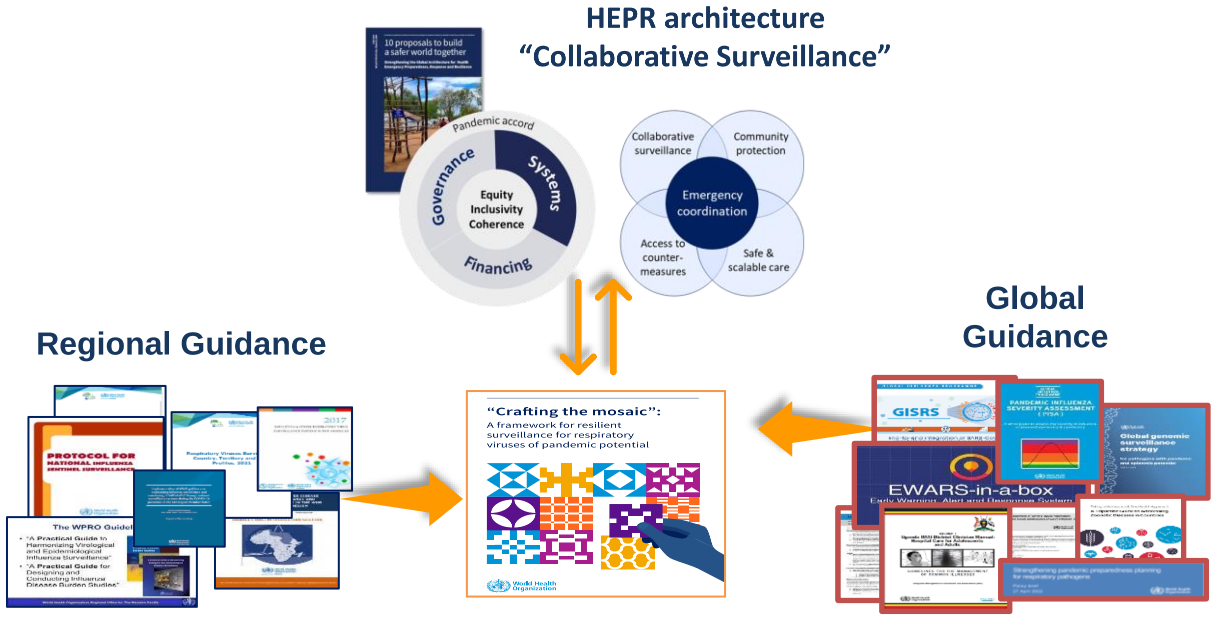
- Adequacy, consistency and timeliness of reporting
- Human resources, sequencing and bioinformatics capacities
- Interpret data in the context of a multi-pathogens surveillance

Ways for improvement

- Linkages with non-sentinel and event-based surveillance,
- Strengthen collaborations with animal and private sector

Integrated surveillance – GISRS in the context of the global surveillance landscape





Expanding GISRS activities beyond influenza envisions

- **An end-to-end integration surveillance package (screening, testing, reporting, sequencing, sharing, risk assessment, response) for influenza and other priority respiratory viruses**
- **Multisource surveillance for an improved risk assessment and response**
- **Aligns with and is a critical player in collaborative surveillance and public health intelligence**

Discussions

1. Access and use of clinical data in the context of national/regional/global surveillance aligned with personal data protection regulations (ex GDPR in EU)

2. Leverage case-based surveillance (and event-based surveillance)

3. Interoperability of data collected between GISHN and RespiMART

4. Uses of GISHN network:
    - During a pandemic (early data on clinical severity, hospital fatality proportion)
    - Clinical interventions
    - Provide signal of risk factors for severe disease, antiviral resistance…

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COMBINATION OF SEVERITY AND WGS FOR STRAIN SELECTION

Dr Wenqing Zhang, Dr Magdi Samaan, WHO, GIP

Foundation for
Influenza
Epidemiology

World Health Organization

GISRS and GIHSN Collaboration

- contribution to vaccine virus selection

Dr Wenqing Zhang
Dr Magdi Samaan
Global Influenza Programme

GIHSN Global Annual Meeting 2023
16-17 November 2023, Salle V WHO

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

Influenza vaccine strain selection

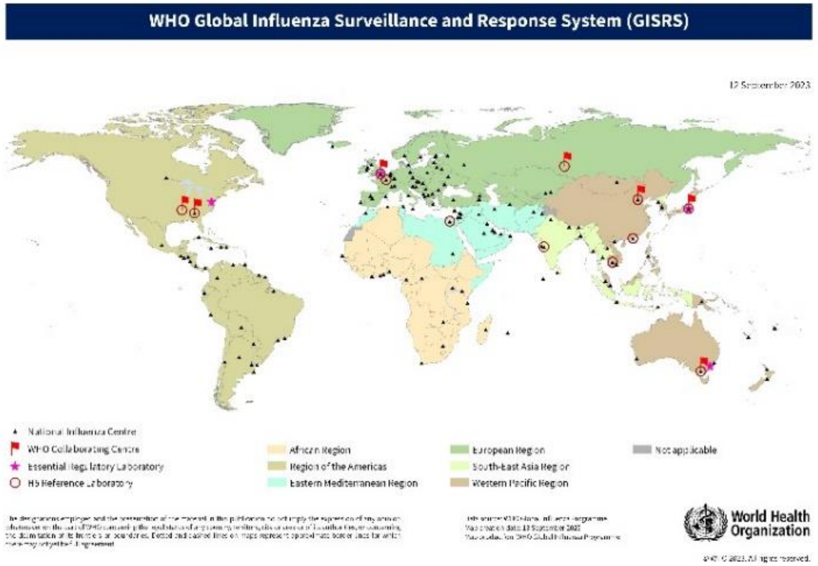
Twice each year WHO makes recommendations on influenza vaccines

mid-February for the Northern Hemisphere

mid-September for the Southern Hemisphere

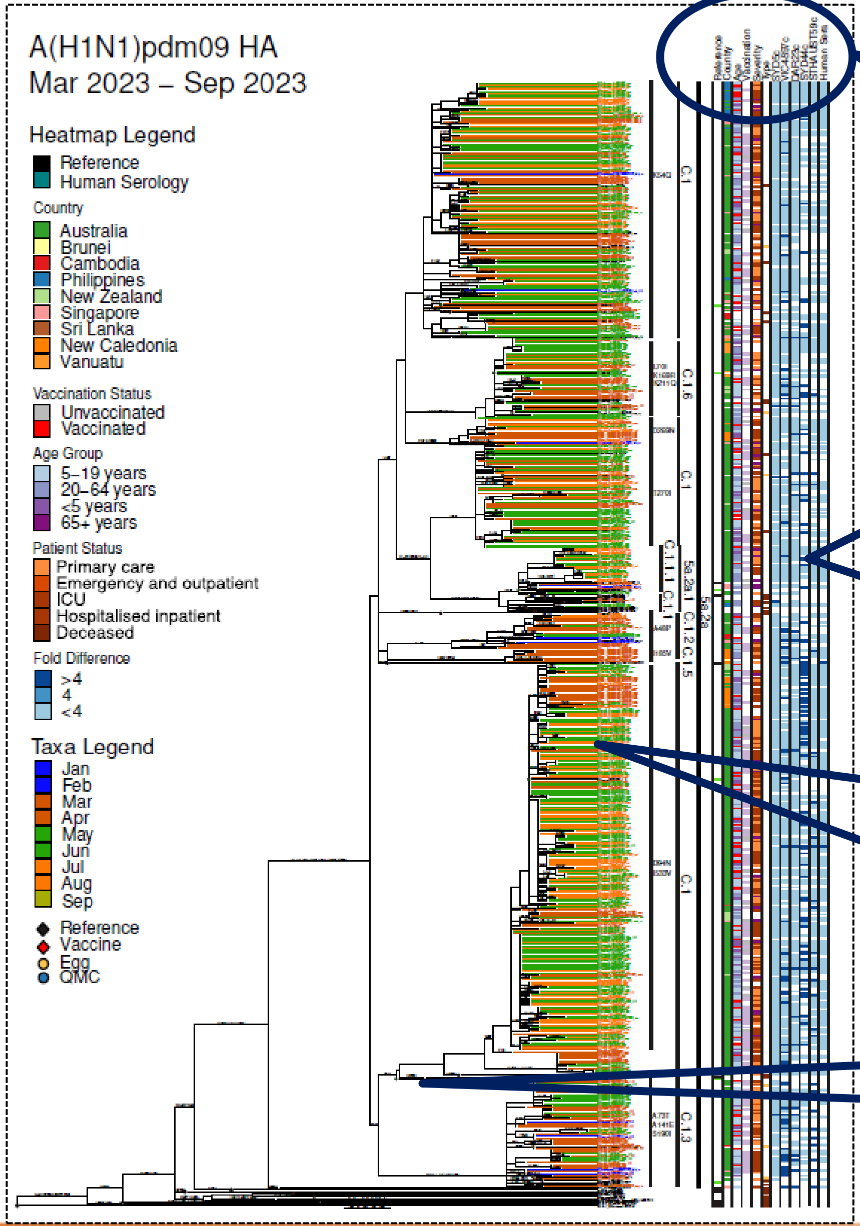
**timely sharing of clinical samples, viruses,
gene sequence data, epidemiological surveillance data year-round**

- Surveillance data: virus surveillance complemented with epidemiologic and clinical findings
- Antigenic characterization of viruses
- Human serology studies with influenza virus vaccines
- Genetic characterisation of viruses
- Virus fitness forecasting
- Antiviral resistance
- Vaccine effectiveness
- Availability of CVVs


WHO Global Influenza Surveillance and Response System (GISRS)

12 September 2023

Influenza vaccine strain selection



Reference
Country
Age
Vaccination
Severity
Type
SYD5c
VIC4897c
DAR23c
SYD44c
STHAUST59c
Human Sera

Country
- 🟩 Australia
- 🟨 Brunei
- 🟥 Cambodia
- 🟦 Philippines
- 🟩 New Zealand
- 🟥 Singapore
- 🟫 Sri Lanka
- 🟧 New Caledonia
- 🟧 Vanuatu

Fold Difference
- 🟦 >4
- 🟦 4
- 🟦 <4

Taxa Legend
- 🟦 Jan
- 🟦 Feb
- 🟧 Mar
- 🟧 Apr
- 🟩 May
- 🟩 Jun
- 🟧 Jul
- 🟧 Aug
- 🟩 Sep

- ◆ Reference
- ◆ Vaccine
- ● Egg
- ● QMC

Vaccination Status
- ⬜ Unvaccinated
- 🟥 Vaccinated

Age Group
- 🟦 5–19 years
- 🟦 20–64 years
- 🟪 <5 years
- 🟪 65+ years

Patient Status
- 🟧 Primary care
- 🟧 Emergency and outpatient
- 🟫 ICU
- 🟫 Hospitalised inpatient
- 🟫 Deceased

From data package of VIDRL for VCM Sept 2023

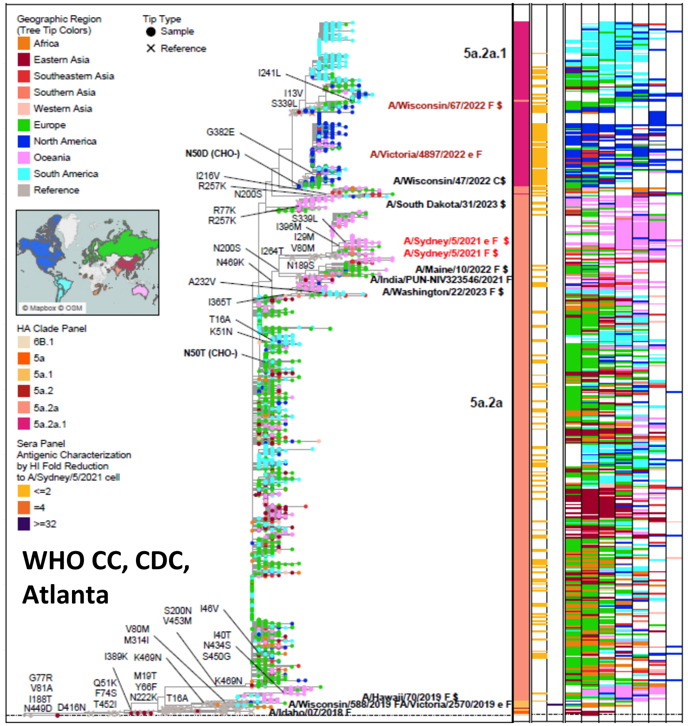
Scales of virus detections *(as of 10 July)*

of influenza B virus surveillance

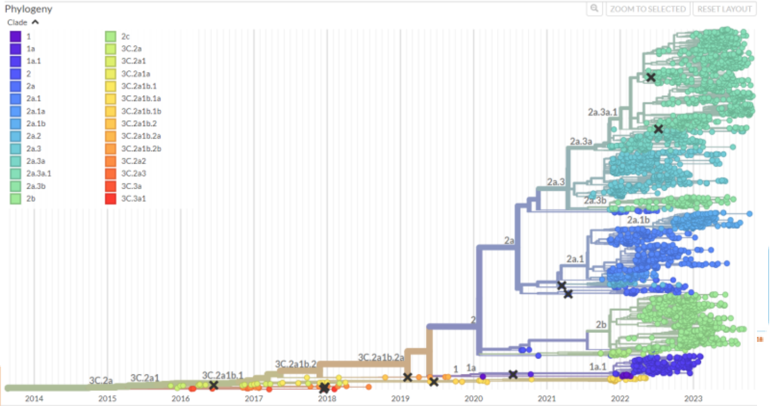
Year	Number of B virus detections			
	Total of B detections	B-Yam detections	B-Vic detections	of B viruses with lineage differentiated
2020	168,301	364	25,531	15%
2021	33,994	42	29,058	86%
2022	62,735	7	34,616	55%
2023	107,600	2	15,336	14%

WGS in influenza surveillance

- **Explain & complement** results of **antigenic** characterization
- Monitoring **antiviral resistance**
- Support **risk assessment** of zoonotic influenza viruses: mammalian adaptation, disease severity, virus origin, evolution (LPAI to HPAI; clade diversity etc.
- Seasonal influenza **vaccine strain** selection
- Markers for **disease severity**
- **Prediction** of virus evolution in terms of natural selection process
- Genomic surveillance – tailored to **public health objectives**



WHO CC, CDC, Atlanta



Discussions

- **Alert** of suspected clusters, especial with severe outcome or exposure to poultry/birds
- **Representative sampling** if not comprehensive sampling

- Contribution from GIHSN to **VCM and beyond**
  - **Timely** generating & reporting **data & viruses**
  - **“Comprehensive” data** attached to each virus specimen to WHO CCs
    - Clinical severity, vaccination history, antiviral use etc.
  - “**Comprehensive” data** for viruses outside of routine surveillance (clinical data including severity to GSD), and share with VCM committee
  - **Lineage** typing for all B virus detections
  - **Sequential/serial sampling** from patients suspected of antiviral resistance and sequence data
  - Human **serum panels**?
  - **Sites** for specific influenza surveillance and pandemic preparedness and response

Thank You

World Health
Organization

Global Influenza
Hospital Surveillance
Network

www.gihsn.org

coordination

IMPACT
Healthcare

GIHSN 11TH ANNUAL MEETING, 16-17 NOVEMBER 2023

BURDEN OF DISEASE ESTIMATION

Stefano Tempia, WHO, GIP

Foundation for
Influenza
Epidemiology

WHO Burden of Disease Pillar under the Pandemic Influenza Preparedness (PIP) Framework

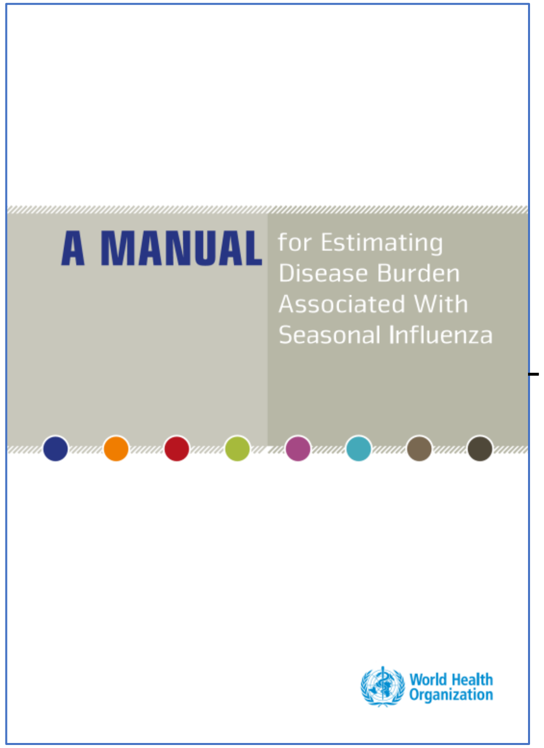
Stefano Tempia

WHO Global Influenza Programme

World Health Organization

Influenza BoD Estimation

BoD Manual



A MANUAL for Estimating Disease Burden Associated With Seasonal Influenza

World Health Organization

Incidence and number of cases

Focus on influenza-associated SARI hospitalization using surveillance data

(robust surveillance data for ≥3 years are needed)

Examples

Chile

ORIGINAL ARTICLE

WILEY

Estimating the burden of influenza-associated hospitalizations and deaths in Chile during 2012-2014

Viviana Sotomayor[1] | Rodrigo A. Fasce[2] | Natalia Vergara[1] | Felipe De la Fuente[1] | Sergio Loayza[1] | Rakhee Palekar[3]

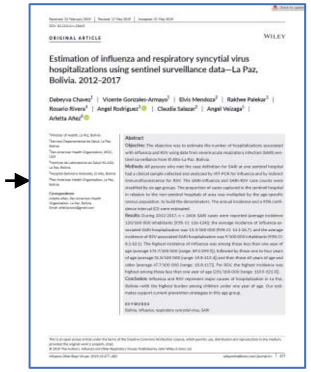
Guatemala

BMC Public Health

RESEARCH Open Access

Hospitalization and death among patients with influenza, Guatemala, 2008–2012

Bolivia



ORIGINAL ARTICLE

WILEY

Estimation of influenza and respiratory syncytial virus hospitalizations using sentinel surveillance data—La Paz, Bolivia. 2012–2017

Dabeyva Chavez[1] | Vicente Gonzales-Armayo[1] | Elvis Mendoza[2] | Rakhee Palekar[3] | Rosario Rivera[4] | Angel Rodriguez[3] | Claudia Salazar[2] | Angel Veizaga[5] | Arletta Añez[6]

New Chapters (3):

- **Extrapolating from base (e.g. sentinel sites/governorate) to national estimates**
- **Estimation of RSV and SARS-CoV-2 BoD**
- **Estimation of the BoD averted through immunization**

Influenza BoD Estimation

From Country-Specific to regional/Global Estimates

Country-Specific Estimates

Regional/Global Estimates

Estimation of influenza and severe acute respiratory illness incidence (burden) in three provinces of the Islamic Republic of Iran, 2012 and 2013

Incidence of influenza virus-associated severe acute respiratory infection in Damanhour district, Egypt, 2013

The national and provincial burden of medically attended influenza-associated influenza-like illness and severe acute respiratory illness in the Democratic Republic of Congo, 2013-2015

The Burden of Influenza-Associated Hospitalizations in Oman, January 2

Estimating the burden of in

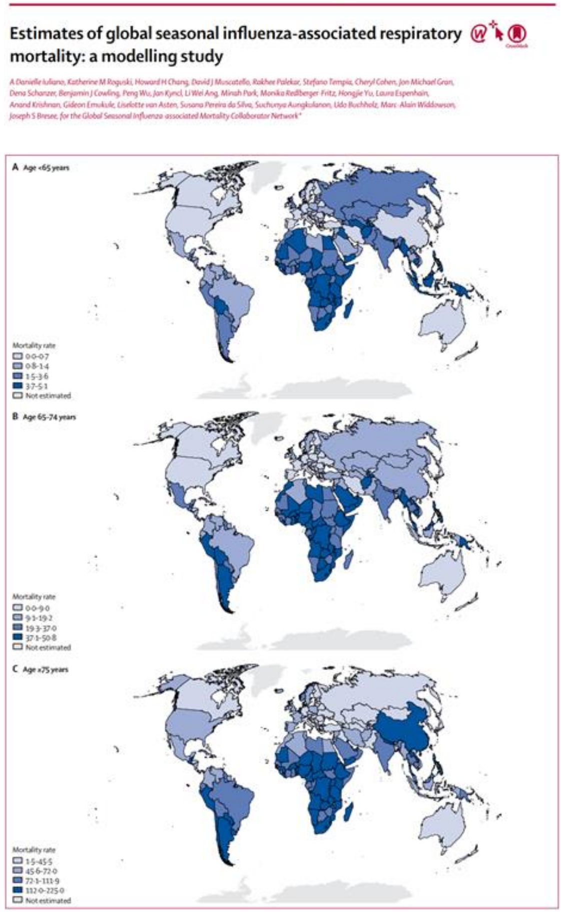
and deaths in Oman (2012-

Quantifying How Different Clinical Presentations, Levels of Severity, and Healthcare Attendance Shape the Burden of Influenza-associated Illness: A Modeling Study From South Africa

Outputs (estimates of incidence and number of cases):

- **Global**
- **Regional**
- **Country-Specific for countries that don't have local estimates**

Example of Global Influenza-Associated Mortality Estimation



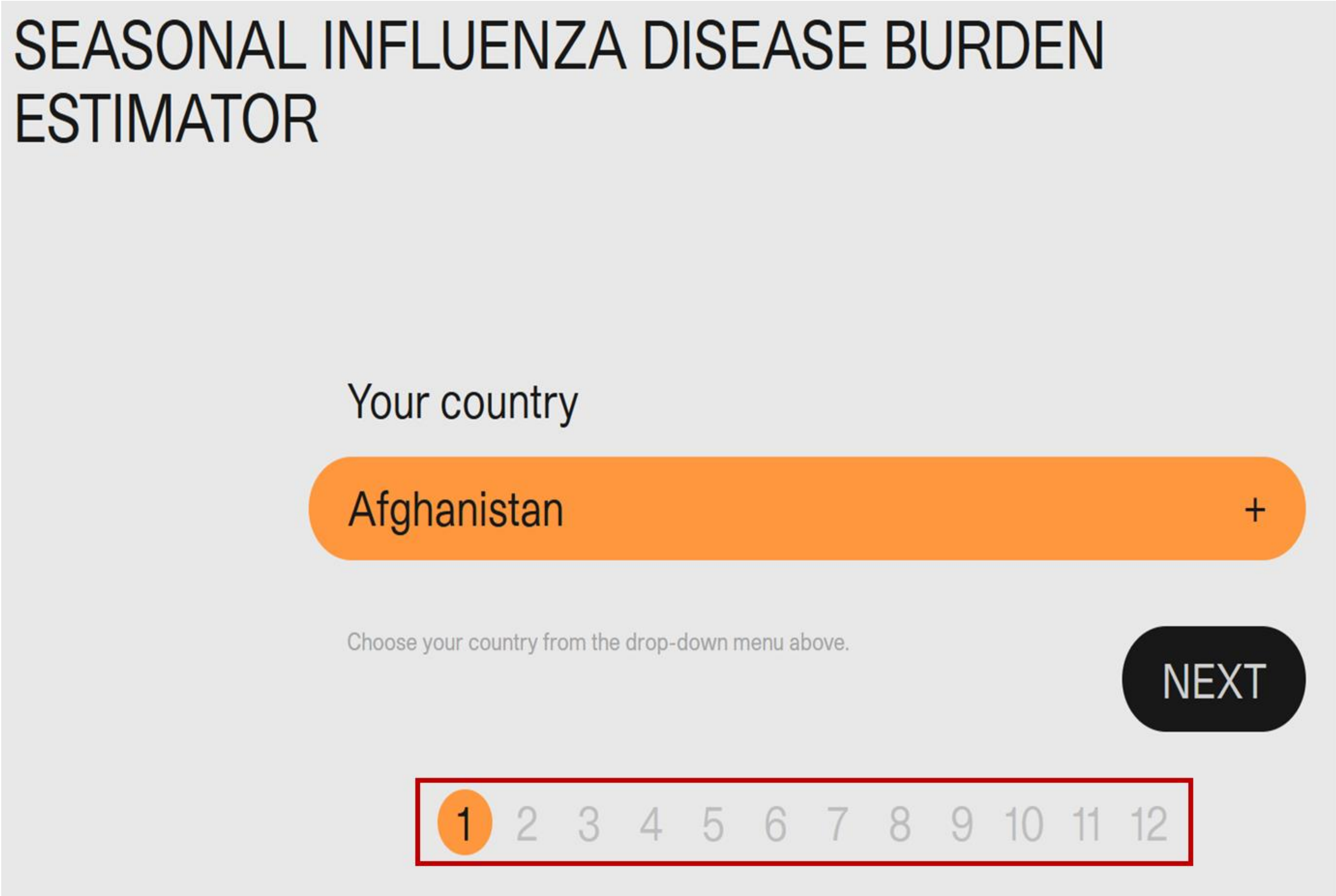
Estimates of global seasonal influenza-associated respiratory mortality: a modelling study

A Danielle Iuliano, Katherine M Roguski, Howard H Chang, David J Muscatello, Rakhee Palekar, Stefano Tempia, Cheryl Cohen, Jon Michael Gran, Dena Schanzer, Benjamin J Cowling, Peng Wu, Jan Kyncl, Li Wei Ang, Minah Park, Monika Redlberger-Fritz, Hongjie Yu, Laura Espenhain, Anand Krishnan, Gideon Emukule, Liselotte van Asten, Susana Pereira da Silva, Suchunya Aungkulanon, Udo Buchholz, Marc-Alain Widdowson, Joseph S Bresee, for the Global Seasonal Influenza-associated Mortality Collaborator Network*

Influenza BoD Estimation

The Tool (www.flutool.org)

World Health Organization



SEASONAL INFLUENZA DISEASE BURDEN ESTIMATOR

Your country: Afghanistan

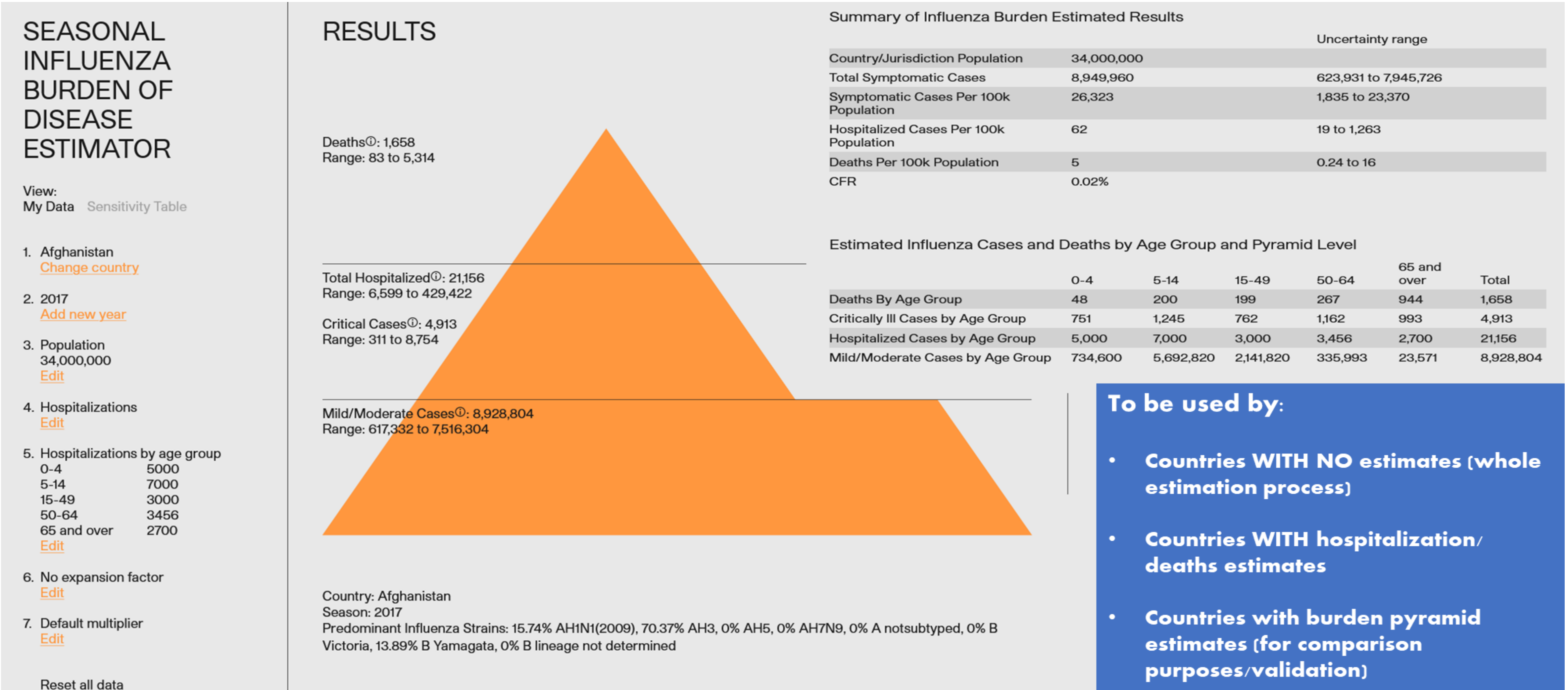
Choose your country from the drop-down menu above.

JOHNS HOPKINS BLOOMBERG SCHOOL of PUBLIC HEALTH | Center for Health Security

World Health Organization

Influenza BoD Estimation

The Tool (output example)



SEASONAL INFLUENZA BURDEN OF DISEASE ESTIMATOR

View:
My Data Sensitivity Table

1. Afghanistan
   Change country
2. 2017
   Add new year
3. Population
   34,000,000
   Edit
4. Hospitalizations
   Edit
5. Hospitalizations by age group

0-4	5000
5-14	7000
15-49	3000
50-64	3456
65 and over	2700

   Edit

6. No expansion factor
   Edit
7. Default multiplier
   Edit

Reset all data

RESULTS

Deathsⓘ: 1,658
Range: 83 to 5,314

Total Hospitalizedⓘ: 21,156
Range: 6,599 to 429,422

Critical Casesⓘ: 4,913
Range: 311 to 8,754

Mild/Moderate Casesⓘ: 8,928,804
Range: 617,332 to 7,516,304

Country: Afghanistan
Season: 2017
Predominant Influenza Strains: 15.74% AH1N1(2009), 70.37% AH3, 0% AH5, 0% AH7N9, 0% A notsubtyped, 0% B Victoria, 13.89% B Yamagata, 0% B lineage not determined

Summary of Influenza Burden Estimated Results

		Uncertainty range
Country/Jurisdiction Population	34,000,000	
Total Symptomatic Cases	8,949,960	623,931 to 7,945,726
Symptomatic Cases Per 100k Population	26,323	1,835 to 23,370
Hospitalized Cases Per 100k Population	62	19 to 1,263
Deaths Per 100k Population	5	0.24 to 16
CFR	0.02%	

Estimated Influenza Cases and Deaths by Age Group and Pyramid Level

	0-4	5-14	15-49	50-64	65 and over	Total
Deaths By Age Group	48	200	199	267	944	1,658
Critically Ill Cases by Age Group	751	1,245	762	1,162	993	4,913
Hospitalized Cases by Age Group	5,000	7,000	3,000	3,456	2,700	21,156
Mild/Moderate Cases by Age Group	734,600	5,692,820	2,141,820	335,993	23,571	8,928,804

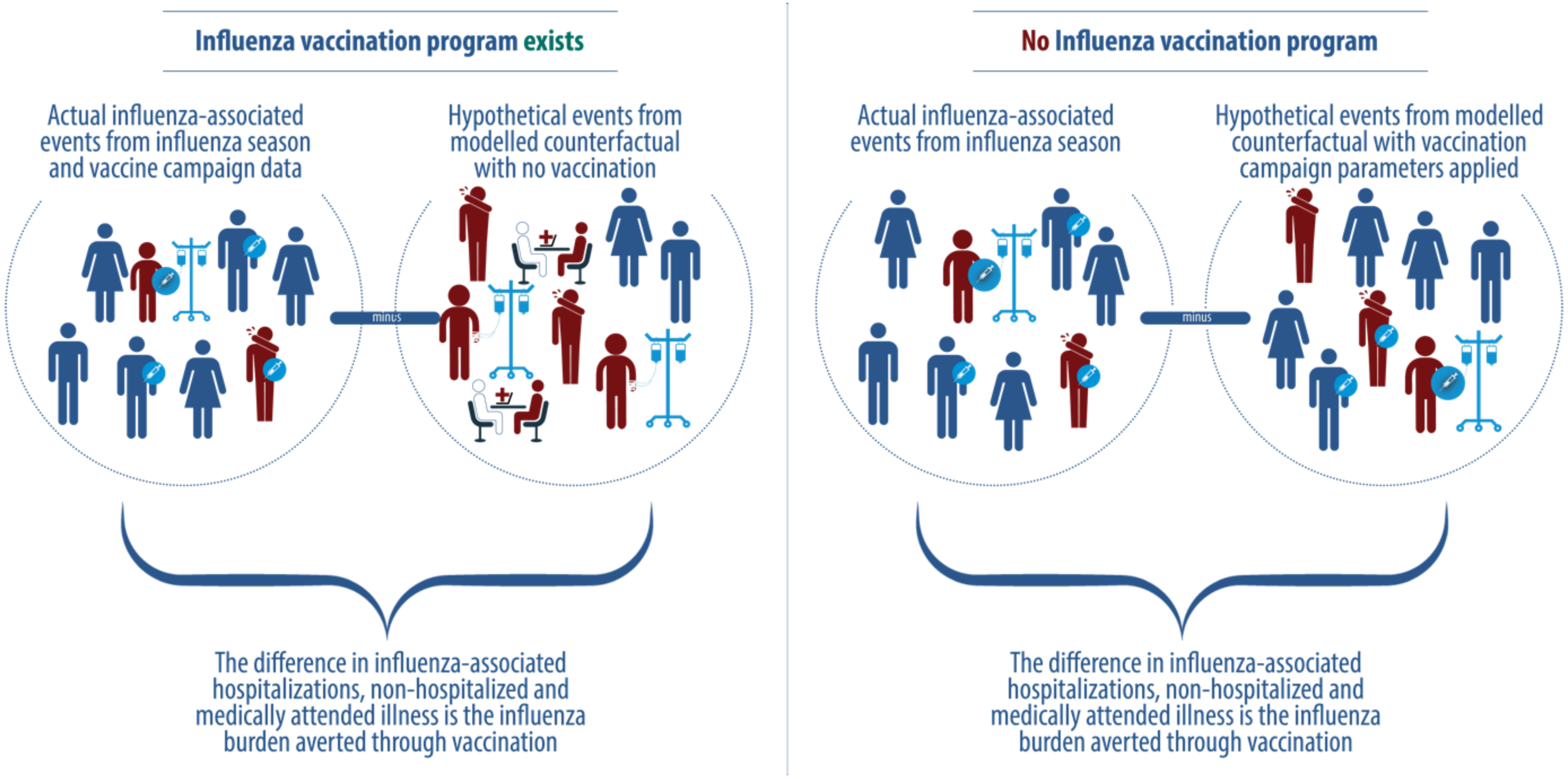
To be used by:

- **Countries WITH NO estimates (whole estimation process)**
- **Countries WITH hospitalization/ deaths estimates**
- **Countries with burden pyramid estimates (for comparison purposes/validation)**

Influenza BoD Estimation

Influenza Burden Averted though Vaccination: Current or Potential Immunization Programmes

World Health Organization



Influenza vaccination program exists

Actual influenza-associated events from influenza season and vaccine campaign data

Hypothetical events from modelled counterfactual with no vaccination

The difference in influenza-associated hospitalizations, non-hospitalized and medically attended illness is the influenza burden averted through vaccination

No Influenza vaccination program

Actual influenza-associated events from influenza season

Hypothetical events from modelled counterfactual with vaccination campaign parameters applied

The difference in influenza-associated hospitalizations, non-hospitalized and medically attended illness is the influenza burden averted through vaccination

Influenza BoD Estimation

Influenza Burden Averted though Vaccination: Linkage with Pyramid Webtool


RESULTS

Deathsⓘ: 1,658
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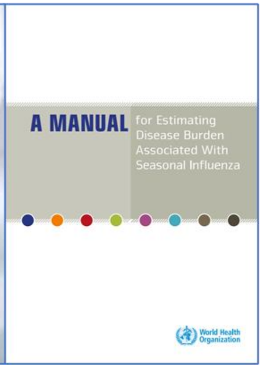
Integration in the tool not yet finalized


A MANUAL for Estimating Disease Burden Associated With Seasonal Influenza

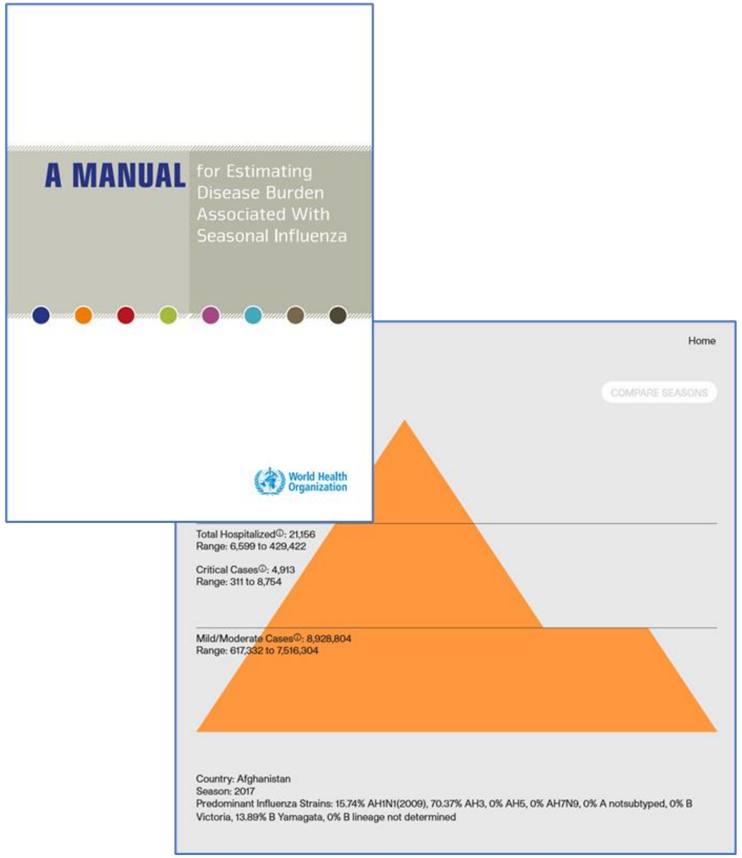
Methods of burden averted through immunization chapter

- Estimate the burden averted through current immunization programs
- Estimate the burden averted through scale-up/introduction of influenza immunization programs
- Additional tool to support evidence-based policy making

Influenza BoD Estimation

Cost burden and Cost Effectiveness Analysis

Disease Burden



A MANUAL for Estimating Disease Burden Associated With Seasonal Influenza

World Health Organization

Home

COMPARE SEASONS

Total Hospitalized①: 21,156
Range: 6,599 to 429,422

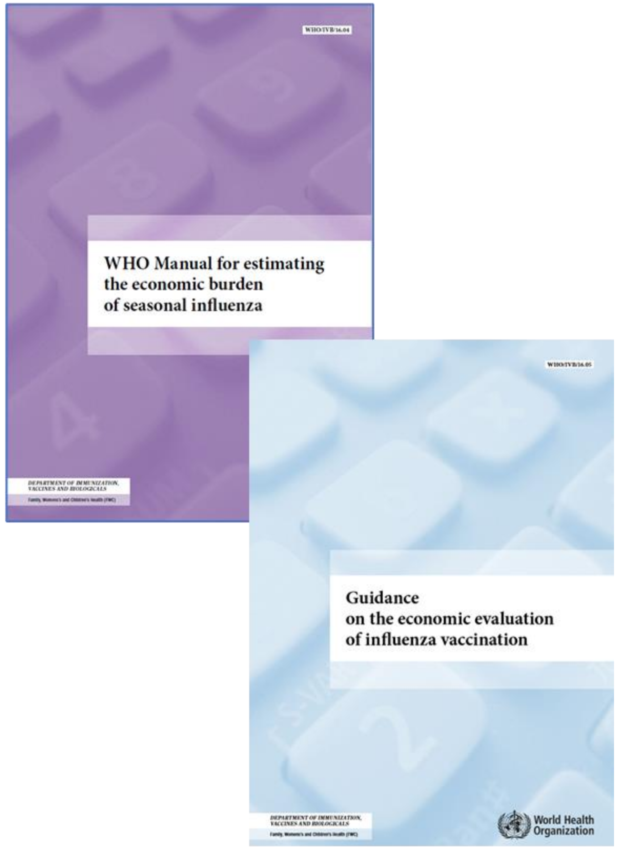
Critical Cases①: 4,913
Range: 311 to 8,754

Mild/Moderate Cases①: 8,928,804
Range: 617,332 to 7,516,304

Country: Afghanistan
Season: 2017
Predominant Influenza Strains: 15.74% AH1N1(2009), 70.37% AH3, 0% AH5, 0% AH7N9, 0% A notsubtyped, 0% B Victoria, 13.89% B Yamagata, 0% B lineage not determined

GIP/IVB Collaboration

Economic Burden



WHO/IVB/16.04

WHO Manual for estimating
the economic burden
of seasonal influenza

DEPARTMENT OF IMMUNIZATION, VACCINES AND BIOLOGICALS
Family, Women's and Children's Health (FWC)

WHO/IVB/16.05

Guidance
on the economic evaluation
of influenza vaccination

DEPARTMENT OF IMMUNIZATION, VACCINES AND BIOLOGICALS
Family, Women's and Children's Health (FWC)

World Health Organization

BoD Estimation

Next Steps

World Health Organization

- Improve understanding of influenza- and RSV-severe disease burden
- Monitor the impact of influenza and RSV control measures (e.g., vaccination)
- Pilot disease/economic and impact tools
- Develop approaches for annual/intra-season influenza and RSV BoD estimates

BoD Estimation

Possible areas of collaboration

World Health Organization

- Pilot novel approaches for catchment areas estimation (e.g., probabilistic method(s))

- Improve understanding of (influenza- and) RSV-severe disease burden (with emphasis on RSV BoD baselines before possible vaccine introduction)

- Pilot systems to monitor the impact of influenza and RSV control measures (e.g., vaccination) – Network/Multi-center Approach

- Pilot approaches for annual/intra-season influenza and RSV BoD estimates

PIP FRAMEWORK

PAHO

Pan American Health Organization

World Health Organization
REGIONAL OFFICE FOR THE Americas

SARInet plus
Severe Acute Respiratory Infections Network

CLOSING OF DAY 1

THANK YOU!

Global Influenza Hospital Surveillance Network