Global Influenza
Hospital Surveillance
Network

www.gihsn.org

GIHSN 12TH GLOBAL ANNUAL MEETING

24-26 November 2024

Foundation for
Influenza
Epidemiology

Sous l'égide de
Fondation
de
France

Coordination
IMPACT
Healthcare

WELCOME TO THE GIHSN GLOBAL ANNUAL MEETING!

DOMAINE DE CHÂTEAUNEUF, 24-26 NOVEMBER 2024

Global Influenza
Hospital Surveillance
Network

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Hospital Surveillance
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www.gihsn.org

GIHSN 12TH ANNUAL MEETING, 25-26 NOVEMBER 2024

GISAID ROLE IN WGS ACTIVITIES

Sebastian MAURER-STROH, GISAID

Foundation for
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France

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IMPACT
Healthcare

GISAID

Data Science Initiative

GISAID – Data Governance begins with respecting submitters’ rights

Ownership
Data submitters retain ownership of their data and intellectual property

Quality
GISAID curation team works with submitters to ensure highest standard of quality for genomic data and metadata

Stewardship
Trust built over a decade of partnerships.
GISAID provides consistent reliability and accountability for data management and service

Security
Protecting digital content and infrastructure
Reliability of systems

Privacy
GISAID commits to data privacy for users and submitters.
GISAID strives to ensure case patient anonymity through robust checks, policies and systems.

GISAID – Empowering Rapid Response to Disease X

2009

H1N1 pandemic
- <36hrs collection to data
- Diagnostics development

2013

H7N9 influenza epidemic
- <48hrs collection to data
- Diagnostics and mRNA vaccine development

2020

COVID-19 pandemic
- <36hrs collection to data
- Diagnostics and mRNA vaccine development

20??

EpiX for Disease X
- Ready for Disease X

2008

Launch of GISAID and **EpiFlu**™

2013-2019

Integration of tools for Influenza

2020-2021

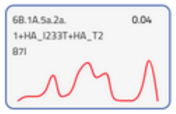
Launch of **EpiCoV**™ and **EpiRSV**™
Expansion of tools
Creation of live dashboards

2022-2024

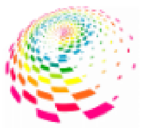
Launch of **EpiPox**™ and **EpiArbo**™ (Dengue, Zika, Chikungunya. Oropouche)

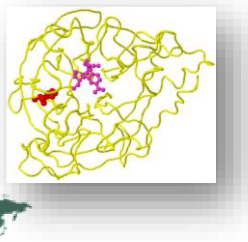

Audacity*Instant*


Lineage Frequency

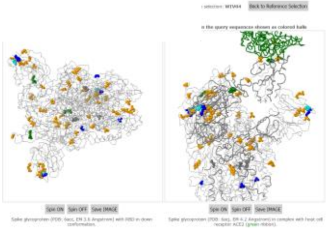


FluCluster-AI


PrimerChecker




Emerging Variants




EpiCharts


Submission tracker

from Equitable Data Access to enabling Equitable Data Science

GISAID's *enduring commitment to education and capacity building*

GISAID Academy

UID Campus, Kura Kura | Bali

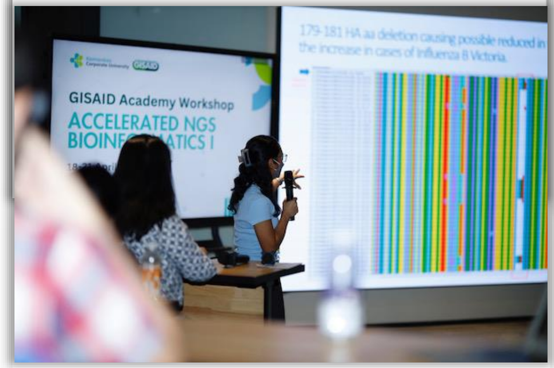
- Consolidating GISAID's global training efforts
- Collaboration with Indonesia Health Ministry
- Supported by private partnerships
- Comprehensive year-round courses
- End-to-end vocational training (wet & dry lab)
- From basic PCR techniques to NGS preparing for advanced bioinformatics training
- Graduates receive academic credits

Kemenkes Corporate University

GISAID
ACADEMY
KURA KURA BALI

CERTIFICATE OF COMPLETION

PRESENTED TO



Accelerated NGS Bioinformatics Training

State-of-the-art learning facilities

International Conferences and Symposia

e.g. Arbovirus Summit

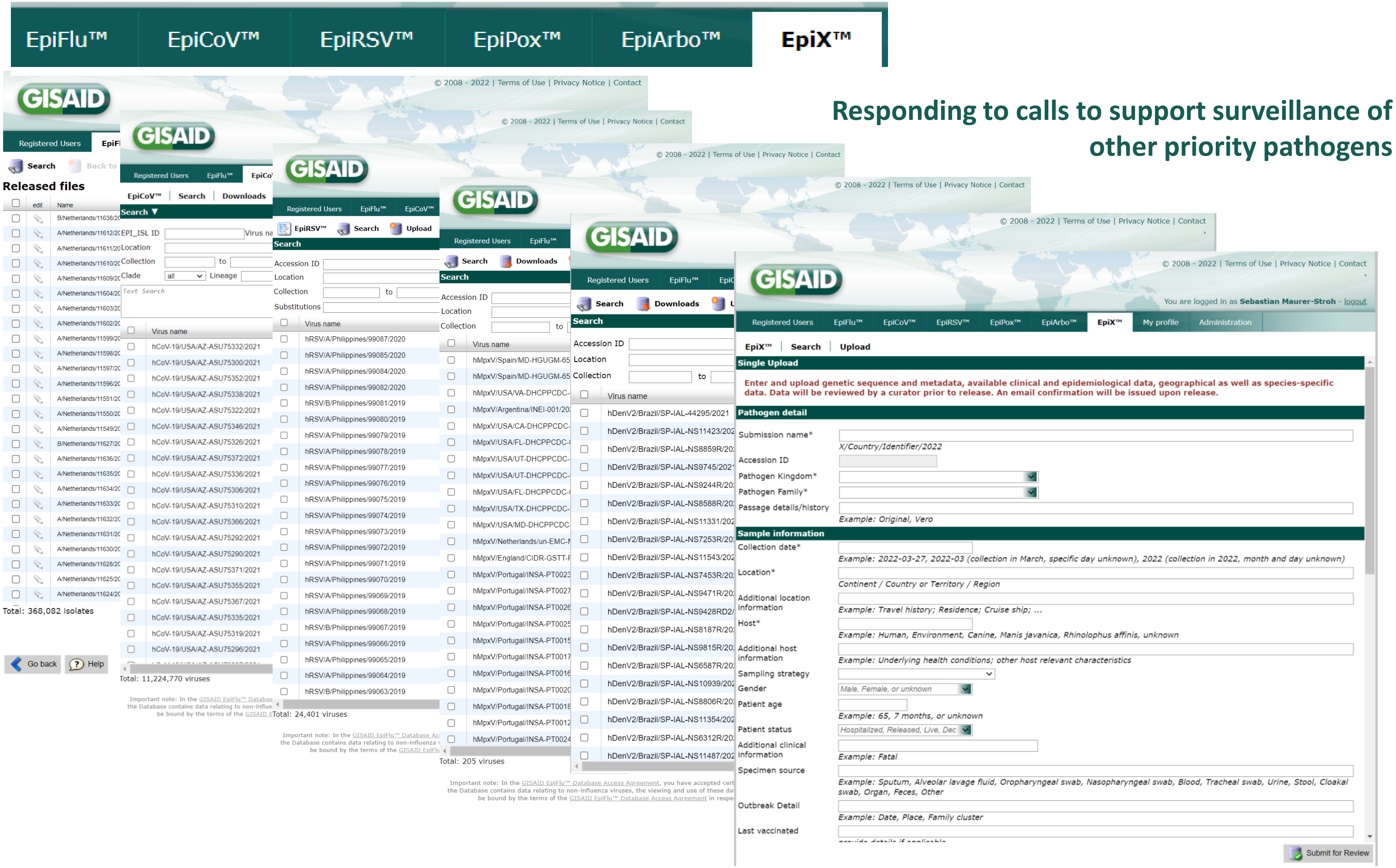
Cohosted by

MoH Brazil & Indonesia

April 2024

GISAID ACADEMY 18 th - 21 st April 2024 (PUSJAK KGTK,BKPK)

Responding to calls to support surveillance of other priority pathogens



You are logged in as **Sebastian Maurer-Stroh** - logout

Registered Users | EpiFlu™ | EpiCoV™ | EpiRSV™ | EpiPox™ | EpiArbo™ | EpiX™ | My profile | Administration

EpiX™ | Search | Upload

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

Submit for Review

Seamless evolution of GISAID Database Architecture

Continuous development with uninterrupted user experience

Migration of all GISAID pathogens to single platform

EpiFlu™ EpiCoV™ EpiRSV™ EpiPox™ EpiArbo™

12 Dec 2021
Switch to PostgreSQL

1 May 2020
Switch to MongoDB

10 Jan 2020
Deployment of temp EpiCoV JSON-File based Database

14 Sept 2009
Launch of replacement EpiFlu with Oracle Database

19 May 2008
Launch of first GISAID EpiFlu proprietary code

10 Oct 2024 Twenty-millionth genetic sequence submission to GISAID platform

21 Feb 2023 Fifteen-millionth hCoV-19 submission

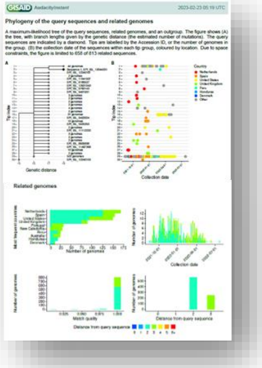
11 Dec 2021 Six-millionth hCoV-19 submission

5 Apr 2021 One-millionth hCoV-19 submission

10 Jan 2020 First hCoV-19 genomes released

31 Dec 2019 1,2 million Influenza genetic sequences (286k viruses)

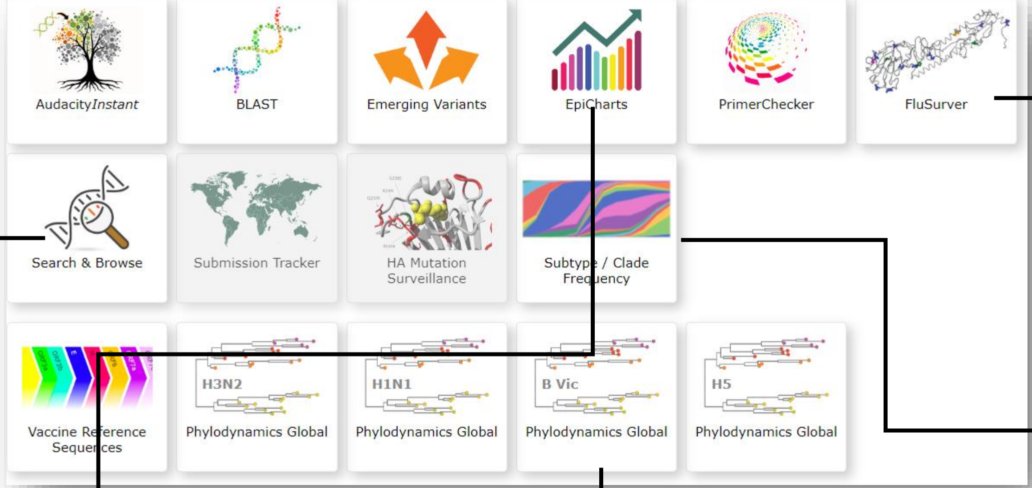
Empowering Actionable Data– Answering YOUR Questions



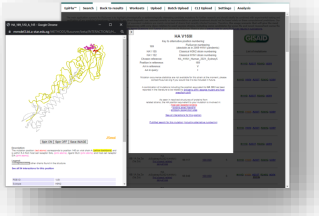
Question:
Which sequences in the database are most similar to my own sequence?

Question:
Any emerging variant with unique constellation of mutations?

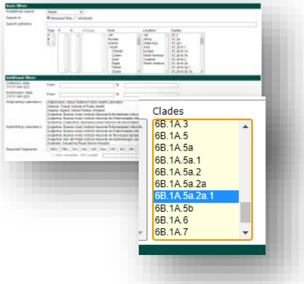
Question:
Any mutation affecting common or my primers?



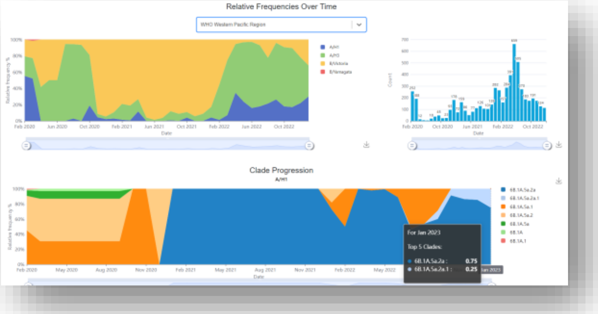
Question:
Any phenotypically important mutation in my sequences (host specificity, antibody binding, drug resistance, glycosylation, virulence)?



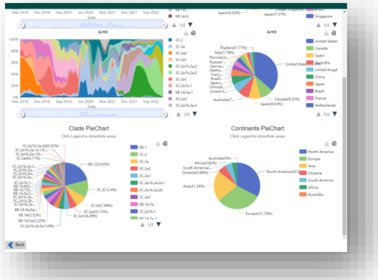
Question:
Can I browse, search and filter entries in the database?



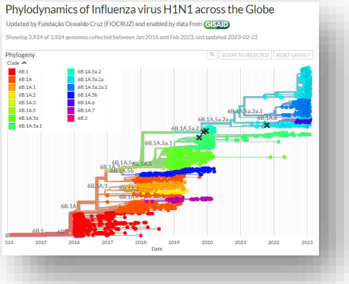
Question:
Which clades are currently dominant or rising in my country/region?



Question:
How can I create summary graphs for hits from a custom database search?



Question:
Summary of phylogenetic evolution in subsampled tree?



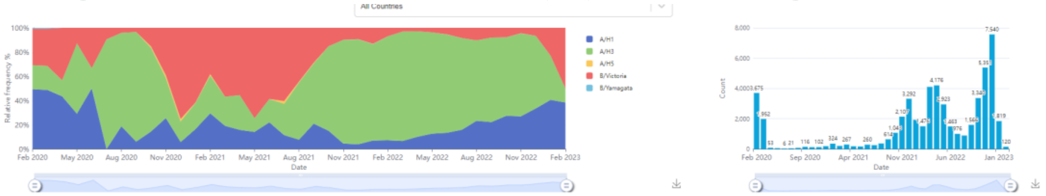
Ecosystem of integrated tools supporting scale-free view of virus evolution

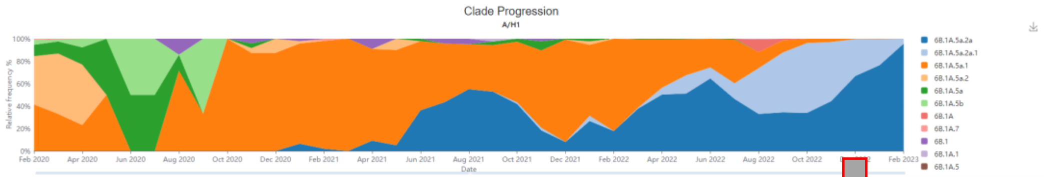
Subtype

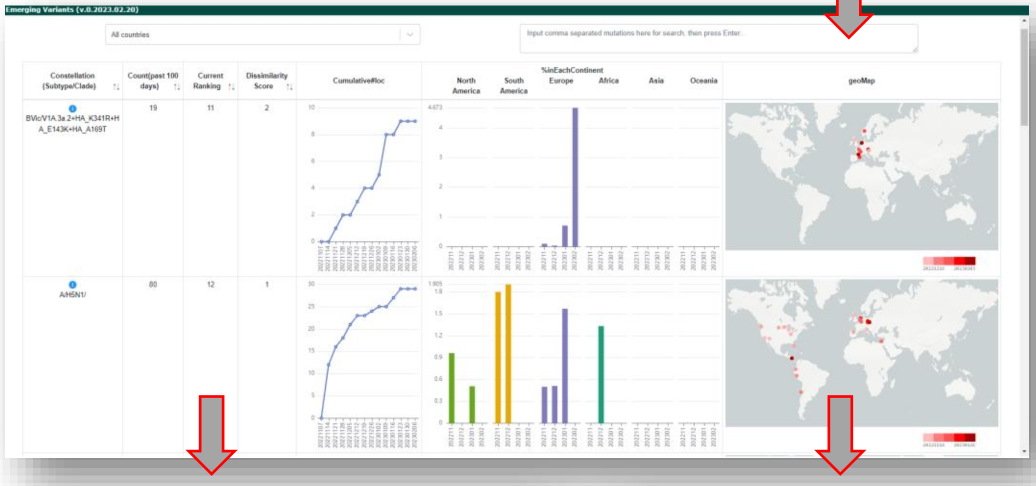
Clade

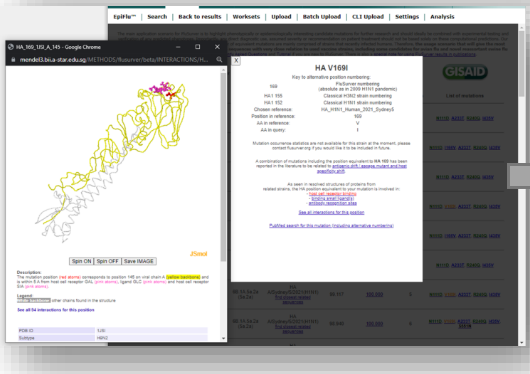
Emerging Variant
(unique set of mutations)

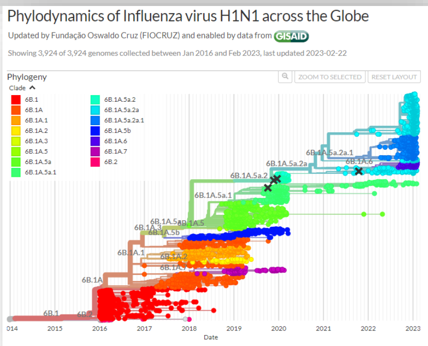
Individual
mutation

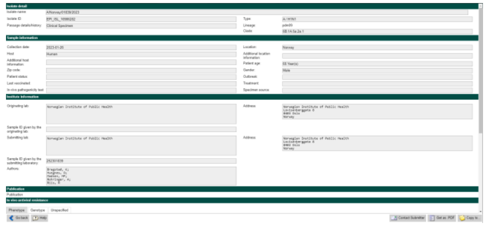




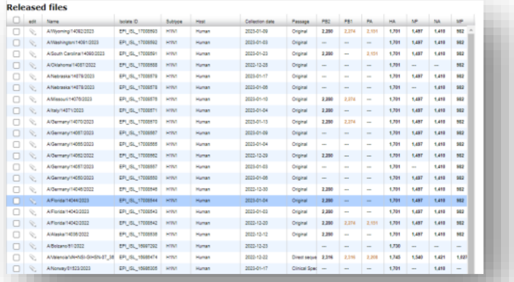




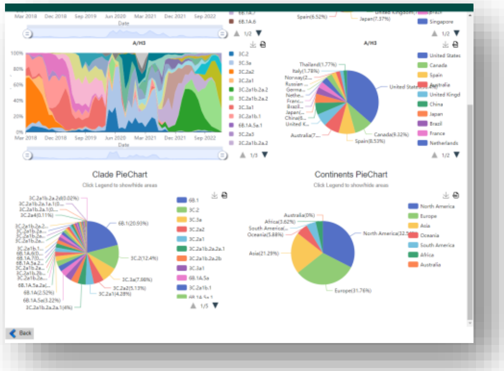




Single entry detail



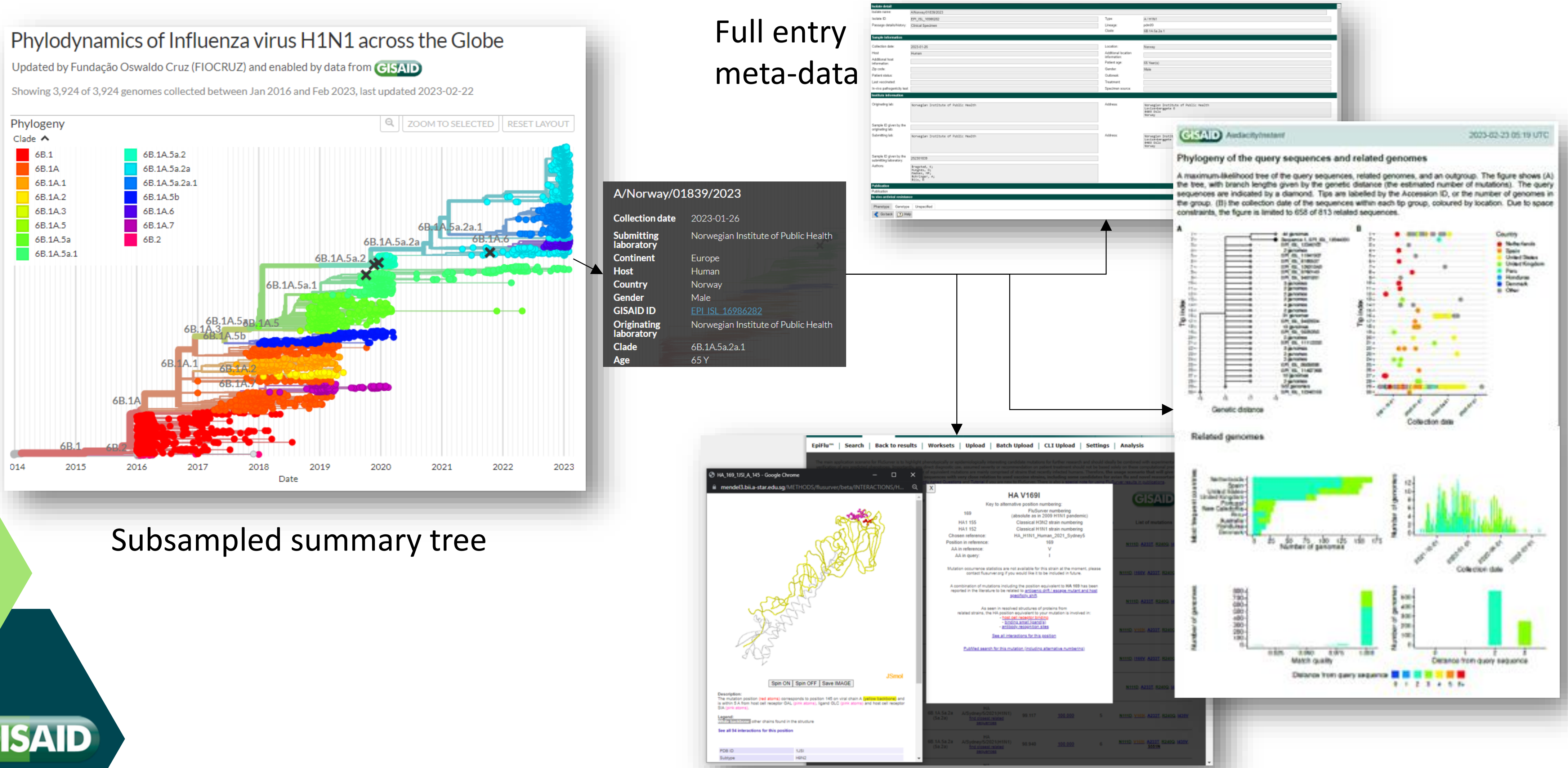
Set of entries in the database



Set of entries graphical summary

GISAID

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.1A5a.2a.1
Age 65 Y

Subsampled summary tree

Full entry meta-data

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

Tracking the viral evolution and identifying fast spreading variants

Emerging Variants

Monitoring emerging Fast Spreading hCoV-19 variants

Ranked by 2 Methods

- Recent Spread
- Acceleration

Monitor AA changes with potential effects on receptor or antibody binding as annotated in CoVsurver

CoVsurver

356 antibody binding sites

2388 literature entries (antibody escape, ACE2 binding, Spike expression and stability)

Constellation

E_T11A, N_P13L, Spike_D405N, Spike_D614G, Spike_D796Y, Spike_E484A, Spike_G257S, Spike_G339H, Spike_G446S, Spike_K147E, Spike_K417N, Spike_N440K, Spike_N460K, Spike_N501Y, Spike_P681H, Spike_Q498R, Spike_R408S, Spike_S371F, Spike_S373P, Spike_S375F, Spike_S477N, Spike_T376A, Spike_T478K, Spike_W152R, Spike_Y505H

Constellation (Clade/Lineage) (New Lineage) BA.2.75	Count(past 100 days) ↑↓	Current Ranking ↑↓	Dissimilarity Score ↑↓
GRA/BA.2.75+Spike_F486S+Spike_R346T Search EpiCoV Spike 3D	652	3	4

Filter by Country

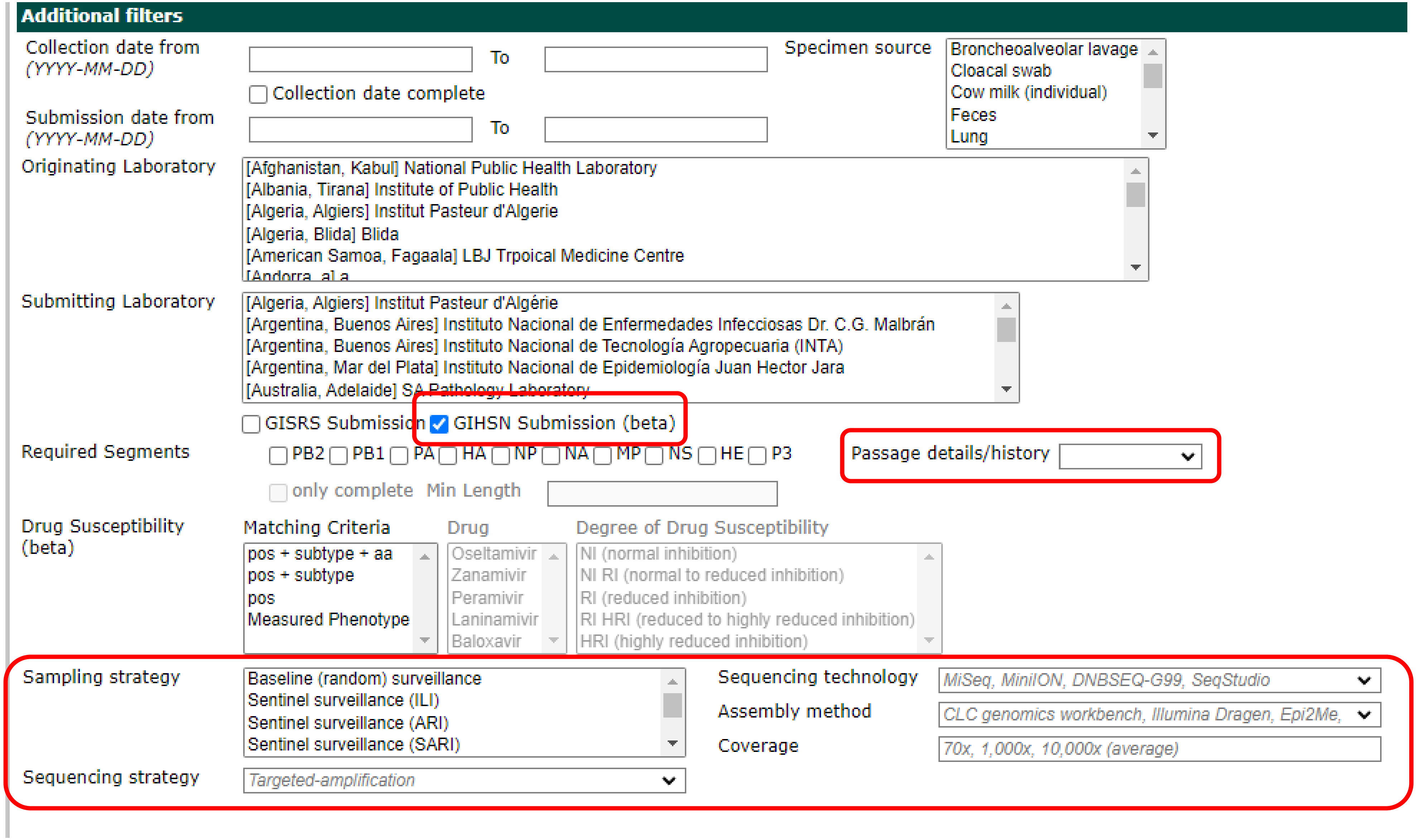
Filter by Mutation

Search GISAID EpiCoV database!

View mutations in Spike 3D Structure

Tool to see new variants before they have a lineage name

New in EpiFlu



Additional filters

Collection date from *(YYYY-MM-DD)* To

☐ Collection date complete

Submission date from *(YYYY-MM-DD)* To

Specimen source
- Broncheoalveolar lavage
- Cloacal swab
- Cow milk (individual)
- Feces
- Lung

Originating Laboratory
- [Afghanistan, Kabul] National Public Health Laboratory
- [Albania, Tirana] Institute of Public Health
- [Algeria, Algiers] Institut Pasteur d'Algerie
- [Algeria, Blida] Blida
- [American Samoa, Fagaala] LBJ Trpoical Medicine Centre
- [Andorra,

Submitting Laboratory
- [Algeria, Algiers] Institut Pasteur d'Algérie
- [Argentina, Buenos Aires] Instituto Nacional de Enfermedades Infecciosas Dr. C.G. Malbrán
- [Argentina, Buenos Aires] Instituto Nacional de Tecnología Agropecuaria (INTA)
- [Argentina, Mar del Plata] Instituto Nacional de Epidemiología Juan Hector Jara
- [Australia, Adelaide] SA Pathology Laboratory

☐ GISRS Submission ☑ GIHSN Submission (beta)

Required Segments ☐ PB2 ☐ PB1 ☐ PA ☐ HA ☐ NP ☐ NA ☐ MP ☐ NS ☐ HE ☐ P3

☐ only complete Min Length

Passage details/history

Drug Susceptibility (beta)

Matching Criteria
- pos + subtype + aa
- pos + subtype
- pos
- Measured Phenotype

Drug
- Oseltamivir
- Zanamivir
- Peramivir
- Laninamivir
- Baloxavir

Degree of Drug Susceptibility
- NI (normal inhibition)
- NI RI (normal to reduced inhibition)
- RI (reduced inhibition)
- RI HRI (reduced to highly reduced inhibition)
- HRI (highly reduced inhibition)

Sampling strategy
- Baseline (random) surveillance
- Sentinel surveillance (ILI)
- Sentinel surveillance (ARI)
- Sentinel surveillance (SARI)

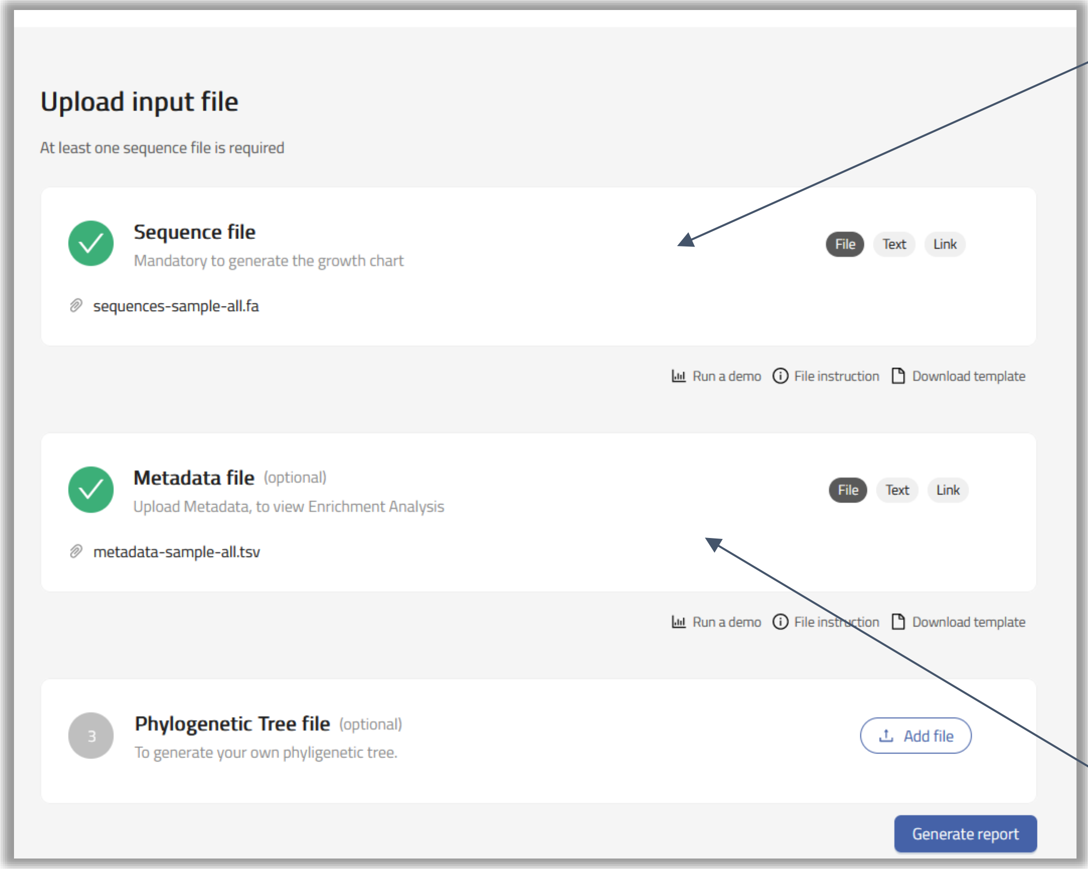
Sequencing strategy *Targeted-amplification*

Sequencing technology *MiSeq, MinION, DNBSEQ-G99, SeqStudio*

Assembly method *CLC genomics workbench, Illumina Dragen, Epi2Me,*

Coverage *70x, 1,000x, 10,000x (average)*

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)

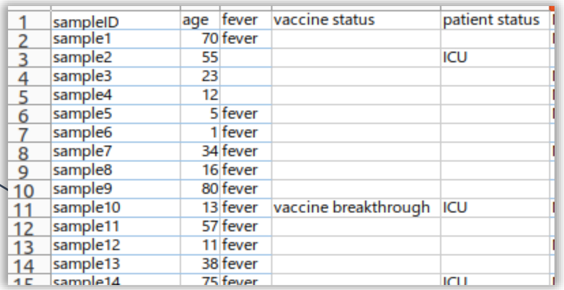
Upload Metadata, to view Enrichment Analysis

metadata-sample-all.tsv

Phylogenetic Tree file (optional)

To generate your own phyligenetic tree.

fasta file(.fasta,.fa)



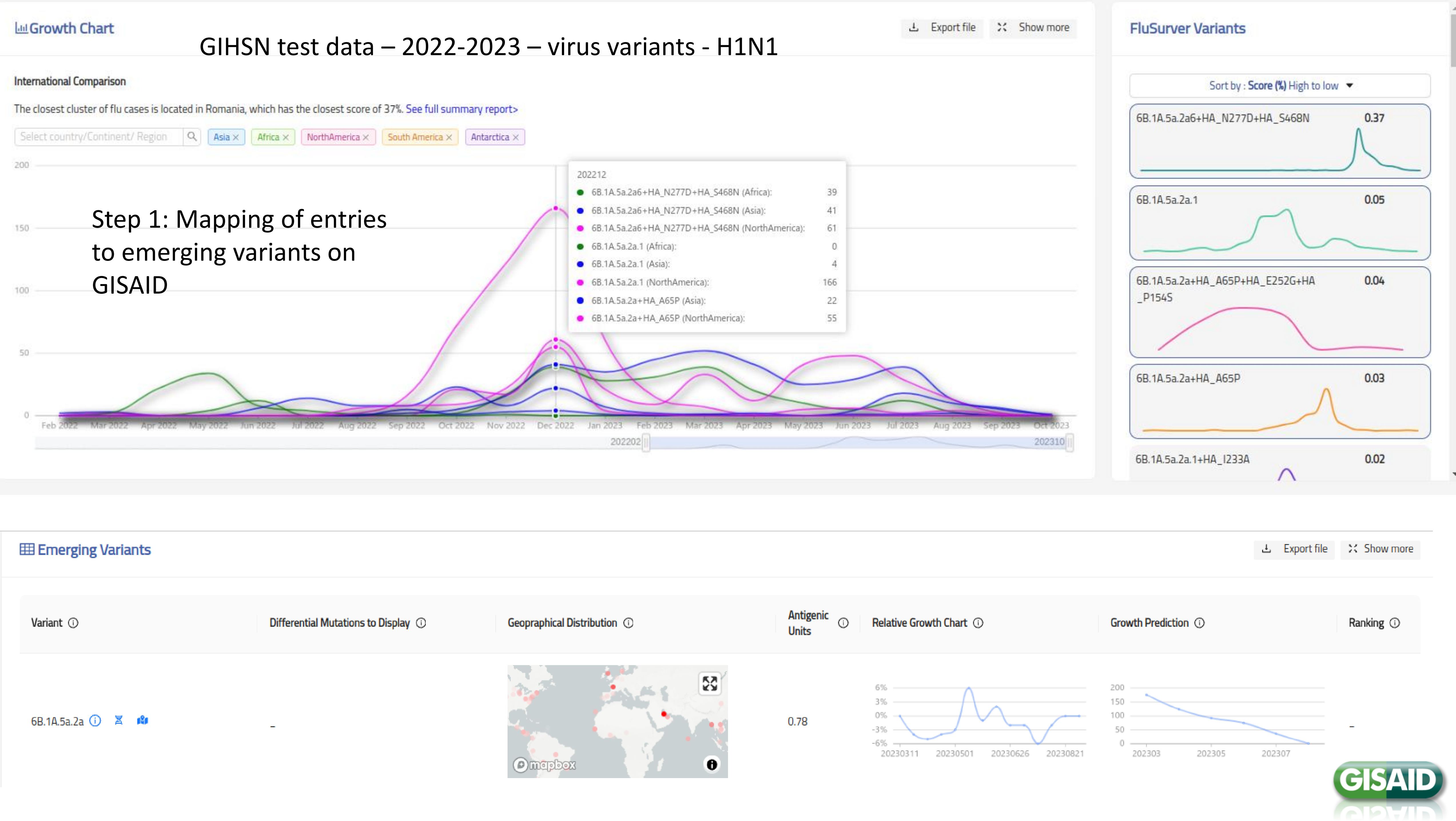
1	sampleID	age	fever	vaccine status	patient status
2	sample1	70	fever		
3	sample2	55			ICU
4	sample3	23			
5	sample4	12			
6	sample5	5	fever		
7	sample6	1	fever		
8	sample7	34	fever		
9	sample8	16	fever		
10	sample9	80	fever		
11	sample10	13	fever	vaccine breakthrough	ICU
12	sample11	57	fever		
13	sample12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

International Comparison

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

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

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

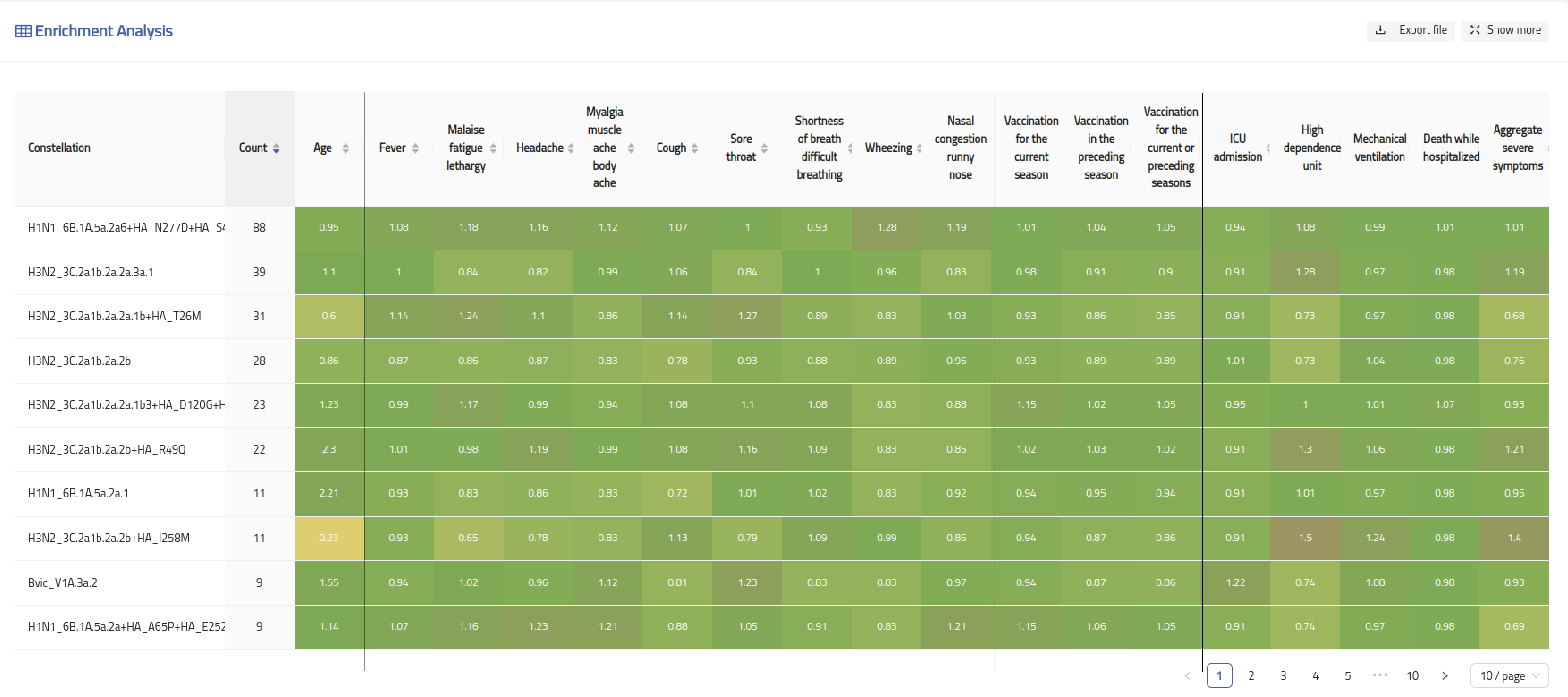
GIHSN test data – 2022-2023 – Clinical correlations - H1N1

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

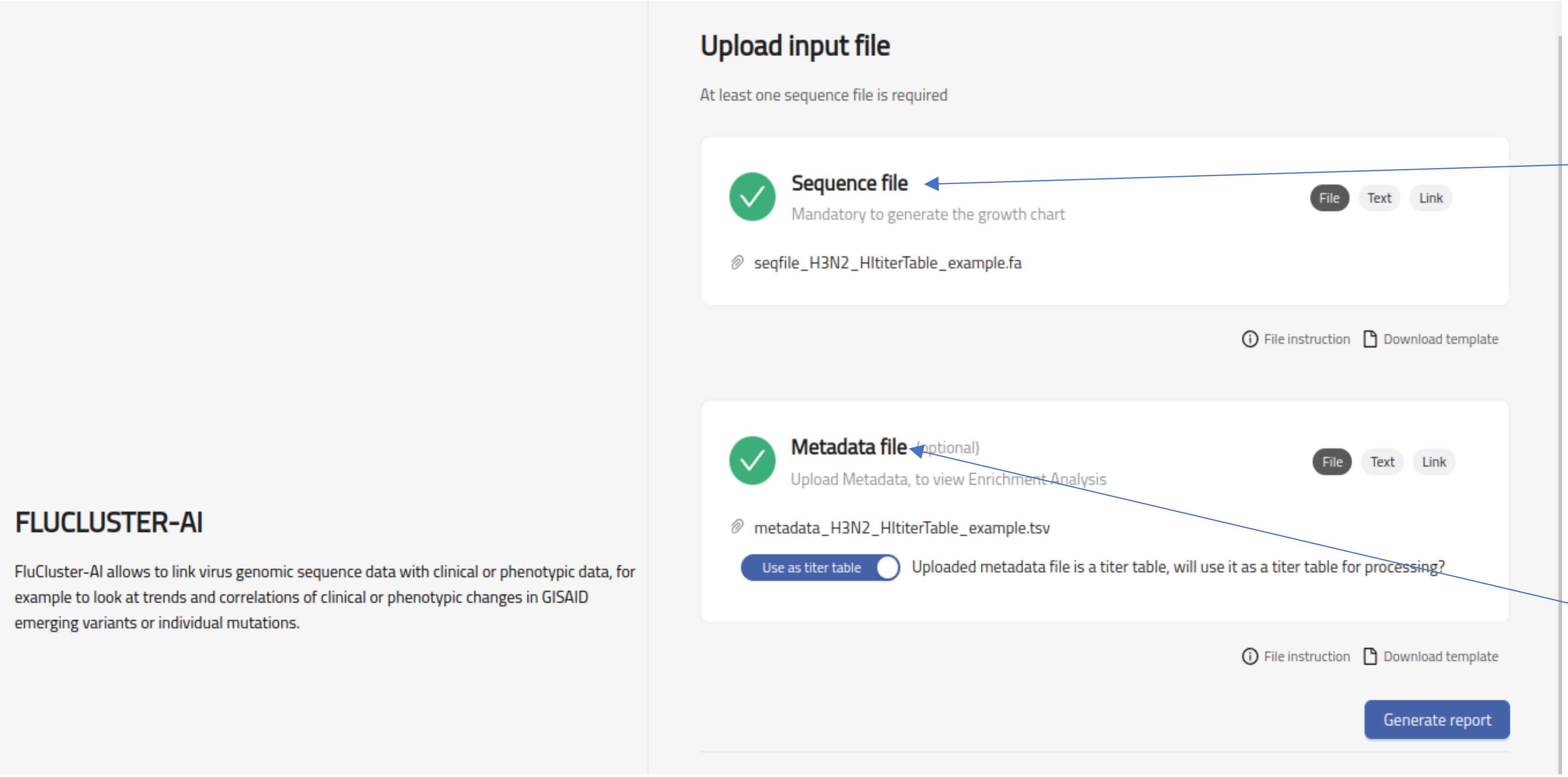
Step 2: Odds ratio analysis of clinical variables for enrichment or depletion association with the emerging variants

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



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

GISAID FluCluster-AI – new functionality for HI titres and antigenic change



FLUCLUSTER-AI

FluCluster-AI allows to link virus genomic sequence data with clinical or phenotypic data, for example to look at trends and correlations of clinical or phenotypic changes in GISAID emerging variants or individual mutations.

Upload input file

At least one sequence file is required

Sequence file

Mandatory to generate the growth chart

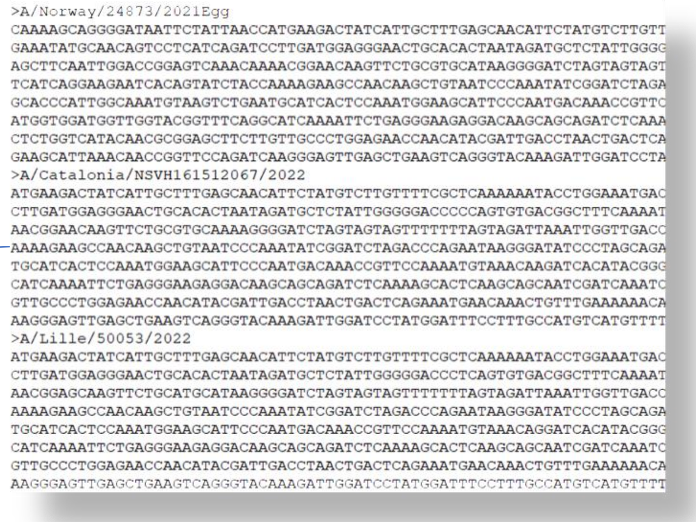
seqfile_H3N2_HItiterTable_example.fa

Metadata file (optional)

Upload Metadata, to view Enrichment Analysis

metadata_H3N2_HItiterTable_example.tsv

Use as titer table: Uploaded metadata file is a titer table, will use it as a titer table for processing?



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>A/Norway/24873/2021Egg
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>A/Catalonia/NSVH161512067/2022
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>A/Lille/50053/2022
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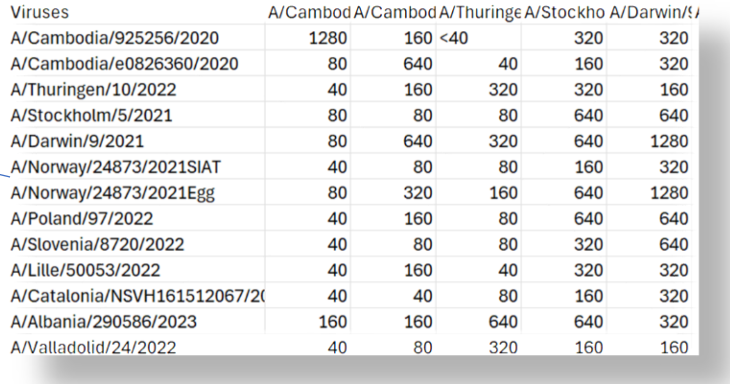
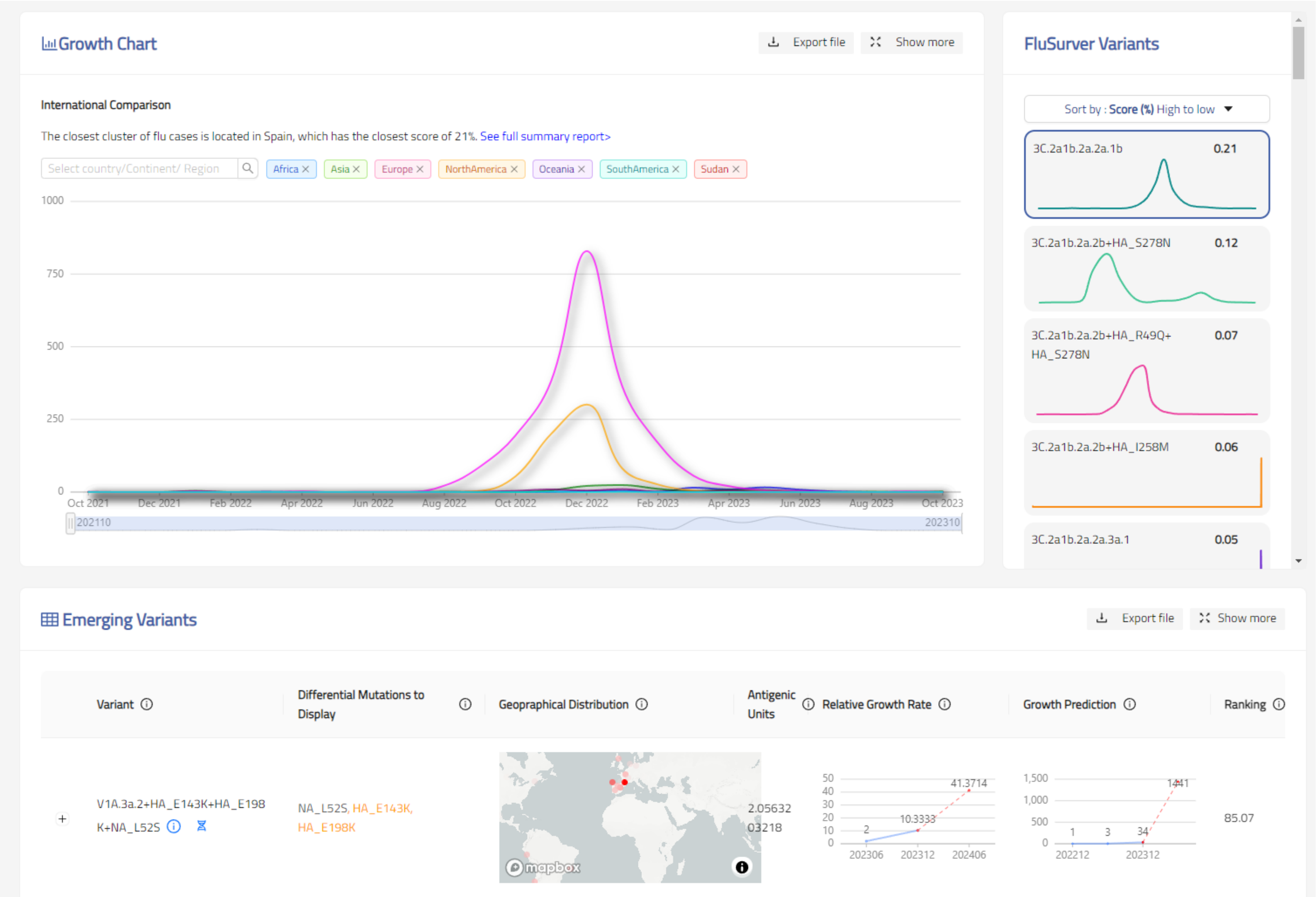


Viruses	A/Cambod	A/Cambod	A/Thuringe	A/Stockho	A/Darwin/
A/Cambodia/925256/2020	1280	160	<40	320	320
A/Cambodia/e0826360/2020	80	640	40	160	320
A/Thuringen/10/2022	40	160	320	320	160
A/Stockholm/5/2021	80	80	80	640	640
A/Darwin/9/2021	80	640	320	640	1280
A/Norway/24873/2021SIAT	40	80	80	160	320
A/Norway/24873/2021Egg	80	320	160	640	1280
A/Poland/97/2022	40	160	80	640	640
A/Slovenia/8720/2022	40	80	80	320	640
A/Lille/50053/2022	40	160	40	320	320
A/Catalonia/NSVH161512067/2(	40	40	80	160	320
A/Albania/290586/2023	160	160	640	640	320
A/Valladolid/24/2022	40	80	320	160	160

"Use as titer table" switch will show only system auto detected the metadata file is likely a titer table. User can choose to use as titer table or not use.

Step 1: map input sequences to emerging variants on GISAID



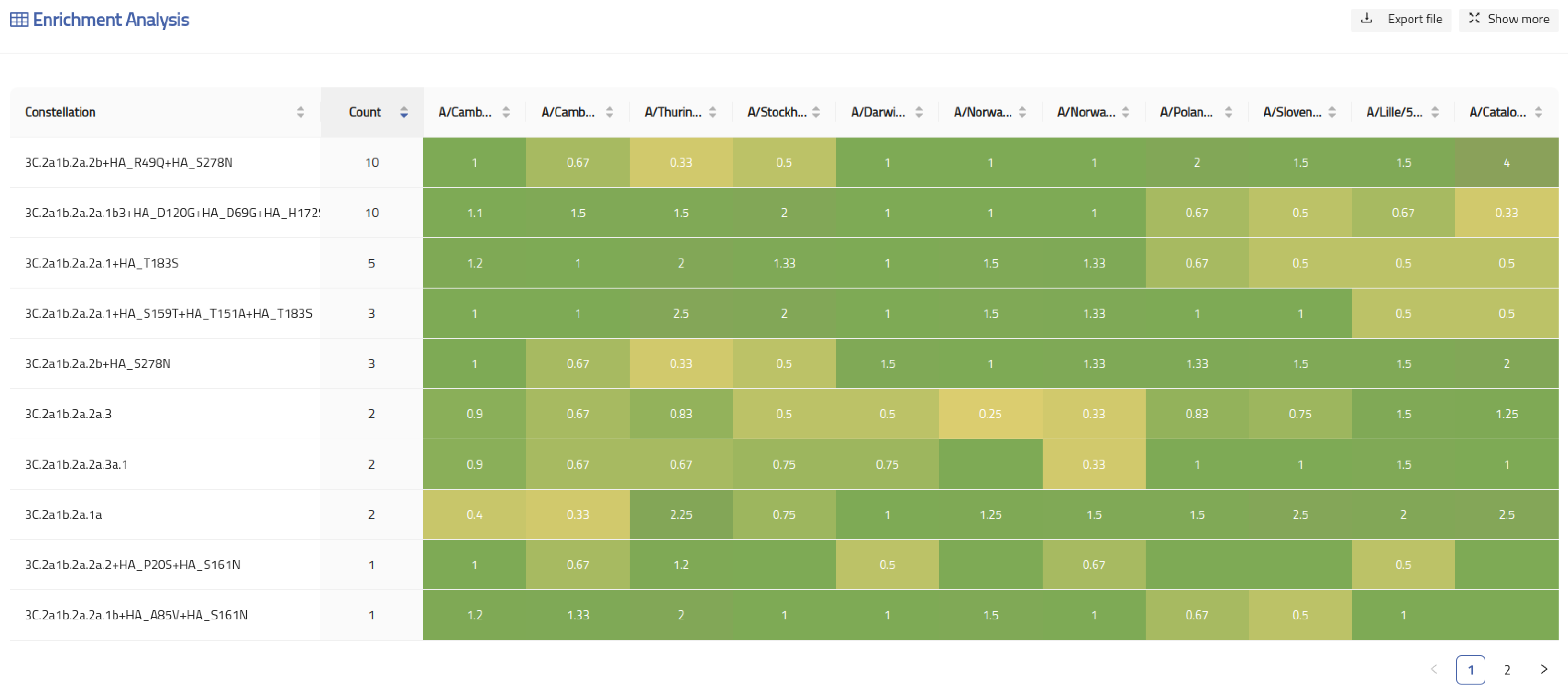
International Comparison

The closest cluster of flu cases is located in Spain, which has the closest score of 21%. See full summary report>

FluSurver Variants	Score
3C.2a1b.2a.2a.1b	0.21
3C.2a1b.2a.2b+HA_S278N	0.12
3C.2a1b.2a.2b+HA_R49Q+HA_S278N	0.07
3C.2a1b.2a.2b+HA_I258M	0.06
3C.2a1b.2a.2a.3a.1	0.05

	Variant	Differential Mutations to Display	Geographical Distribution	Antigenic Units	Relative Growth Rate	Growth Prediction	Ranking
+	V1A.3a.2+HA_E143K+HA_E198K+NA_L52S	NA_L52S, HA_E143K, HA_E198K		2.0563203218			85.07

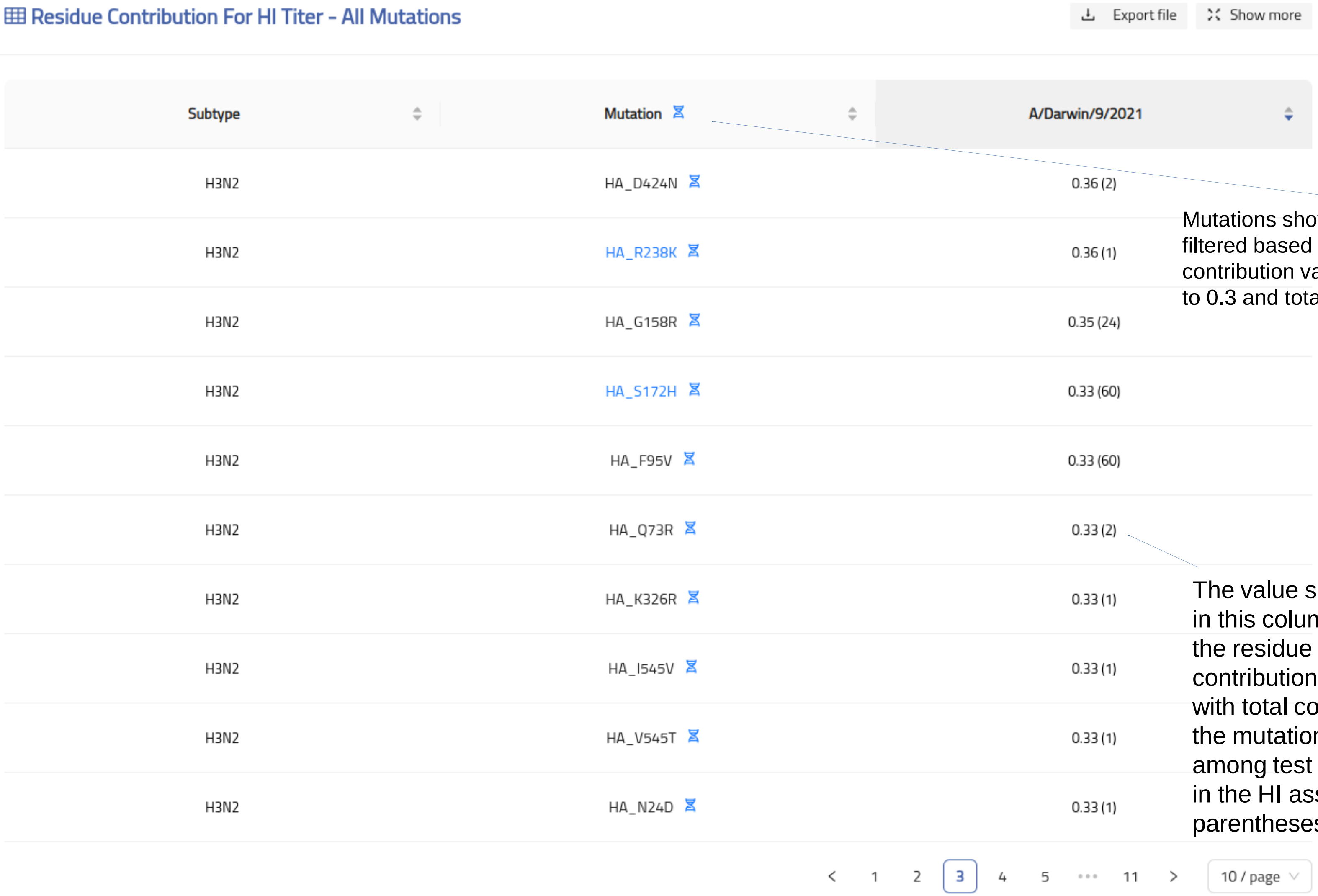
Step 2: correlate phenotype with emerging variants



Constellation	Count	A/Camb...	A/Camb...	A/Thurin...	A/Stockh...	A/Darwi...	A/Norwa...	A/Norwa...	A/Polan...	A/Sloven...	A/Lille/5...	A/Catalo...
3C.2a1b.2a.2b+HA_R49Q+HA_S278N	10	1	0.67	0.33	0.5	1	1	1	2	1.5	1.5	4
3C.2a1b.2a.2a.1b3+HA_D120G+HA_D69G+HA_H172	10	1.1	1.5	1.5	2	1	1	1	0.67	0.5	0.67	0.33
3C.2a1b.2a.2a.1+HA_T183S	5	1.2	1	2	1.33	1	1.5	1.33	0.67	0.5	0.5	0.5
3C.2a1b.2a.2a.1+HA_S159T+HA_T151A+HA_T183S	3	1	1	2.5	2	1	1.5	1.33	1	1	0.5	0.5
3C.2a1b.2a.2b+HA_S278N	3	1	0.67	0.33	0.5	1.5	1	1.33	1.33	1.5	1.5	2
3C.2a1b.2a.2a.3	2	0.9	0.67	0.83	0.5	0.5	0.25	0.33	0.83	0.75	1.5	1.25
3C.2a1b.2a.2a.3a.1	2	0.9	0.67	0.67	0.75	0.75		0.33	1	1	1.5	1
3C.2a1b.2a.1a	2	0.4	0.33	2.25	0.75	1	1.25	1.5	1.5	2.5	2	2.5
3C.2a1b.2a.2a.2+HA_P20S+HA_S161N	1	1	0.67	1.2		0.5		0.67			0.5	
3C.2a1b.2a.2a.1b+HA_A85V+HA_S161N	1	1.2	1.33	2	1	1	1.5	1	0.67	0.5	1	

Note that this step preserves privacy of user phenotype data as all data and analysis remains on the user's computer

Correlation with phenotype is also shown as per residue contribution

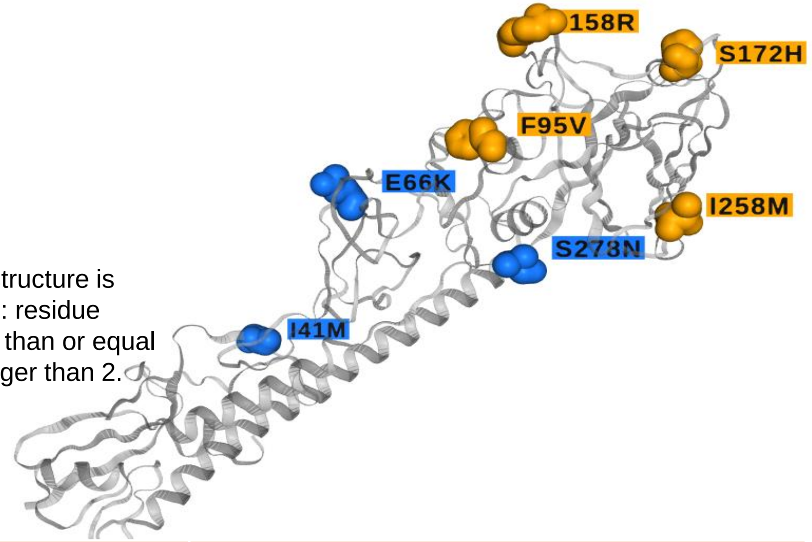


Residue Contribution For HI Titer - All Mutations

Subtype	Mutation	A/Darwin/9/2021
H3N2	HA_D424N	0.36 (2)
H3N2	HA_R238K	0.36 (1)
H3N2	HA_G158R	0.35 (24)
H3N2	HA_S172H	0.33 (60)
H3N2	HA_F95V	0.33 (60)
H3N2	HA_Q73R	0.33 (2)
H3N2	HA_K326R	0.33 (1)
H3N2	HA_I545V	0.33 (1)
H3N2	HA_V545T	0.33 (1)
H3N2	HA_N24D	0.33 (1)

Mutations shown in the structure is filtered based on the rule: residue contribution value bigger than or equal to 0.3 and total count bigger than 2.

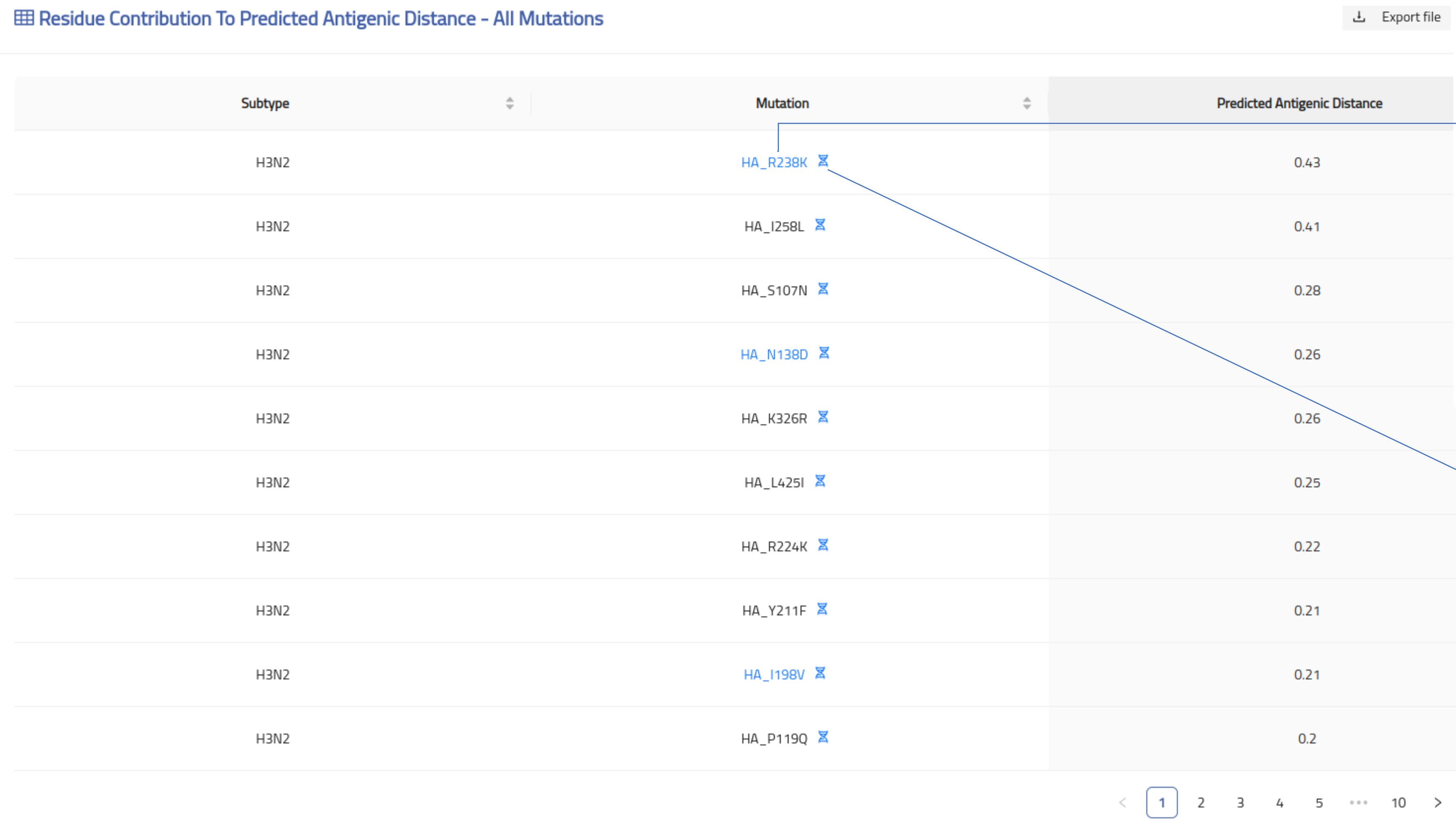
The value shown in this column is the residue contribution value with total count of the mutation found among test viruses in the HI assay in parentheses.



aa change	(FluSurver) annotations
I41M	Viral oligomerization, binds NAG
E66K	Binds Ab (1EO8), viral oligomerization, binds SO4
F95V	Binds Ab (1EO8), viral oligomerization, binds EDO
G158R	Binds Ab (4HF5), viral oligomerization, binds NAG
S172H	Binds Ab (4GMS), host cell receptor site, viral oligomerization, binds BGC
I258M*	Viral oligomerization, binds NAG
S278M	Viral oligomerization

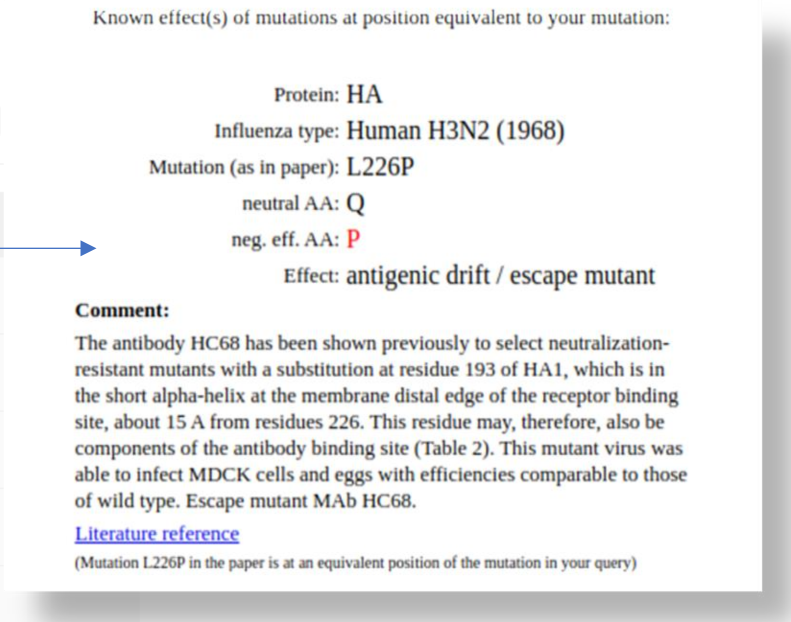
*found in many test viruses that are greater than eight-fold of heterologous titres in recent ECDC influenza virus characterization summary report

If no phenotype is available, we also provide antigenic distance prediction



Residue Contribution To Predicted Antigenic Distance - All Mutations

Subtype	Mutation	Predicted Antigenic Distance
H3N2	HA_R238K	0.43
H3N2	HA_I258L	0.41
H3N2	HA_S107N	0.28
H3N2	HA_N138D	0.26
H3N2	HA_K326R	0.26
H3N2	HA_L425I	0.25
H3N2	HA_R224K	0.22
H3N2	HA_Y211F	0.21
H3N2	HA_I198V	0.21
H3N2	HA_P119Q	0.2



Known effect(s) of mutations at position equivalent to your mutation:

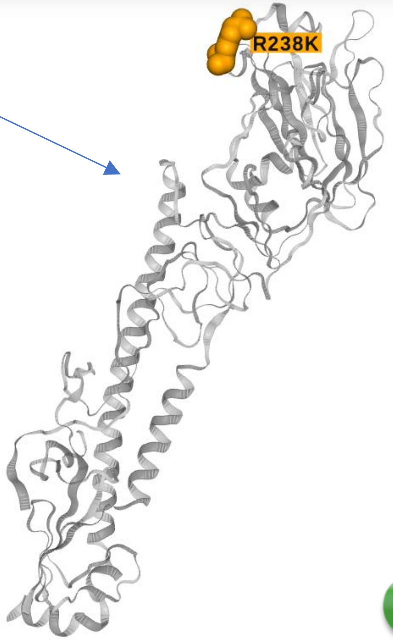
Protein: HA
Influenza type: Human H3N2 (1968)
Mutation (as in paper): L226P
neutral AA: Q
neg. eff. AA: P
Effect: antigenic drift / escape mutant

Comment:

The antibody HC68 has been shown previously to select neutralization-resistant mutants with a substitution at residue 193 of HA1, which is in the short alpha-helix at the membrane distal edge of the receptor binding site, about 15 A from residues 226. This residue may, therefore, also be components of the antibody binding site (Table 2). This mutant virus was able to infect MDCK cells and eggs with efficiencies comparable to those of wild type. Escape mutant MAb HC68.

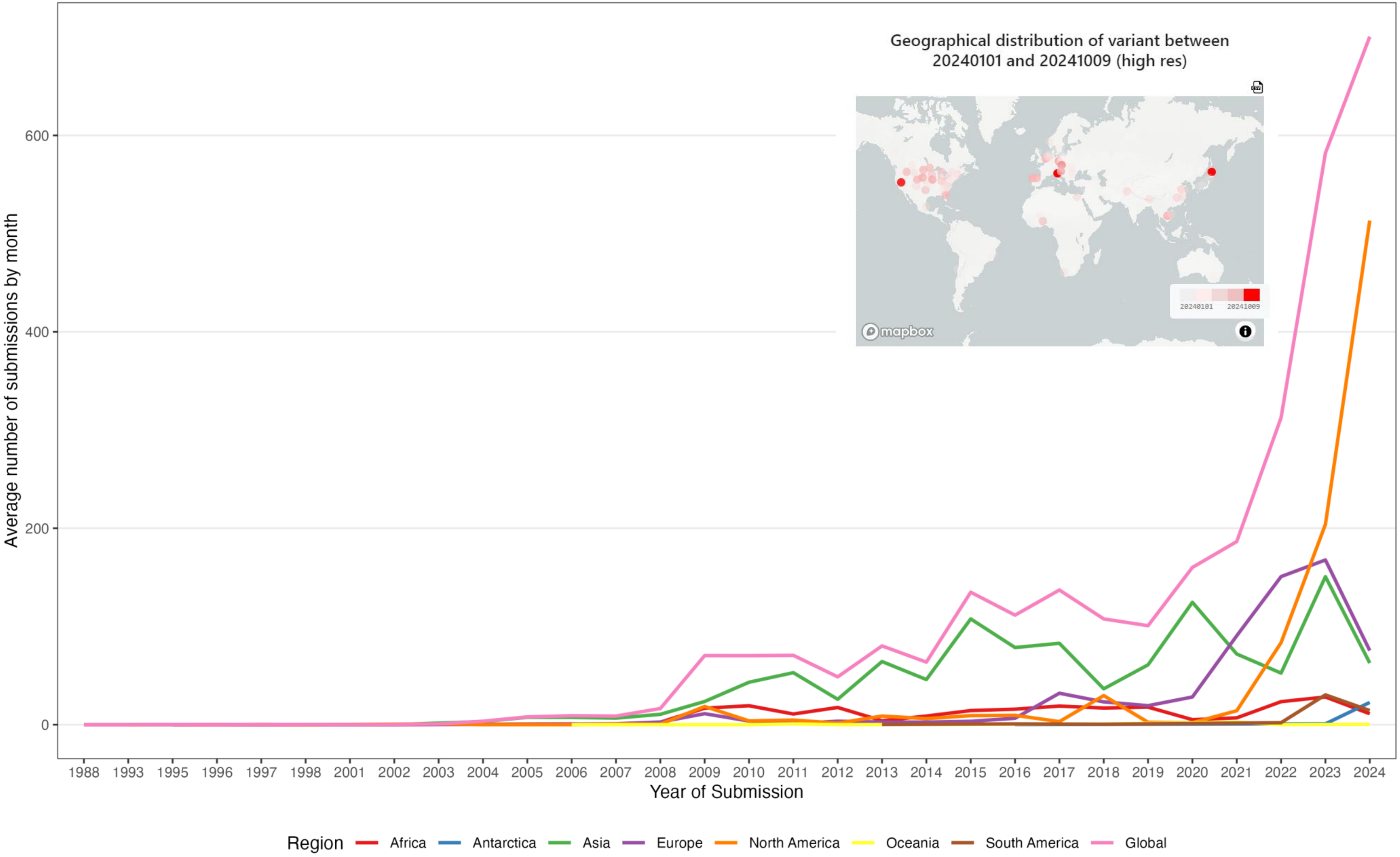
Literature reference

(Mutation L226P in the paper is at an equivalent position of the mutation in your query)



News on zoonotic human infections

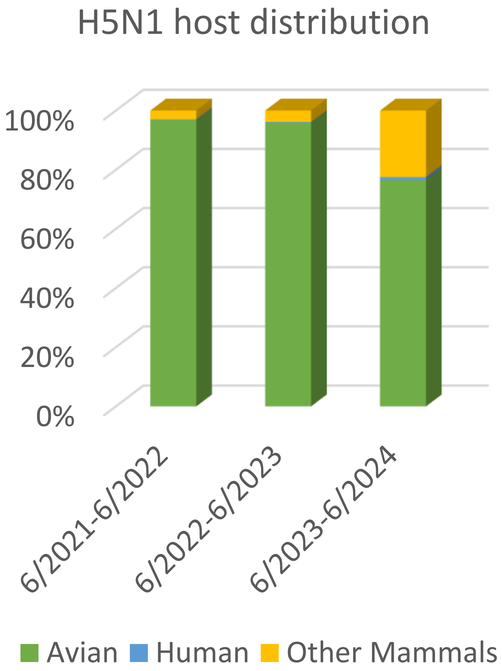
Influenza (H5*) GSD globally and by continent

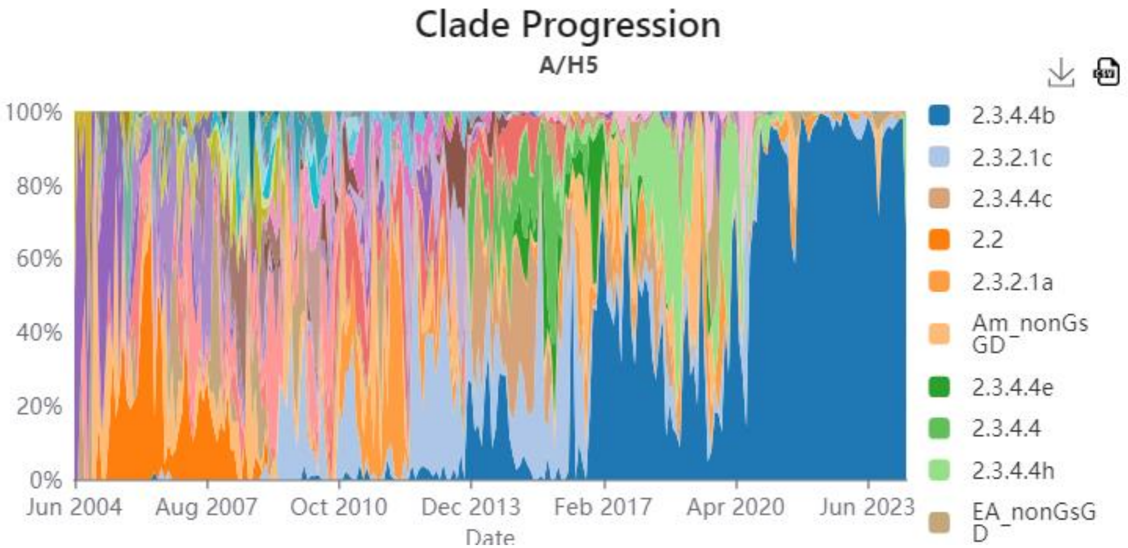


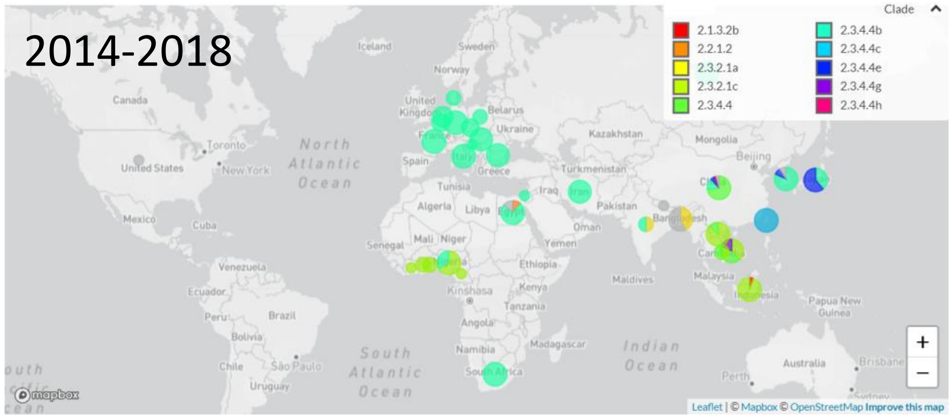
We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the statistics are based.

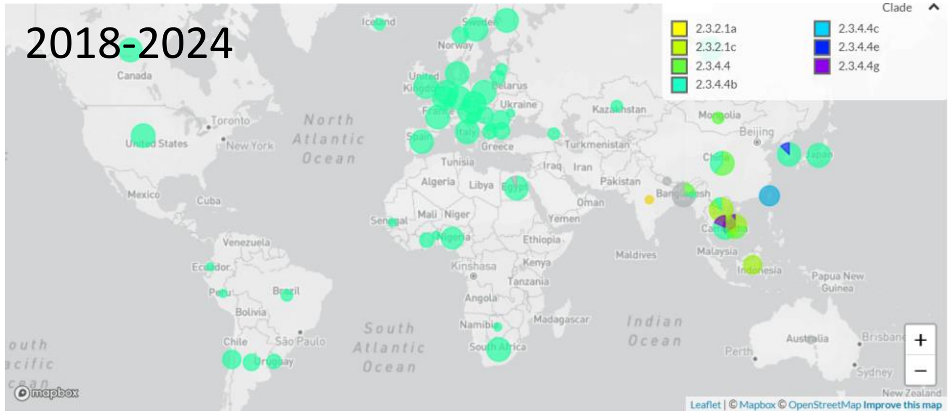
by BII/GIS, A*STAR Singapore

- **Rise of a new dominant H5N1 avian influenza lineage 2.3.4.4b**
- **Spread to all continents**
- **Outbreak in dairy cows in US**
- **Increasing infections in multiple mammalian species**
- **18 human cases detected**



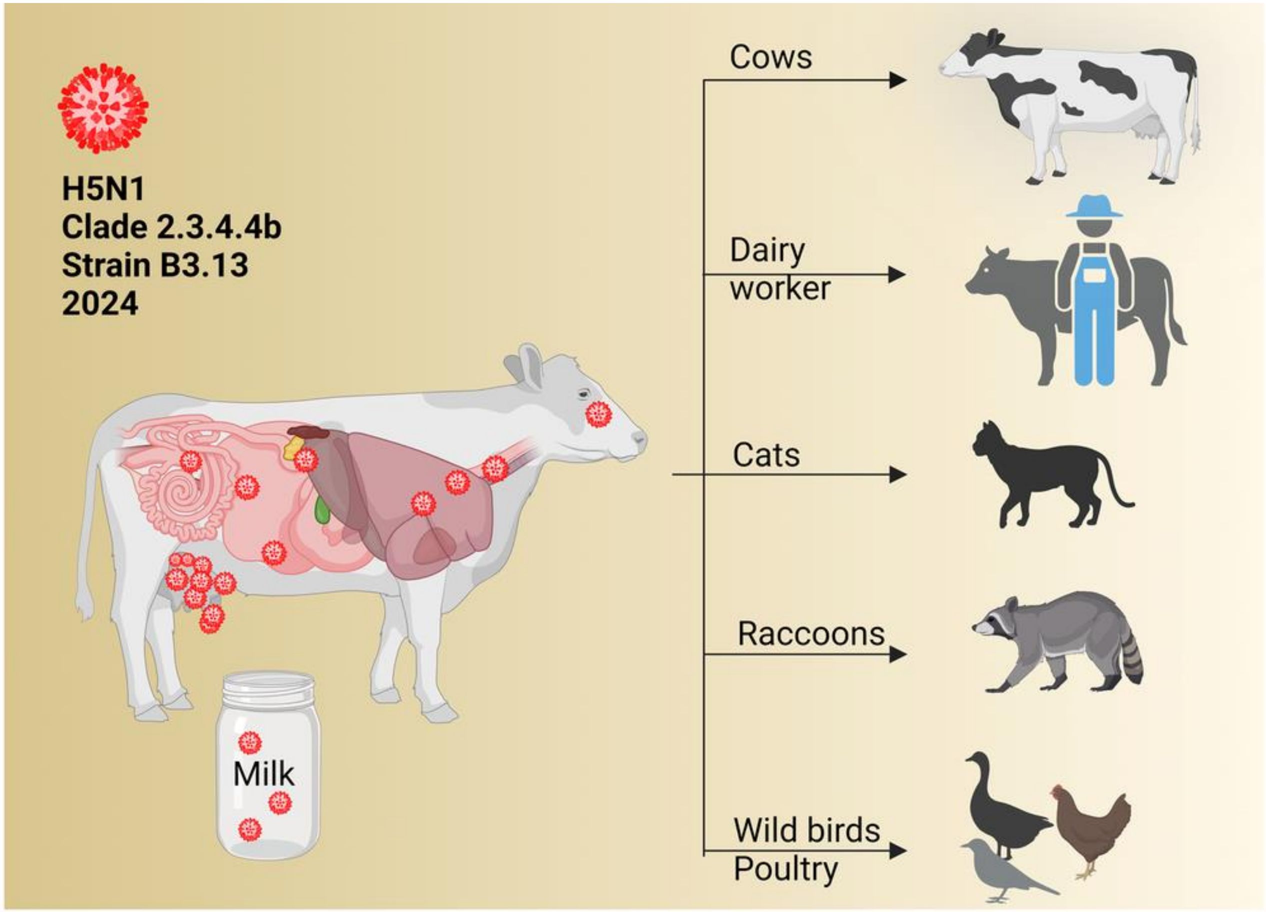






GISAID

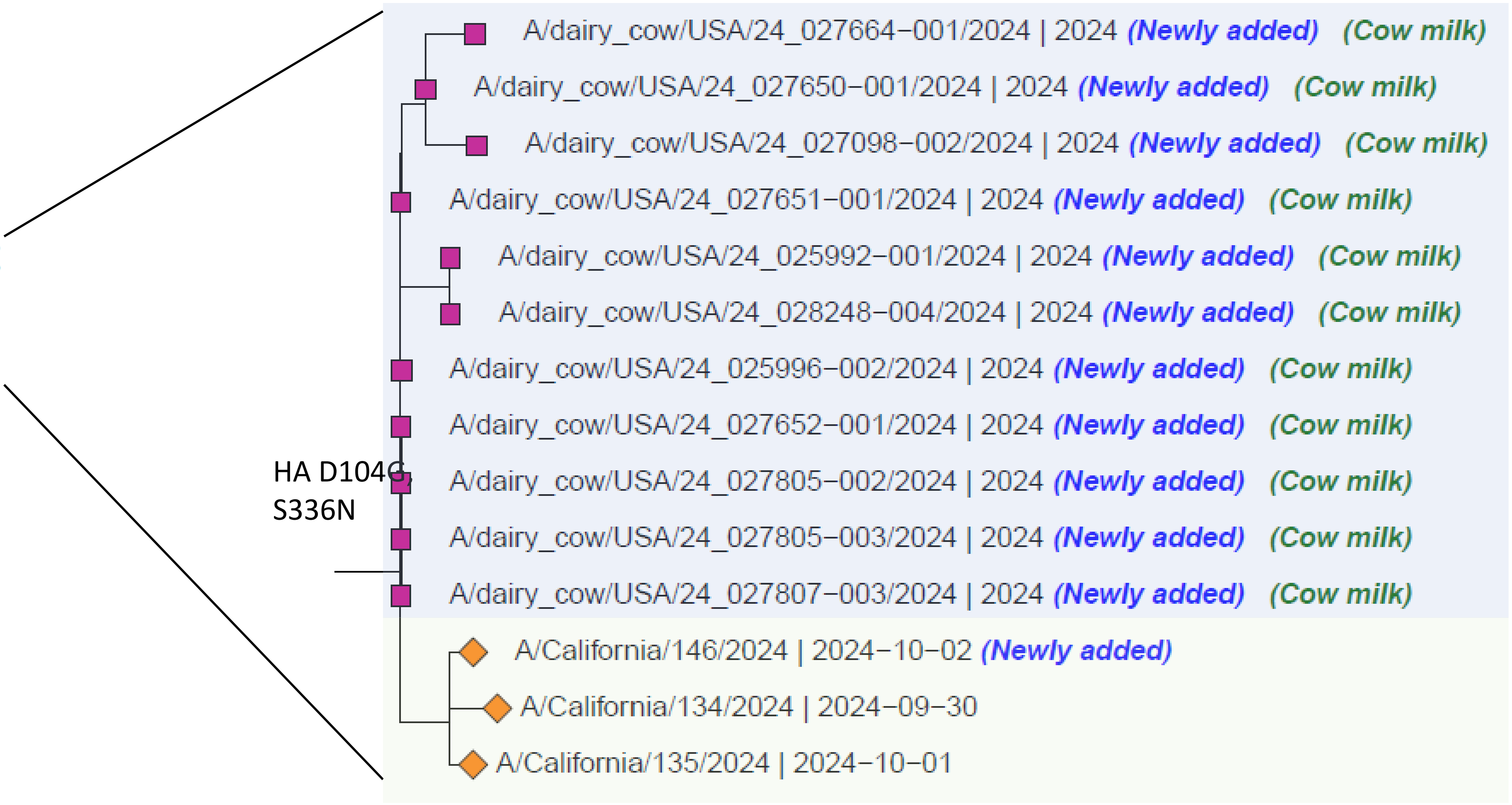
H5N1 Bird Flu circulating in the U.S. in Dairy Cows, Poultry and now found in pigs



The 2.3.4.4b clade of the highly pathogenic avian influenza (HPAI) virus causing outbreaks in wild and domestic birds around the world, continues to spread in dairy farms across the United States since March 2024, with **over 50 human cases reported thus far**. These HPAI viruses recently caused morbidity and mortality in multiple mammalian species, mostly carnivores, after consuming infected carcasses. Although cows had not been considered to be at risk of infection, the current outbreak in the U.S. demonstrates influenza remains unpredictable.

Over a thousand full virus genome sequences from this outbreak, collected from mammalian and avian specimens in at least 18 States, have thus far been made available in GISAID EpiFlu.

Dairy cow H5N1, submitted by USDA missing state info and incomplete collection date

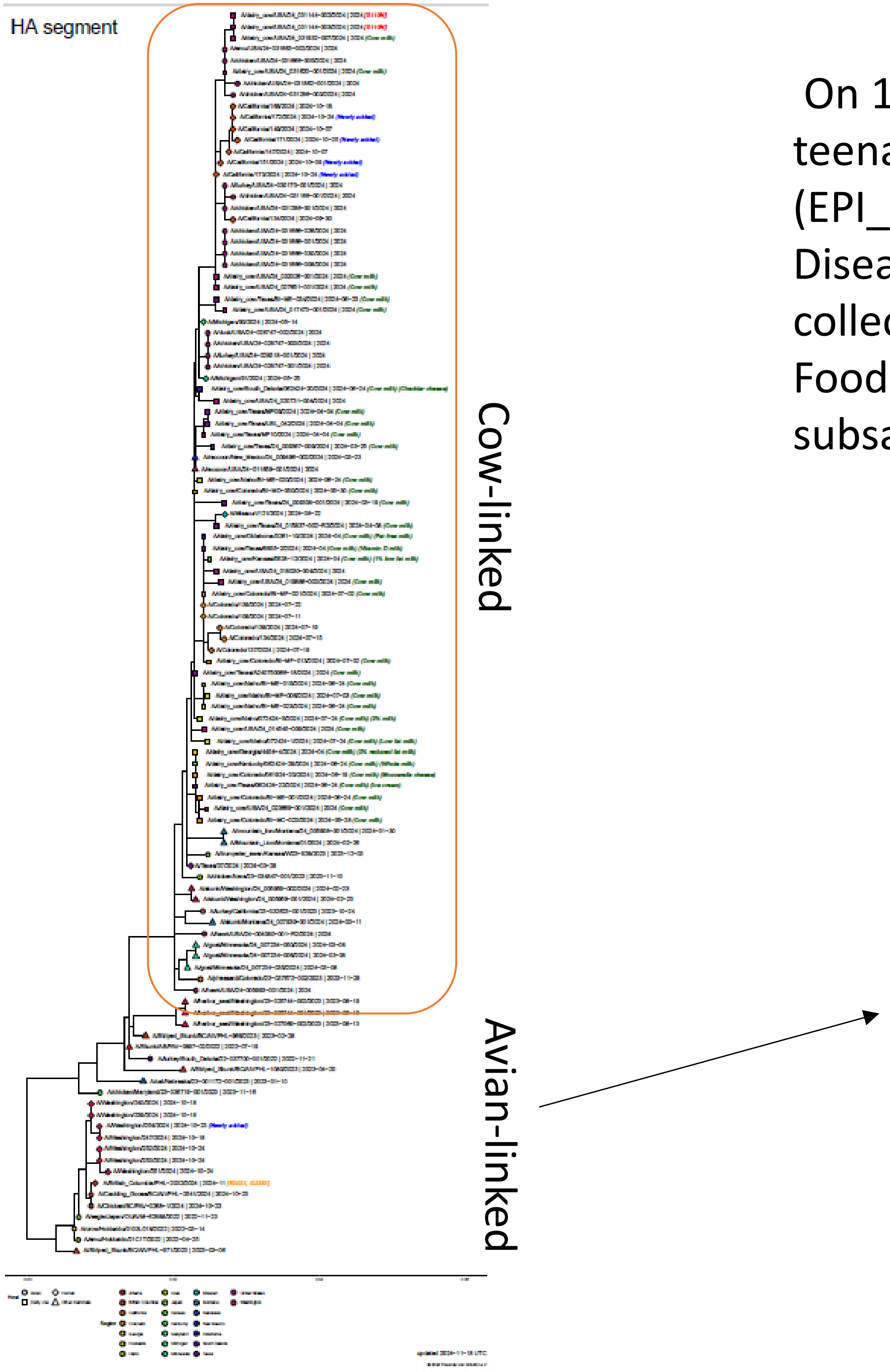


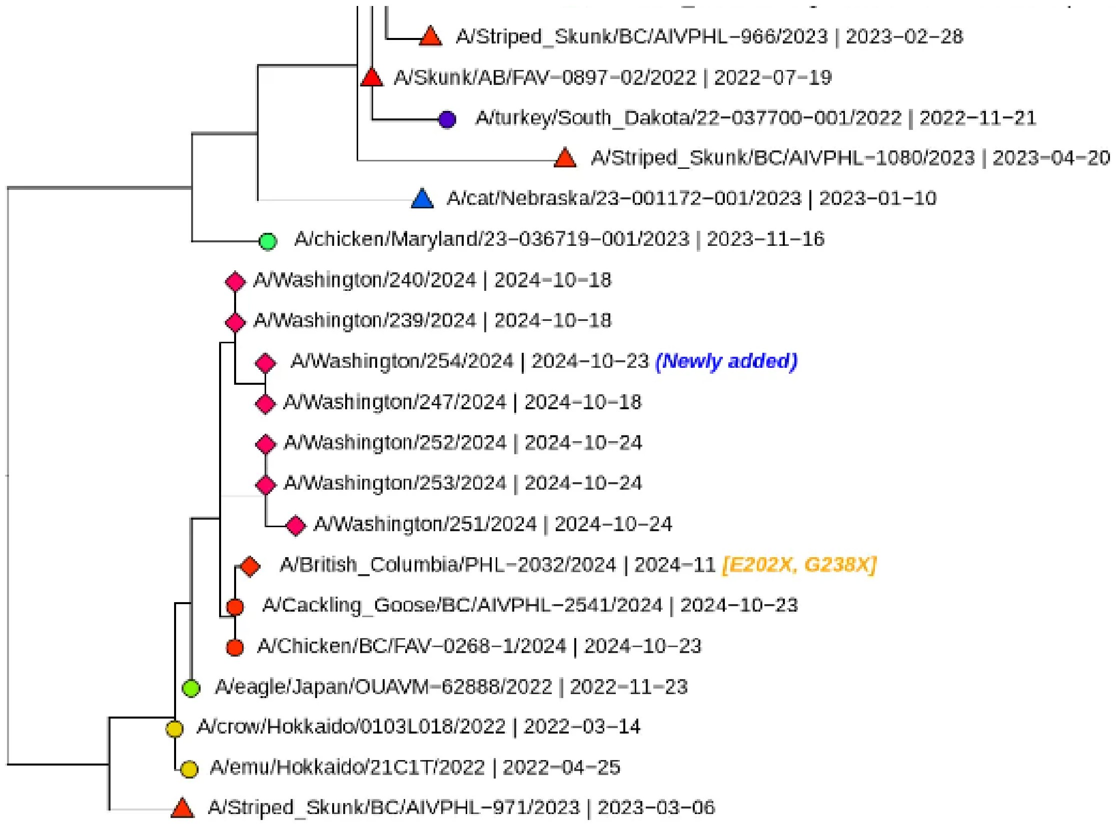
HA D104G, S336N

Human H5N1, submitted by US CDC with state info and complete collection date

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

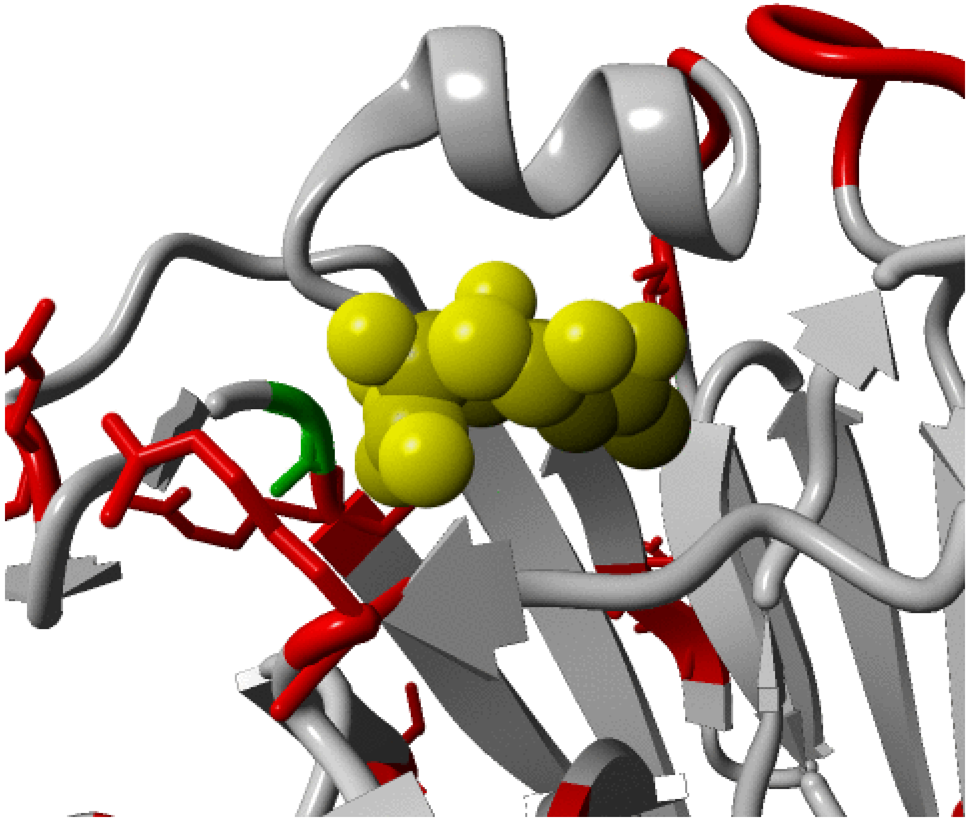
On 15. November, specimen data of British Columbia's first human case, a teenager who is currently hospitalized, with an unknown route of exposure (EPI_ISL_19548836) was made available by British Columbia Centre for Disease Control (BCCDC). Additionally, specimen data from poultry, collected between 20. and 23. October, was made available by the Canadian Food Inspection Agency. The latest trees, based on representative subsamples, are dated to 18 November 2024.

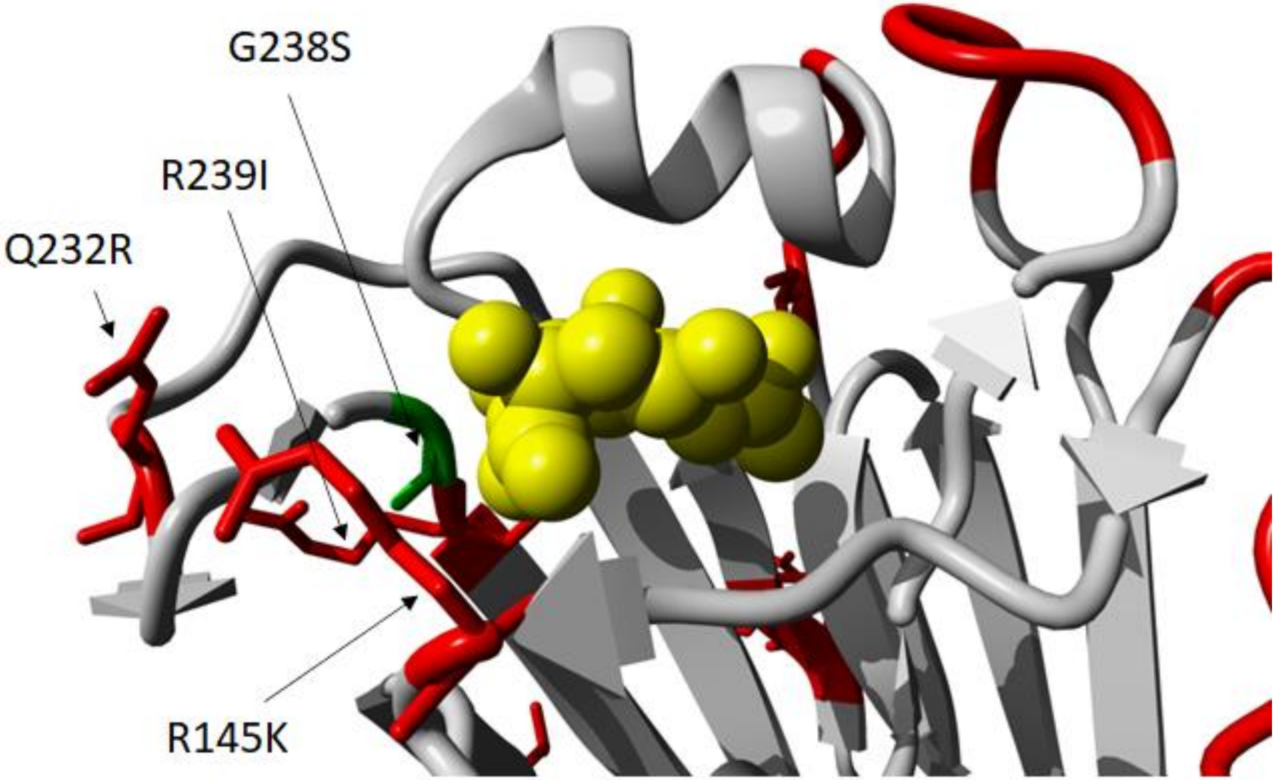




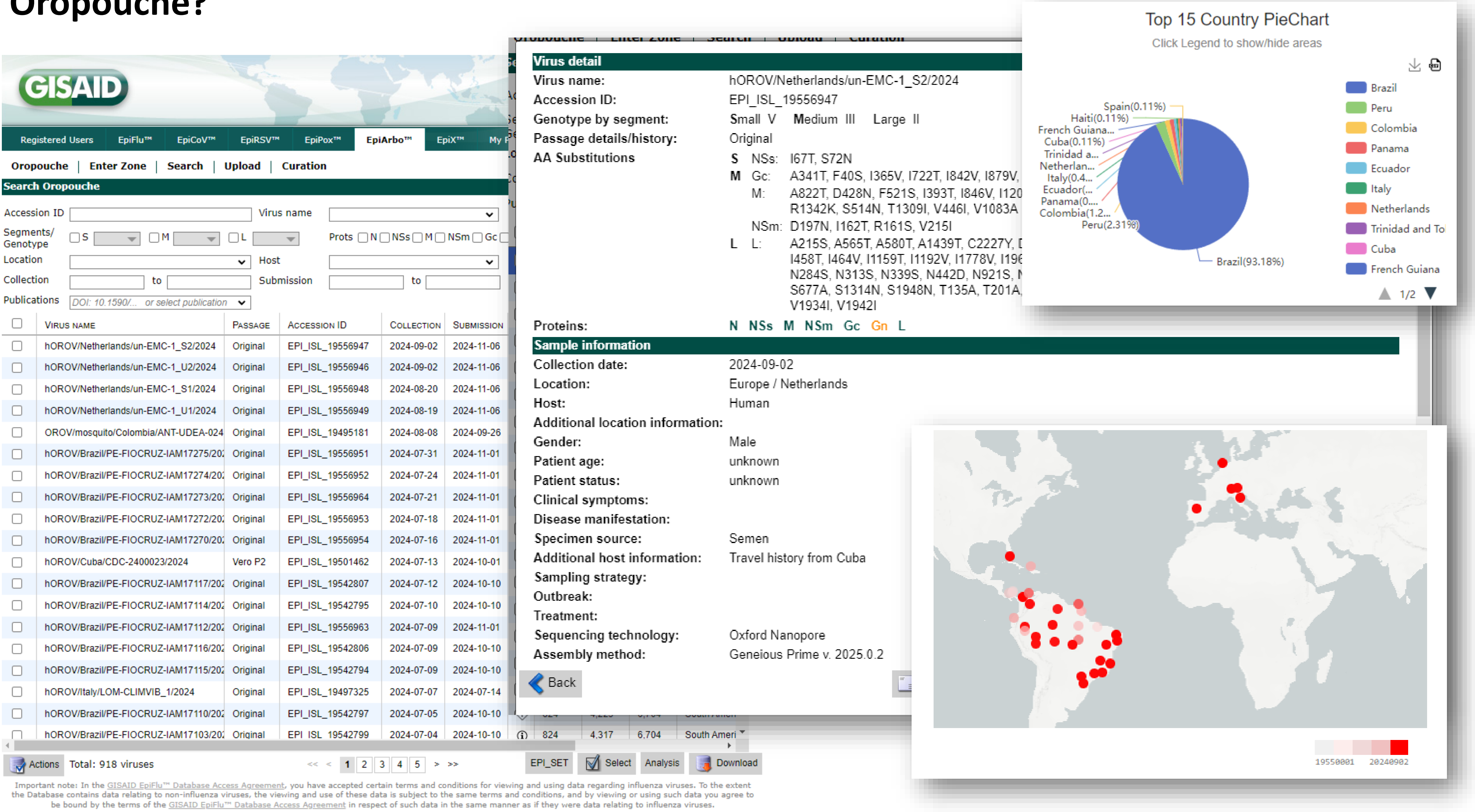
Or H10N3 as next possible pandemic?

First human case 2021 in Jiangsu Province, China. Reoccurrence 2024 in Yunnan. Human host adaptation marker G228S (G238S) in 31 of 45 avian samples (Asia, since 2020).





Or Oropouche?



Search Oropouche

Accession ID
Virus name
Segments/ Genotype ☐ S ☐ M ☐ L
Prots ☐ N ☐ NSs ☐ M ☐ NSm ☐ Gc
Location
Host
Collection to
Submission to
Publications *DOI: 10.1590/... or select publication*

☐	Virus name	Passage	Accession ID	Collection	Submission
☐	hOROV/Netherlands/un-EMC-1_S2/2024	Original	EPI_ISL_19556947	2024-09-02	2024-11-06
☐	hOROV/Netherlands/un-EMC-1_U2/2024	Original	EPI_ISL_19556946	2024-09-02	2024-11-06
☐	hOROV/Netherlands/un-EMC-1_S1/2024	Original	EPI_ISL_19556948	2024-08-20	2024-11-06
☐	hOROV/Netherlands/un-EMC-1_U1/2024	Original	EPI_ISL_19556949	2024-08-19	2024-11-06
☐	OROV/mosquito/Colombia/ANT-UDEA-024	Original	EPI_ISL_19495181	2024-08-08	2024-09-26
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17275/202	Original	EPI_ISL_19556951	2024-07-31	2024-11-01
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17274/202	Original	EPI_ISL_19556952	2024-07-24	2024-11-01
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17273/202	Original	EPI_ISL_19556964	2024-07-21	2024-11-01
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17272/202	Original	EPI_ISL_19556953	2024-07-18	2024-11-01
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17270/202	Original	EPI_ISL_19556954	2024-07-16	2024-11-01
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☐	hOROV/Brazil/PE-FIOCRUZ-IAM17117/202	Original	EPI_ISL_19542807	2024-07-12	2024-10-10
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17114/202	Original	EPI_ISL_19542795	2024-07-10	2024-10-10
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17112/202	Original	EPI_ISL_19556963	2024-07-09	2024-11-01
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17116/202	Original	EPI_ISL_19542806	2024-07-09	2024-10-10
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17115/202	Original	EPI_ISL_19542794	2024-07-09	2024-10-10
☐	hOROV/Italy/LOM-CLIMVIB_1/2024	Original	EPI_ISL_19497325	2024-07-07	2024-07-14
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17110/202	Original	EPI_ISL_19542797	2024-07-05	2024-10-10
☐	hOROV/Brazil/PE-FIOCRUZ-IAM17103/202	Original	EPI_ISL_19542799	2024-07-04	2024-10-10

Total: 918 viruses

<< < 1 2 3 4 5 > >>

Important note: In the GISAID EpiFlu™ Database Access Agreement, you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the GISAID EpiFlu™ Database Access Agreement in respect of such data in the same manner as if they were data relating to influenza viruses.

Virus detail

Virus name: hOROV/Netherlands/un-EMC-1_S2/2024
Accession ID: EPI_ISL_19556947
Genotype by segment: **Small** V **Medium** III **Large** II
Passage details/history: Original
AA Substitutions
S NSs: I67T, S72N
M Gc: A341T, F40S, I365V, I722T, I842V, I879V,
M: A822T, D428N, F521S, I393T, I846V, I120
R1342K, S514N, T1309I, V446I, V1083A
NSm: D197N, I162T, R161S, V215I
L L: A215S, A565T, A580T, A1439T, C2227Y,
I458T, I464V, I1159T, I1192V, I1778V, I196
N284S, N313S, N339S, N442D, N921S,
S677A, S1314N, S1948N, T135A, T201A,
V1934I, V1942I
Proteins: N NSs M NSm Gc Gn L

Sample information

Collection date: 2024-09-02
Location: Europe / Netherlands
Host: Human
Additional location information:
Gender: Male
Patient age: unknown
Patient status: unknown
Clinical symptoms:
Disease manifestation:
Specimen source: Semen
Additional host information: Travel history from Cuba
Sampling strategy:
Outbreak:
Treatment:
Sequencing technology: Oxford Nanopore
Assembly method: Geneious Prime v. 2025.0.2

Thank you!

Committed to GIHSN

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GIHSN 12TH ANNUAL MEETING, 25-26 NOVEMBER 2024

PERSPECTIVES AND CHALLENGES FOR INFLUENZA VACCINE SELECTION

Nicola LEWIS, Crick WHO CC

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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

WORKSHOP 1: SCALING UP AND OPTIMIZING WGS

PLENARY BRIEF, BY BRUNO LINA, NIC LYON, FRANCE

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Epidemiology

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WORKSHOP 1 – OBJECTIVES

Scaling up and optimizing WGS in GIHSN, 2024-25 season

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

→ Experience sharing between sites to identify barriers & group discussions to find solutions

Expected outcomes: Set up best practices and improve WGS scale up during upcoming 2024-25 surveillance period

SPECIMEN SELECTION FOR WGS

☐ **Current targets (season 2024-25)**

- WGS for a **minimum** of **50 to 100 influenza viruses** will be expected. **If number of influenza positive cases are low, site is encouraged to complete WGS of SARS-COV-2**
  - **If 50 to 100 Flu+ -> WGS for all samples should be done**
  - **If more than 100 Flu+, the following WGS algorithm should apply:**
    - all severe cases (ICU admission, mechanical ventilation)
    - 10-25 samples per month during the 6 months of flu season stratified by age (<5yo, 5-65, >65)
    - all samples off season

☐ **Aspirational target (starting season 2025-26): 200 WGS per site**

Flu first and completed by SARS-COV2 if flu+ is low

Same algorithm should apply

Next year 2025-26, grant allocation will also consider lab resources for the WGS done locally

WHICH OPTIONS FOR SEQUENCING: LOCALLY / IN LYON (GIHSN PLATFORM) / WITH WHO CC?

What to do for the 2024-25 season

- Can you proceed and scale up with WGS locally?
- If not or only partially, where to send the samples (Lyon ? WHO CC?)

Summarize challenges and main recommendations

CONSIDERATIONS ON SHIPMENT (TO BE OPTIMIZED)

What to do for the 2024-25 season

For those that are not doing locally:

- Shipment of samples is very expensive (between 2000 and 3000 euros) – this should be organized when the batch is big enough
- Batch of 25 minimum with some exceptions (before Vaccine Composition meetings)
- Check for CT value

Summarize challenges and main recommendations

UPLOAD OF RESULTS ON GISAID (GIHSN TAG)

What to do for the 2024-25 season

- WGS data uploaded to GISAID by site in a reasonable timeframe, so results are available for the WHO Vaccine Composition Meetings
- Link between WGS data uploaded in GISAID and clinical data in GIHSN required
- Identification of GIHSN specimens for exhaustive uploads
  - E.g. A/PERU/GIHSN-HCL024130069401/2024

Summarize challenges and main recommendations

WORKSHOP 1 – AGENDA

☐ **14.45 to 14.50:** Split the attendance in 3 predefined groups

Move from plenary room to groups' room

☐ **14.50 to 15.30:** Groups discussions on pre-defined topics/questions

Only for in-person participants

One/two moderators to support discussion – template slides to report outputs

☐ **15.30 to 16.15:** Sharing in Plenary

One rapporteur (site) per group to present outputs (8') and then plenary discussions/wrap-up

WORKSHOP 1 - GROUPS

Group 1

Moderators: Bruno Lina & Cédric Mahé
Room: plenary Salle Ste-Victoire

- Côte d'Ivoire
- Lebanon
- Ukraine
- Brazil
- Peru

Group 2

Moderators: John McCauley & Catherine Commaille-Chapus
Room: Salle Jas de Bouffan

- South Africa
- New Zealand
- Spain - Valencia
- Canada

Group 3

Moderators: Dmitriy Pereyaslov & Laurence Torcel-Pagnon
Room: Salon Olivier

- Kenya
- Uganda
- Pakistan
- Romania
- USA

All participants are invited to join the workshop splitting themselves into the 3 groups

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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

RESEARCH PROJECTS LEVERAGING THE GIHSN PLATFORM

Moderated by Marta Nunes, CERP & Sandra Chaves, Foundation for Influenza Epidemiology

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RESEARCH PROJECTS LEVERAGING THE GIHSN PLATFORM

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

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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

SPECIFIC INFLUENZA ACTIVITY FROM SOUTH AFRICA

Vicky Baillie, University of the Witwatersrand, Johannesburg

WITS VIDA
UNIVERSITY OF THE WITWATERSRAND
VACCINES & INFECTIOUS DISEASES ANALYTICS

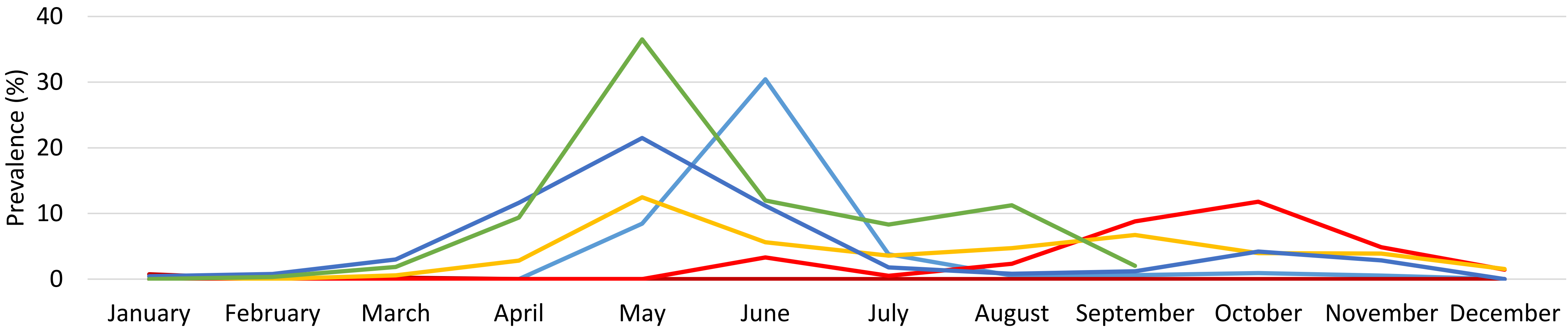
BACKGROUND TO RSA SITE

- The study takes place at the Chris Hani Baragwanath Academic Hospital (CHBAH) in Soweto, South Africa
  - Large (3,400 beds), secondary-tertiary facility
  - Public hospital
- Soweto has a total population approx. 1.9 million people including 190 000 <5 year old
  - Rural, low income population
  - HIV prevalence among pregnant women➔~28%
- Only paediatric patients are enrolled into the study
- Influenza season in South Africa normally peaks between April to September with peak in June
- Pre-pandemic incidence was 54/100 000 children<5years of age

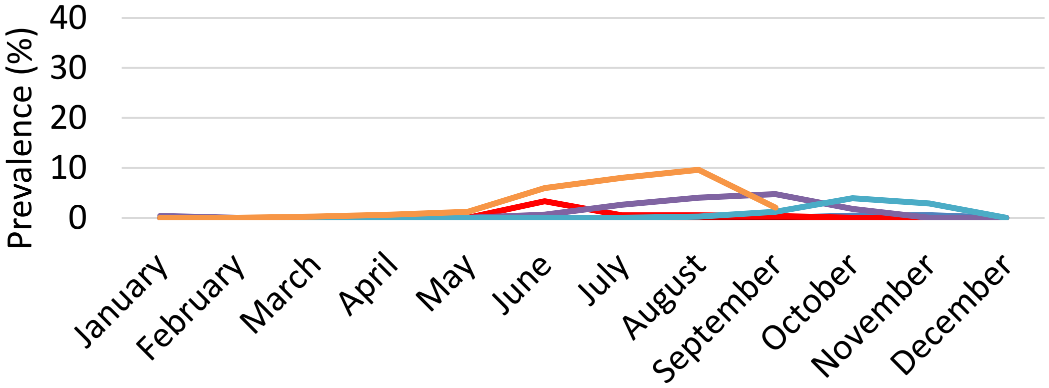
- Previously we have only tested for influenza, RSV, hMPV and *Bordetella pertussis*
- Started testing for SARS-CoV-2 in 2020
- Started testing for hRV, PIV-3, AdenoV and EnteroV in 2023
- Enroll >3500 participants per year

INFLUENZA RESULTS

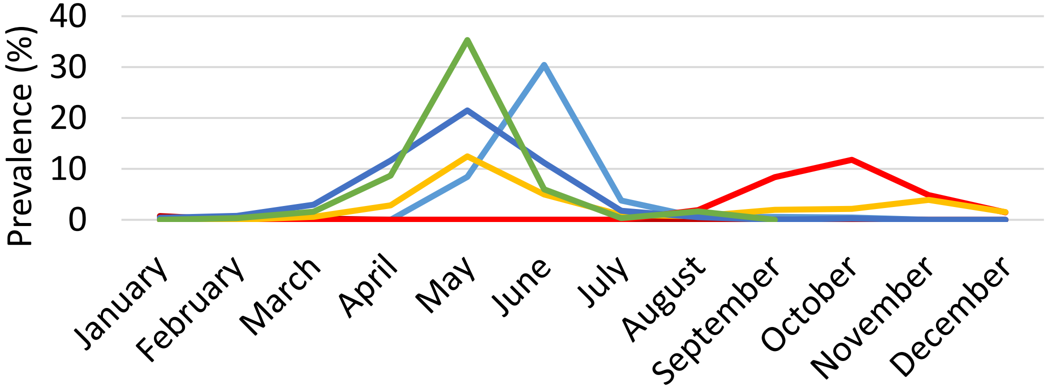
Total Influenza prevalence



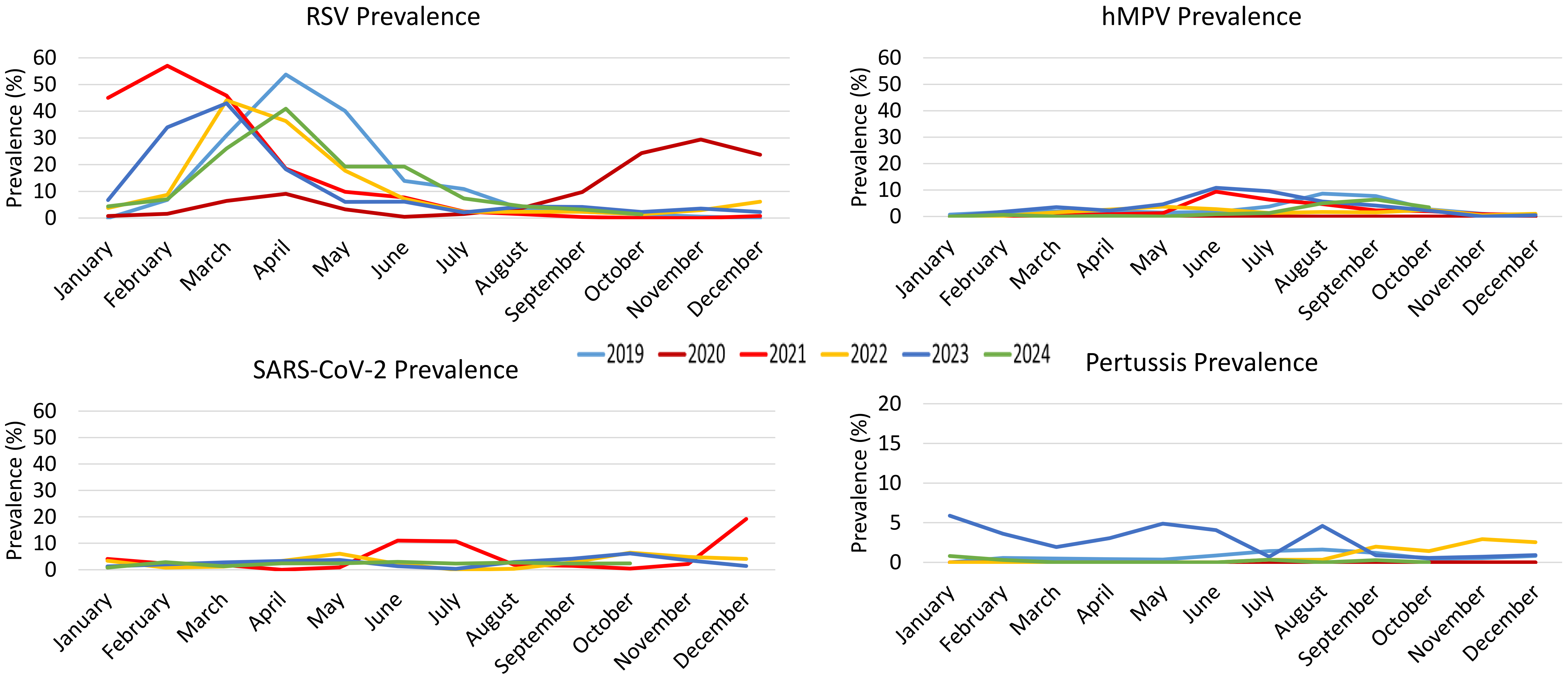
Influenza B prevalence

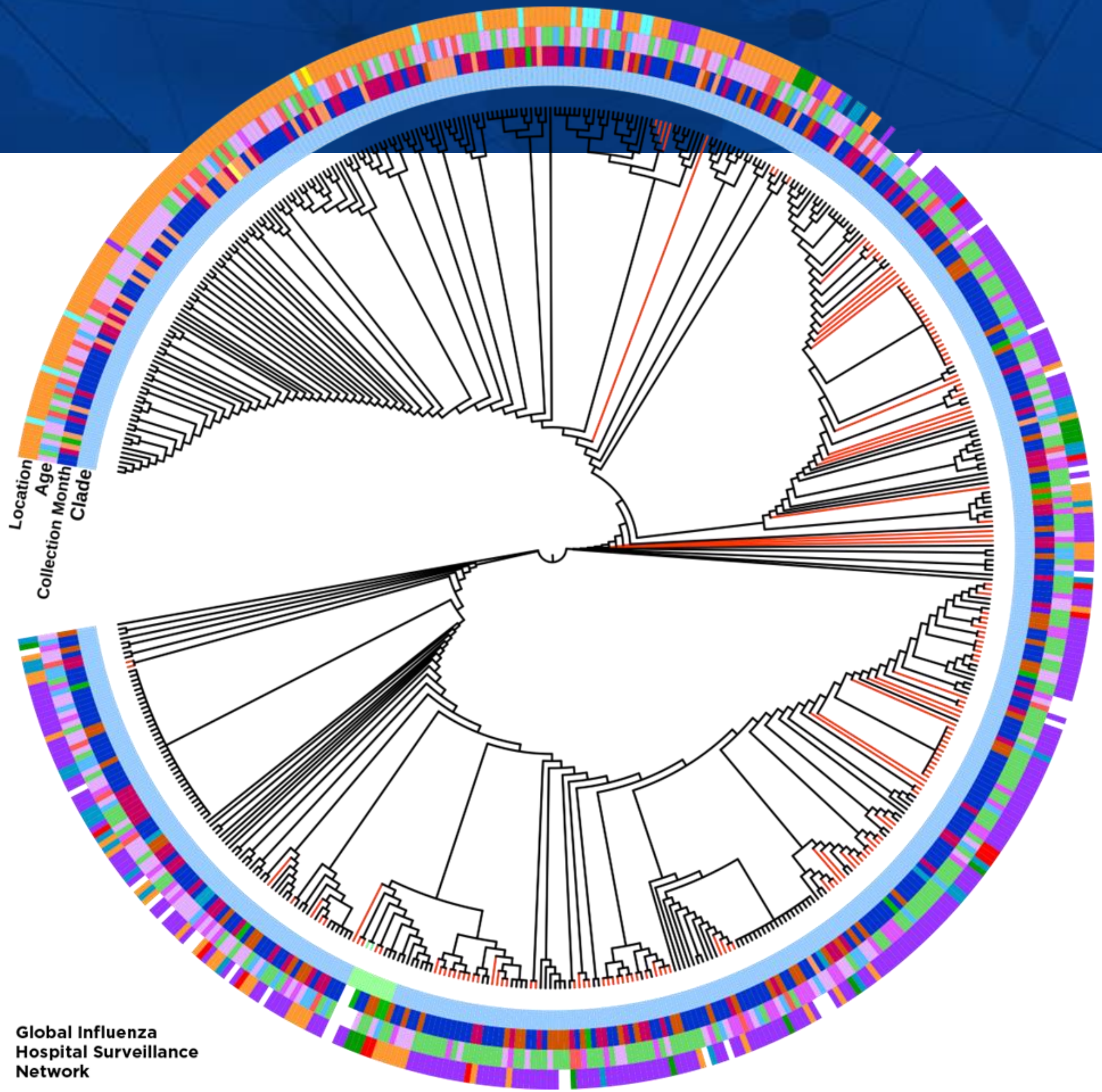


Influenza A prevalence



OTHER TARGETS





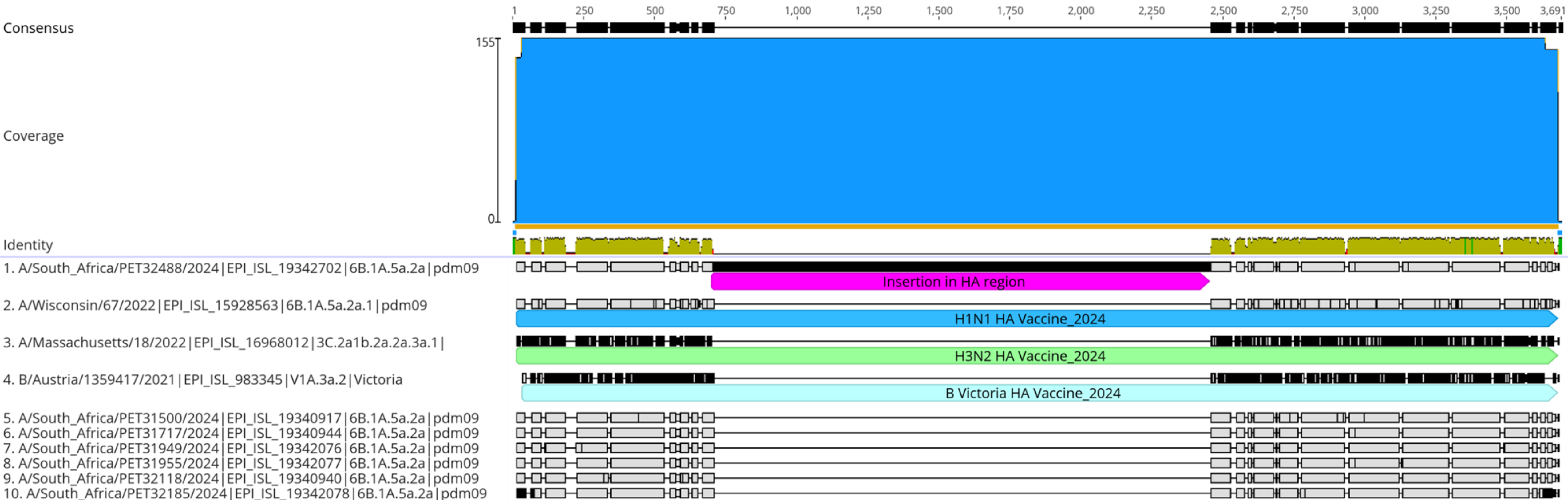
Collection month (2024)	Colour
Jan	🟪
Feb	🟦
Mar	🟩
Apr	🟧
May	🟦
Jun	🟥
Jul	🟧
Aug	🟨

Age (years)	Colour
< 1 year	🟪
1 < age ≤ 5	🟩
5 < age ≤ 18	🟦
19 ≤ age ≤ 60	🟪
years > 60	🟥

Location (RSA)	Color
Gauteng	🟪
Kwazulu Natal	🟩
Limpopo Province	🟨
Mpumalanga	🟥
North West	🟦
Province of Eastern Cape	🟦
Province of the Western Cape	🟧
Not specified	⬜

Subclade	Colour
5a.2a	🟦
5a.2a.1	🟩

SOME INTERESTING RECOMBINATION EVENTS!

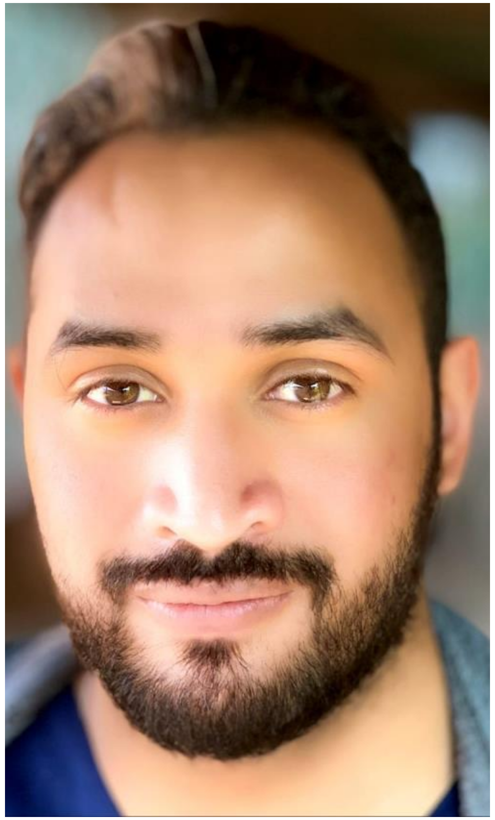


THANK YOU!

THANKS TO ALL THE STAFF AT WITS-VIDA

THE PARTICIPANTS AND THEIR FAMILIES

THE FOUNDATION FOR THE FUNDING



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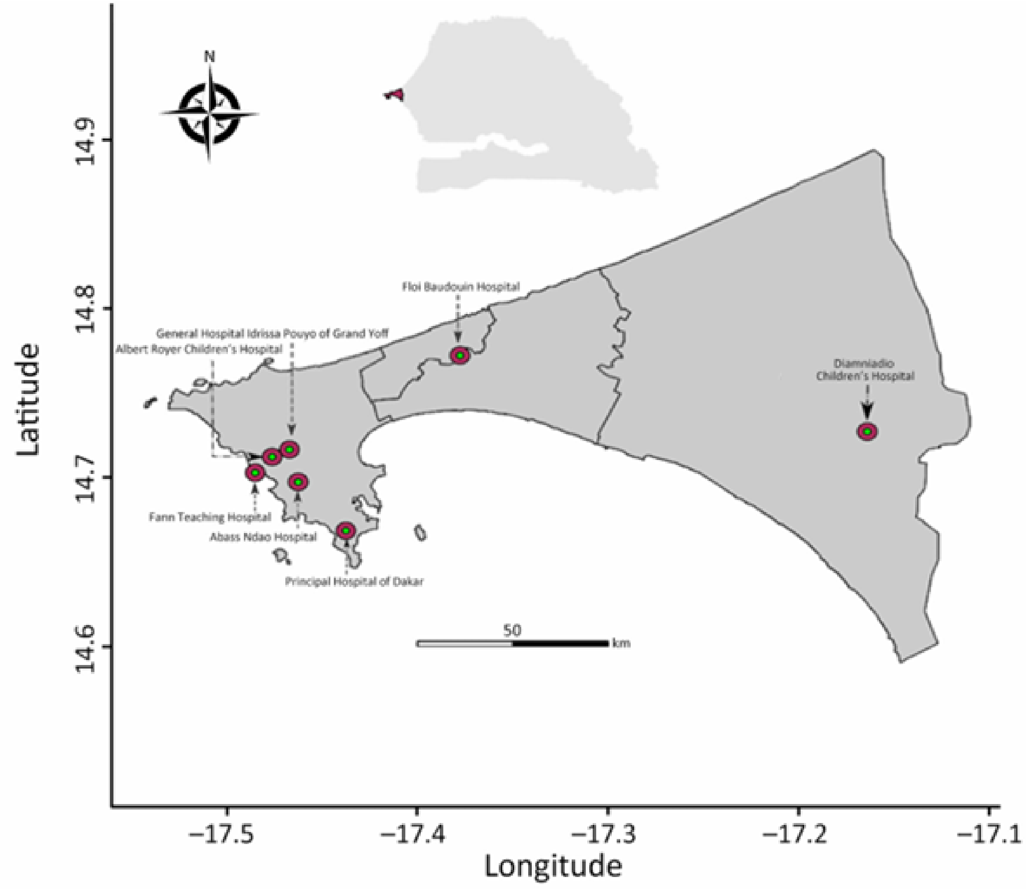
GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

HOSPITAL-BASED SURVEILLANCE OF SARI IN SENEGAL: FOCUS ON RSV

Ndongo DIA, Institut Pasteur of Dakar, Senegal

Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

- ✓ Initiated in 2015, SARI surveillance is conducted in collaboration with 7 reference hospitals
- ✓ **Extended SARI Definition: S**evere (requiring hospitalization) *AND* **A**cute (onset within the last 10 days) *AND* **R**espiratory **I**nfection (having cough or shortness of breath). **In infants <6 months old, also include:** Apnea *OR* Sepsis (fever, hypothermia, shock, seriously ill with no apparent cause)
- ✓ Collect data in relation to RSV infection: burden (especially in infants), vaccination perspectives, genetic monitoring (full genome sequencing)
- ✓ SARI surveillance restricted in DAKAR (capital City): main hospitalization capacities of the country, most densely populated region



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Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

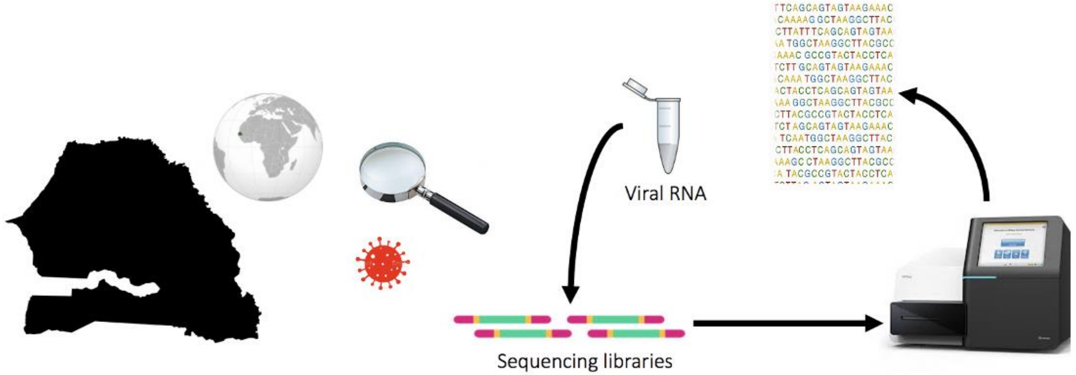
Lab Diagnostic

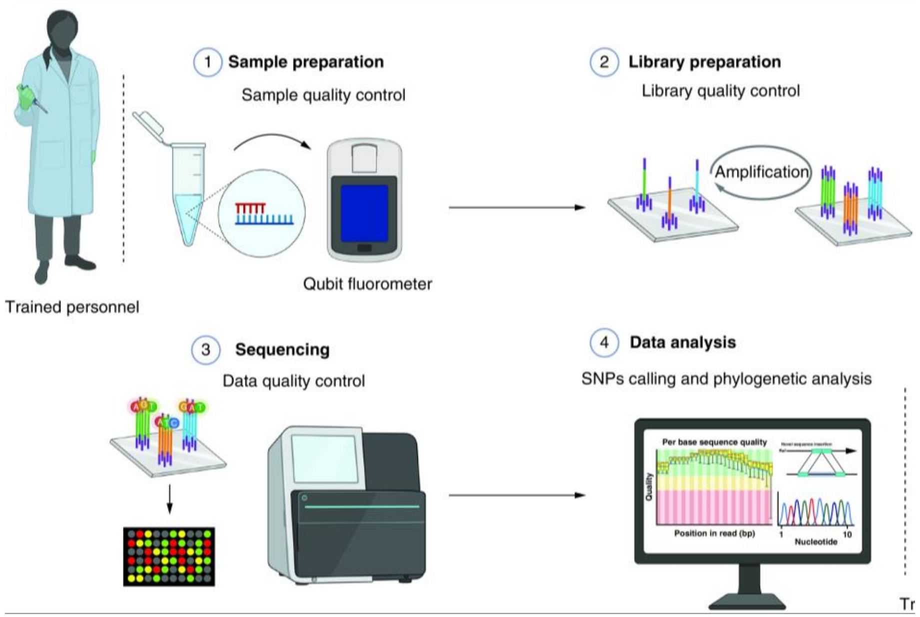
- SARI samples, in addition to being tested for respiratory viruses (Flu, SARS-CoV-2, RSV, RV, EV, HMPV, AdV, BoV, human CoVs, PIVs), are also tested for the most common respiratory bacteria including: *Haemophilus influenzae, Klebsiella Pneumoniae, Moraxella pneumonae, Staphylococcus aureus, Streptococcus pneumoniae, Bordetella Pertussis, Streptococcus Pneumoniae*

- Active surveillance program of EV-D68: all ILI and Rhino/Enterovirus-positive SARI samples are routinely tested for EV-D68.

Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

Genomic surveillance





Routine genomic surveillance of respiratory viruses

(RSV, Flu, SARS_CoV2)

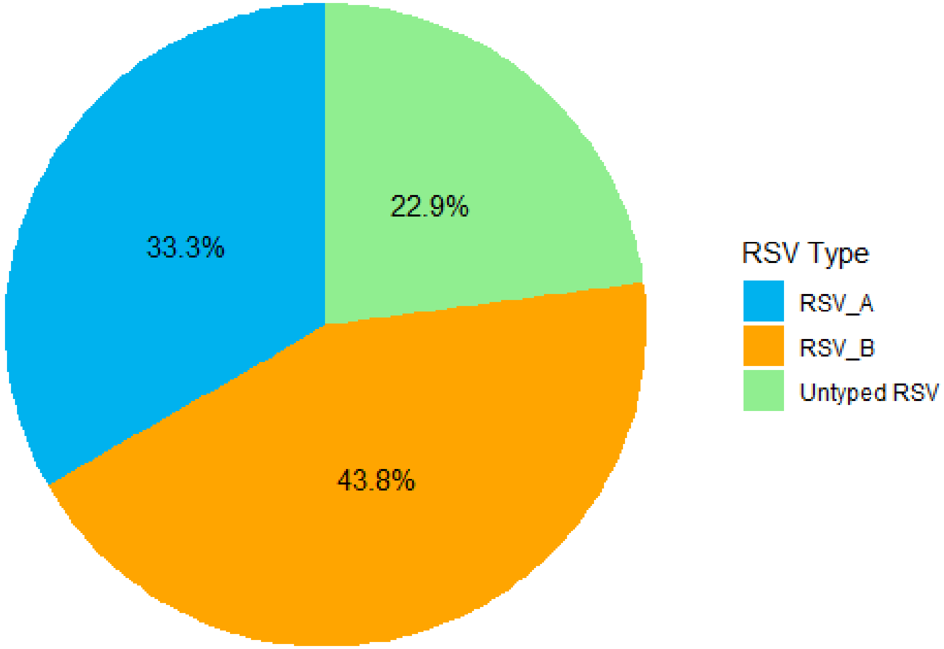
Whole-genome sequencing workflow

GISAID

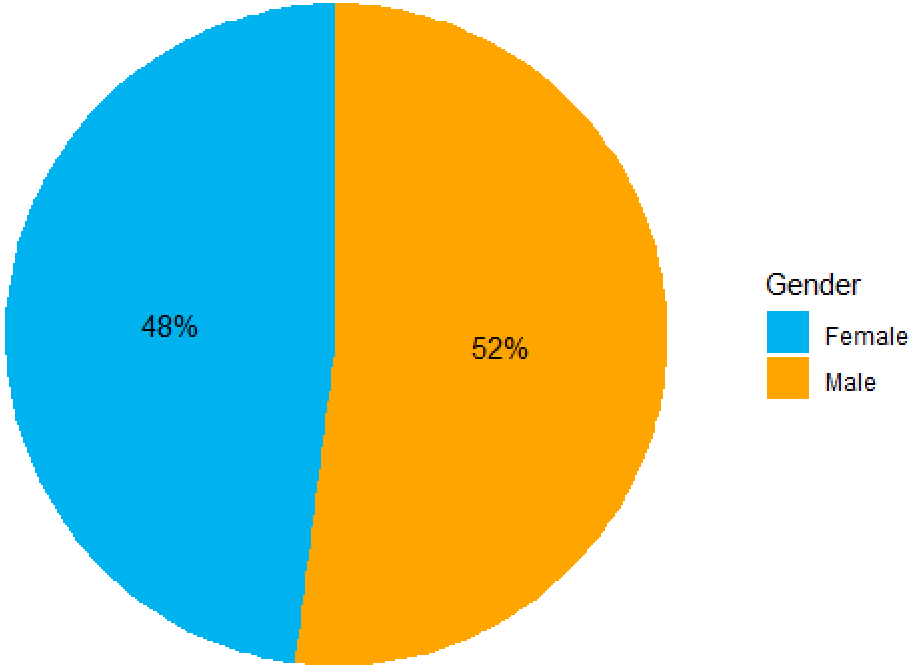
Genomic sequences submitted to the GISAID database

Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

- From January, 1 2022 to October 31 2024, **2850 SARI samples** were received at the NIC and analyzed for RSV
- RSV was detected in **10,7%** (306/2850)



Repartition by RSV subtype



RSV gender repartition

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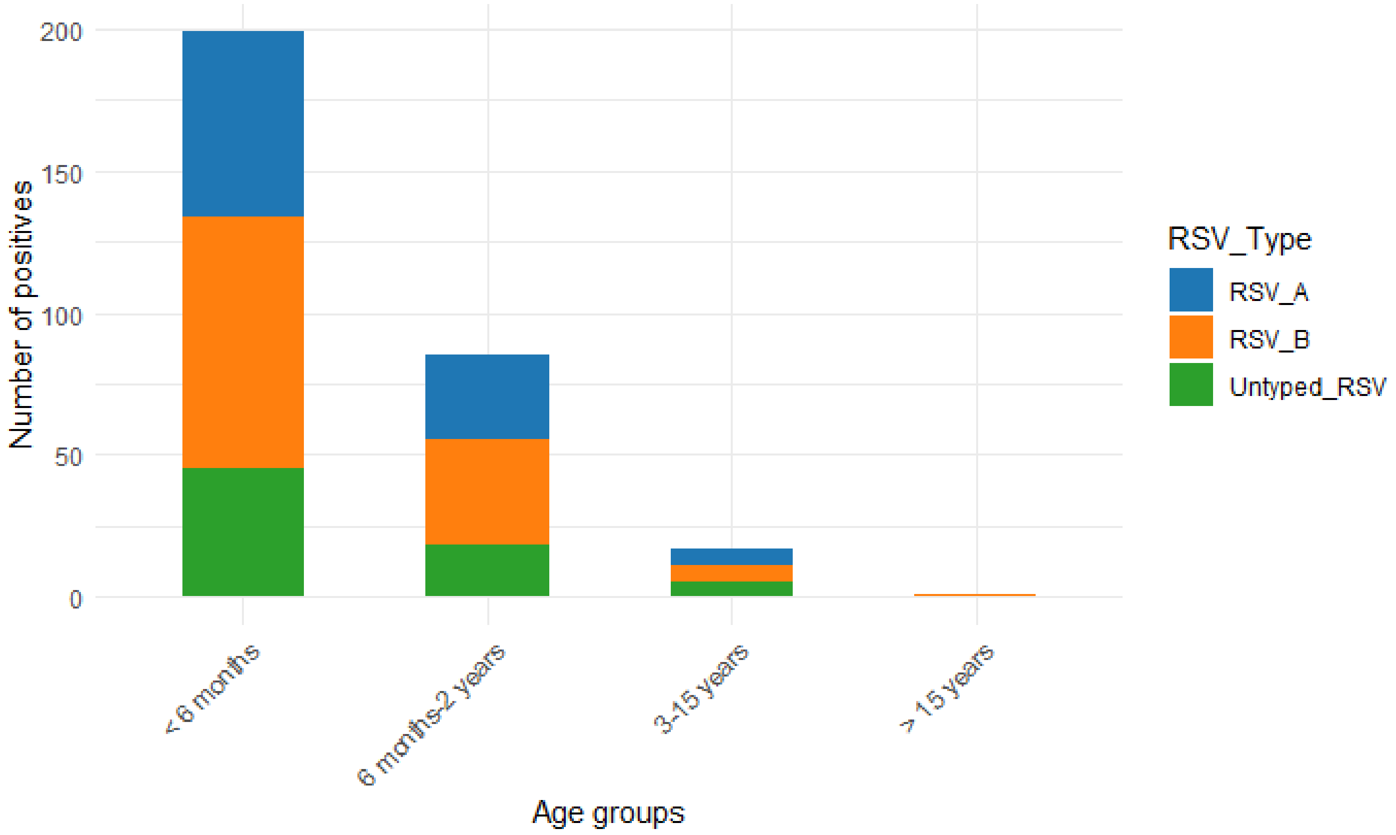
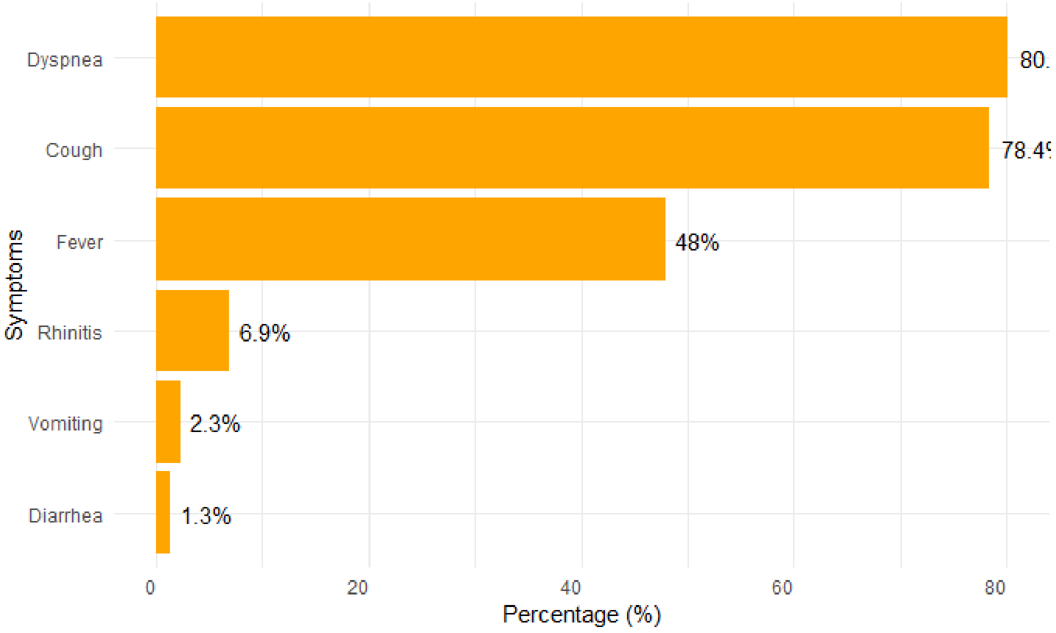
Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal



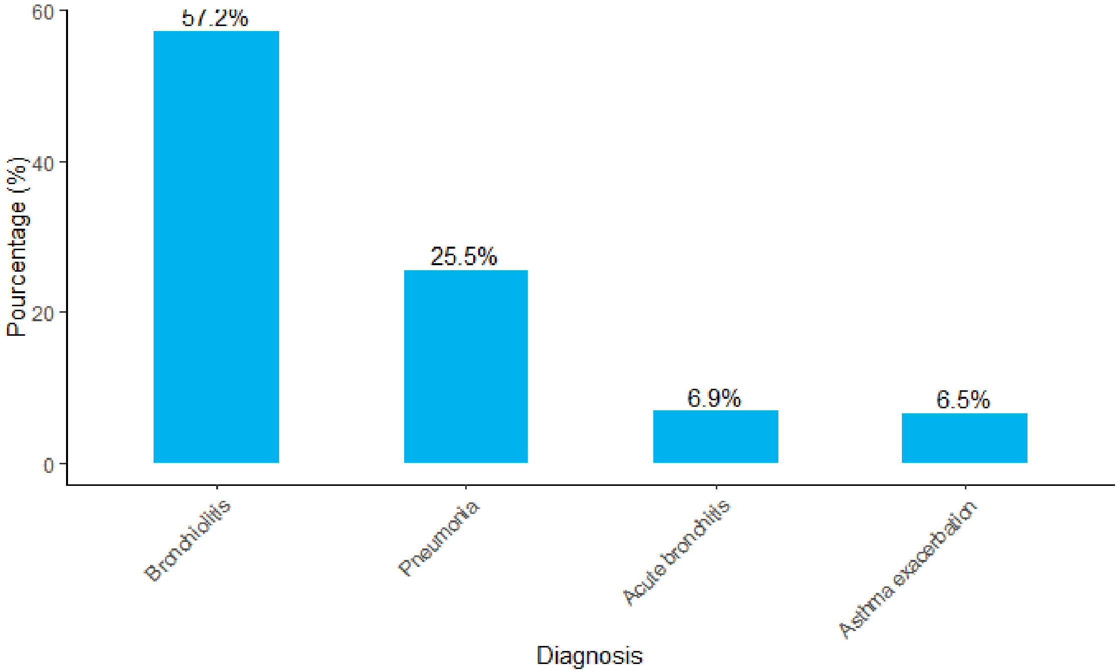
- ➢ Highest RSV detection rate in patients aged < 6 months, (**65%;** 199/306)
- ➢ Lowest detection rate in patients aged > 15 years old with only one case (**0.7%;** 1/306)
- ➢ RSV was detected in **27.8%** (85/306) in the age group 6 months-2 years and 5,5% (17/306) in patients aged 3-15 years.

Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

- At the time of admission, besides cough and fever, breathing difficulties are more commonly reported among RSV positif patients

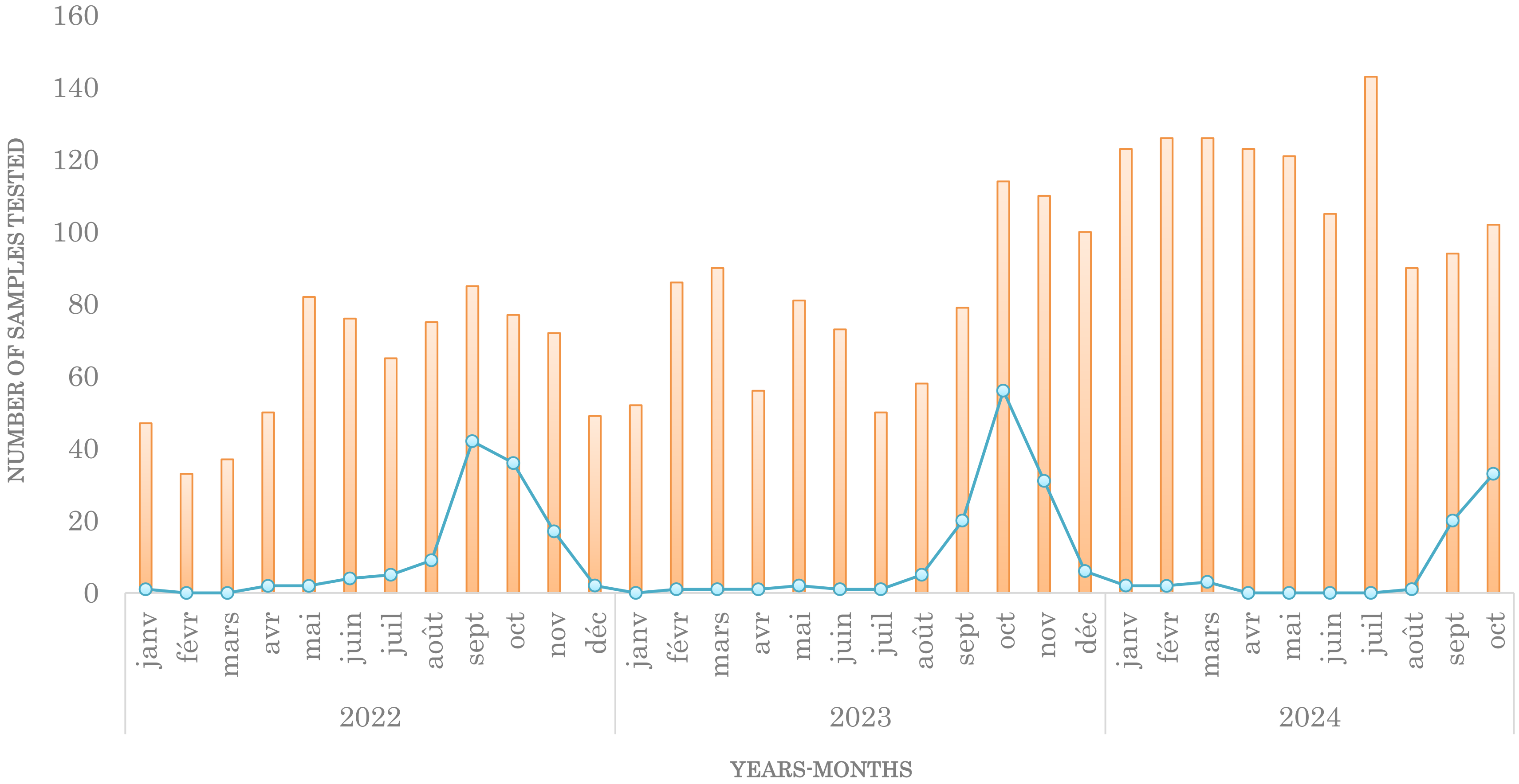


Repartition by symptoms



- More than half (57.2%) of all inpatients infected with RSV had bronchiolitis, whereas pneumonia was diagnosed in **25.5%**.
- Acute bronchitis and asthma exacerbation were diagnosed in **6.9%** and **6.5%** of RSV positive patients respectively

Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal



- ➢ From January 2022 through October 2024, we observed a clear seasonal pattern of RSV activity in Senegal (highest detection rates were observed between August and November each year).

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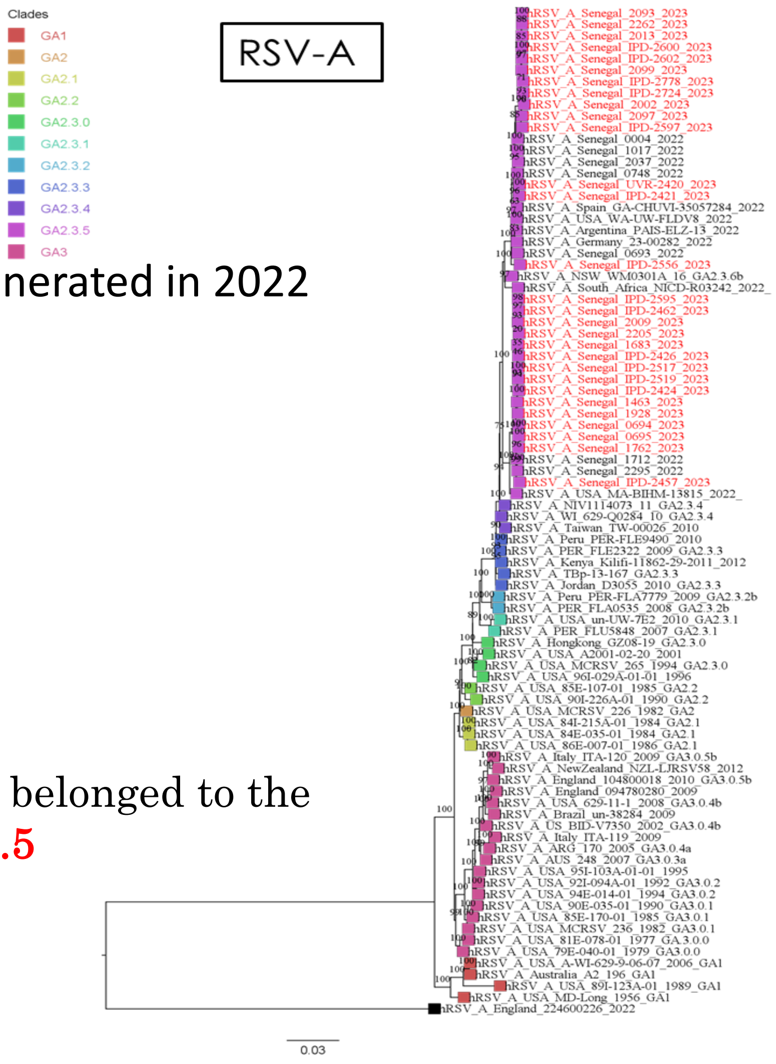
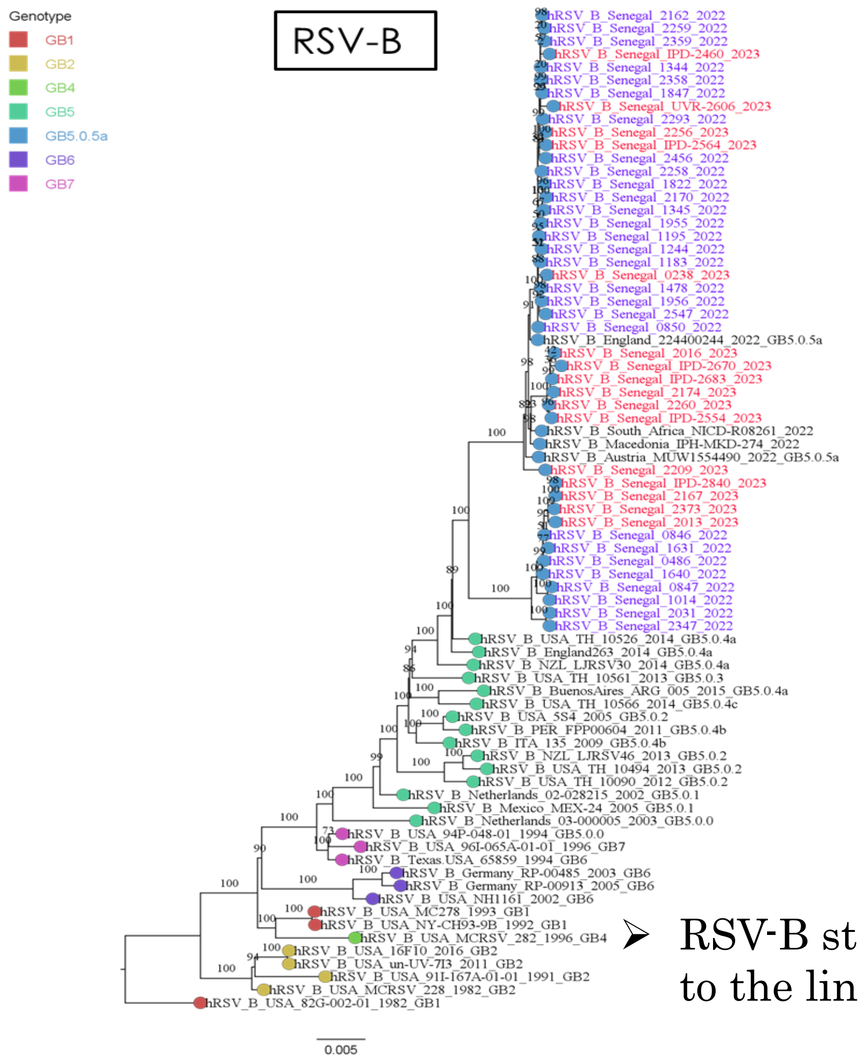
Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

- ➢ 43 full genomes generated in 2022
- ➢ 64 in 2023
- ➢ 7 in 2024



- ➢ RSV-A strains belonged to the lineage GA2.3.5



- ➢ RSV-B strains belonged to the lineage GB5.05a

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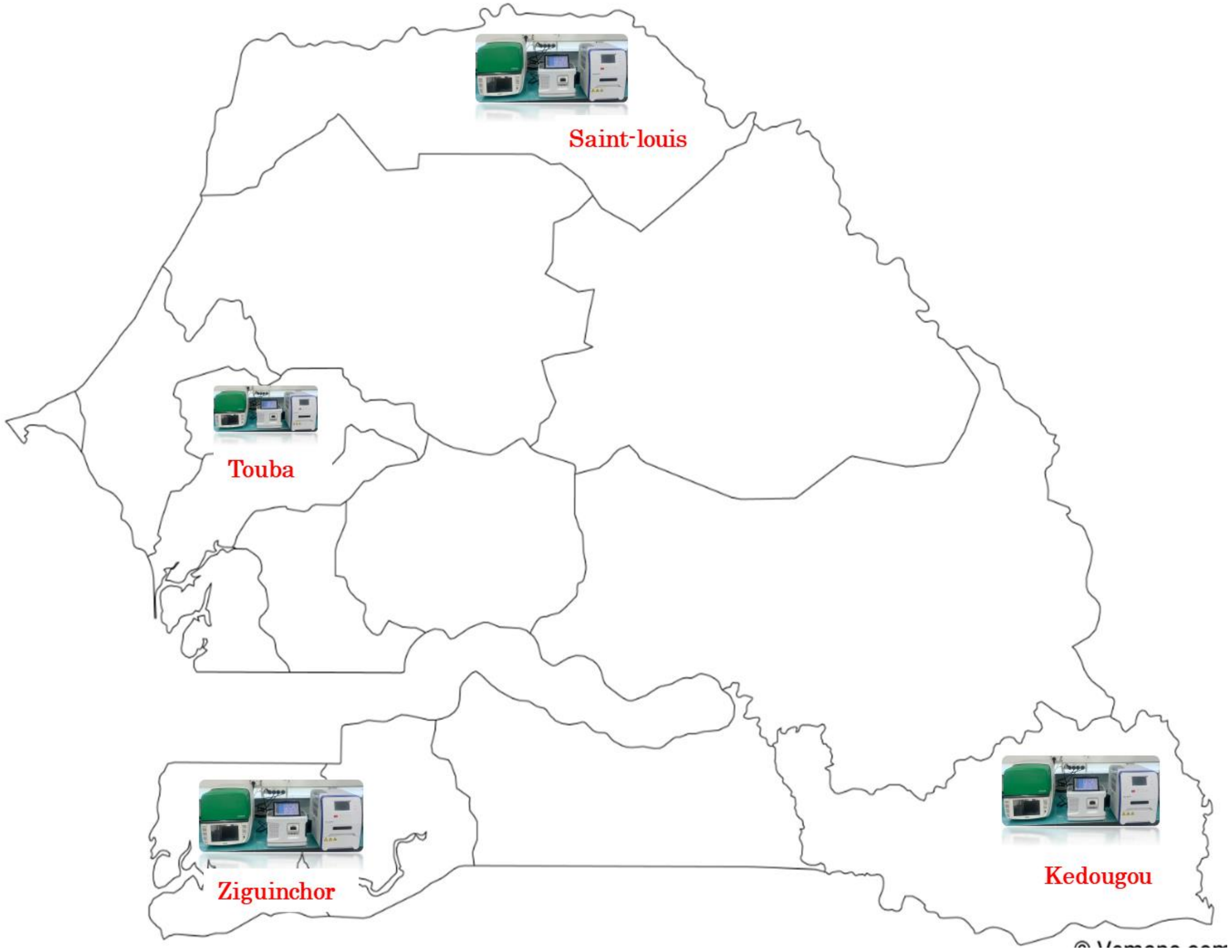
Hospital-based Surveillance of Severe Acute Respiratory Infections in Senegal

Extension of SARI surveillance in other regions: current decentralizing of laboratory activities to cover remote regions of the country.



Thank you!

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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

“PEDIATRIC INFLUENZA 2024 IN PARANÁ, SOUTHERN BRAZIL: CLINICAL AND EPIDEMIOLOGICAL ASPECTS"

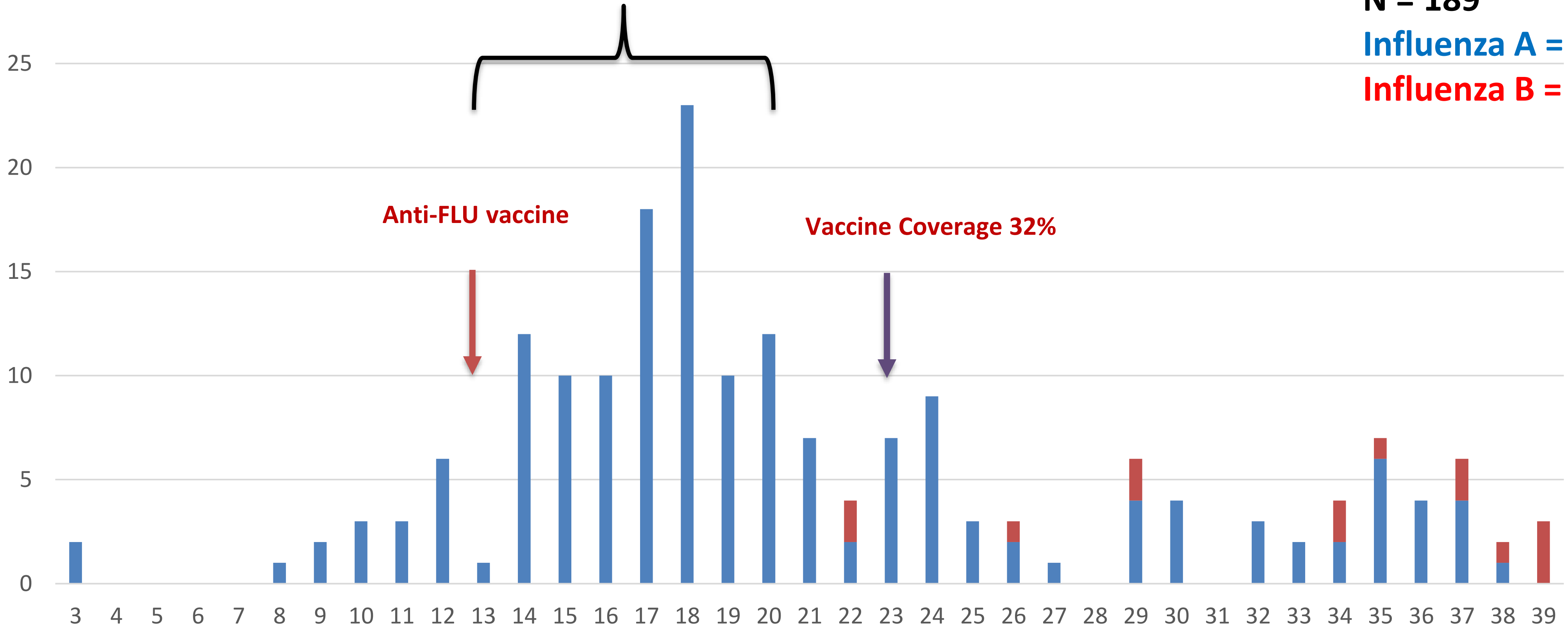
RABONI, Sonia, Pequeno Principe Hospital, Curitiba, Brazil

10 anos HOSPITAL pequeno PRÍNCIPE

UFPR
UNIVERSIDADE FEDERAL DO PARANÁ

NUMBER OF INFLUENZA CASES BY EPIDEMIOLOGICAL WE
2024

N = 189
Influenza A = 175
Influenza B = 14 (7.5%)



Mar 31 – May 19

Anti-FLU vaccine

Vaccine Coverage 32%

Influenza Detection: Rapid Test
Influenza subtype: A H1N1

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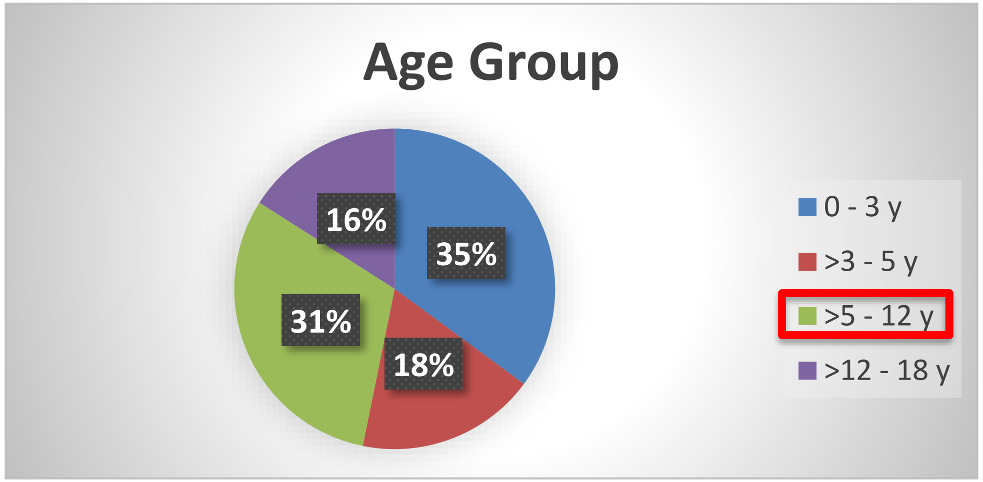
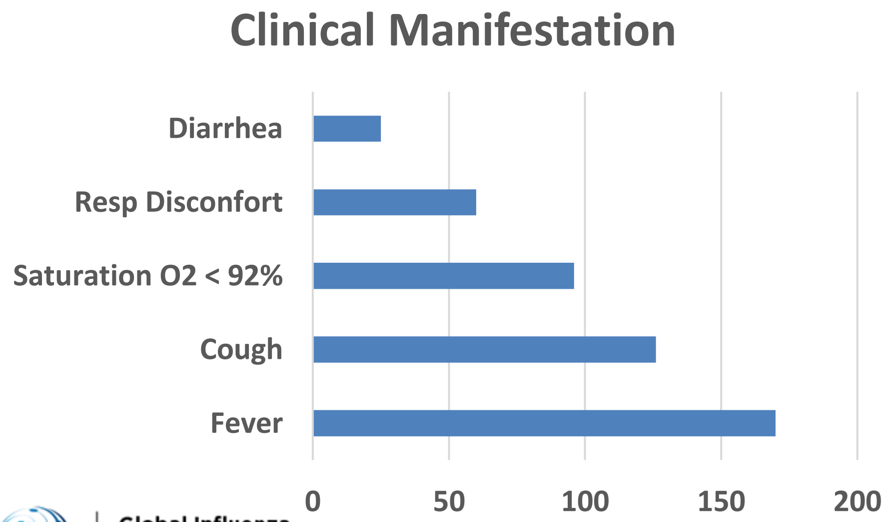
INFLUENZA CASES – CLINICAL AND DEMOGRAPHIC PROF



Age Group

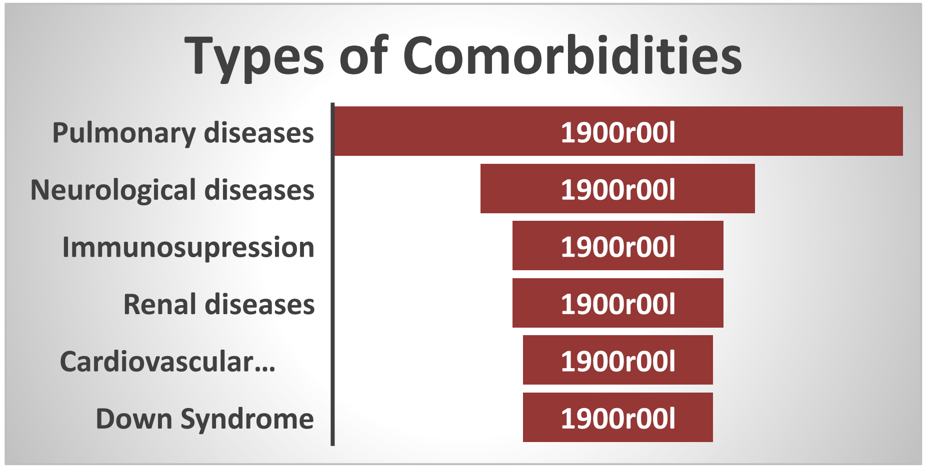
	Non-ICU (n = 170)	ICU (n = 19, 10%)
Male	95 (56%)	5 (26%)
LOS, day (IQR)	3 (2-6)	**12 (8-17)**
Age, y, Median (IQR)	5 (2-9)	6.8 (2-6)
Comorbidities	75 (44%)	**12 (63%)**

LOS = Lenght of stay



Clinical Manifestation

Death = 1 (0.5%)
No comorbidities: 54%

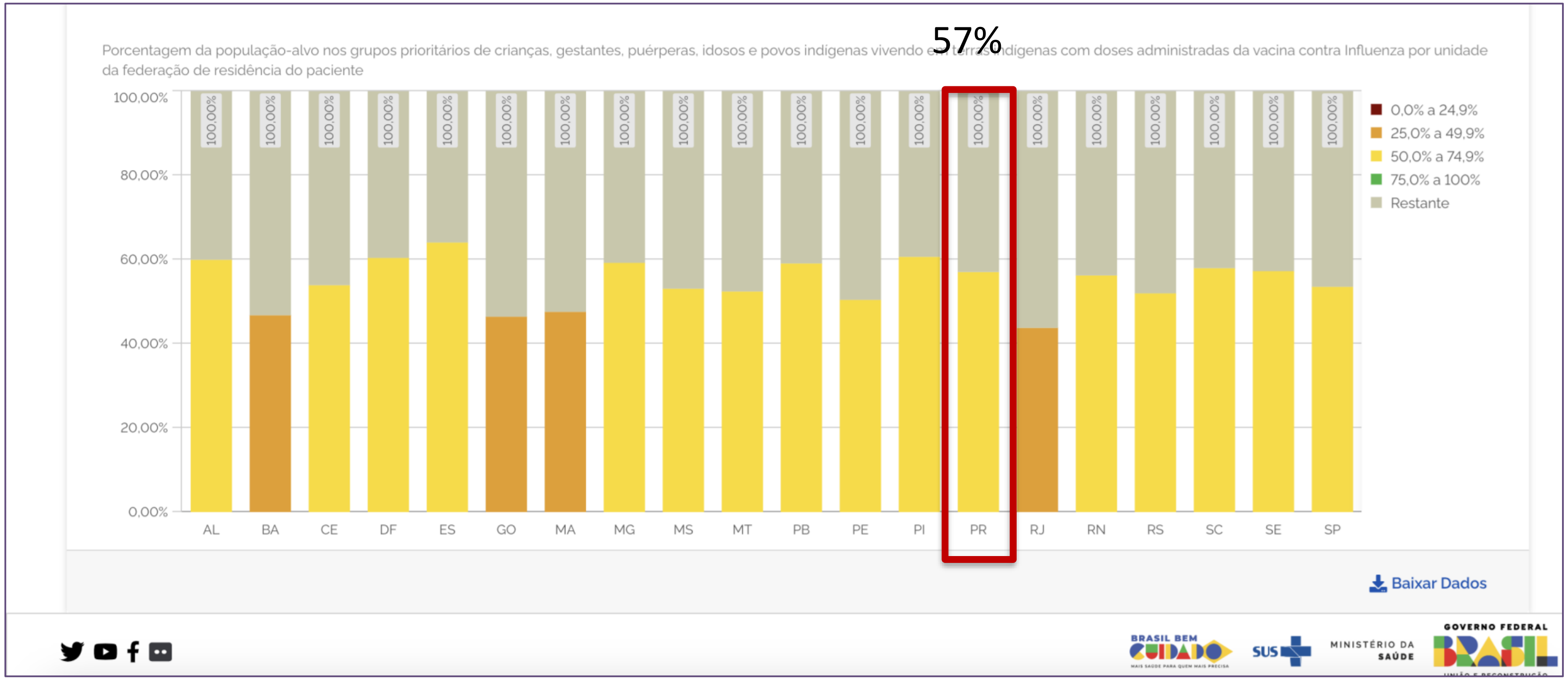


Types of Comorbidities

SARS DATA AND INFLUENZA VACCINE 2024 - BRAZIL

Epidemiological Year 2024

- **97,469 cases SARS**
  - **19.3% influenza A**
  - **0.4% influenza B**
  - **45.0% RSV**
  - **18.8% SARS-CoV-2**


Porcentagem da população-alvo nos grupos prioritários de crianças, gestantes, puérperas, idosos e povos indígenas vivendo em terras indígenas com doses administradas da vacina contra Influenza por unidade da federação de residência do paciente

Idosos	30.304.417	80.292	24.414	14.358.156	154.774	14.617.636	48,24%	-
Crianças	11.744.343	1.455.824	898.728	5.730.557	47.075	8.132.184	69,24%	-
Comorbidades	8.682.264	9.575	3.655	2.544.538	15.604	2.573.372	-	29,64%
Pessoas com deficiência permanente	7.686.383	723	375	209.460	1.451	212.009	-	2,76%

https://infoms.saude.gov.br/extensions/SEIDIGI_DEMAS_INFLUENZA_2024_RESIDENCIA/SEIDIGI_DEMAS_INFLUENZA_2024_RESIDENCIA.html
https://portal.fiocruz.br/noticia/2024/07/infogripe-sudeste-tem-aumento-no-numero-de-hospitalizacoes-por-influenza-vsr-e

CONCLUSION

- In 2024, pediatric influenza hospitalizations surpassed those of the 2009 pandemic.
- Severe cases shifted to children aged 5–12 y, rather than under 3 y.
- Over half of hospitalized children had no comorbidities.
- Rare symptoms like parotitis and neurological issues were reported but had good outcomes.
- Influenza B resurgence (7.4%)
- Seasonal peaks in winter and spring were observed.
- Low vaccination rates likely contributed to increased hospitalizations; further studies are needed.
  - By June 3, Paraná’s vaccination rate was 38.01%, with children at 32.23%.

THANK YOU!

sraboni@ufpr.br

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GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

ASSOCIATION OF INFLUENZA VIRAL GENETIC INFORMATION WITH SEVERITY MARKERS IN HOSPITALIZED PATIENTS

Aung Pone MYINT

Center of excellence in respiratory pathogens (CERP), Hospices Civils de Lyon, and Université Claude Bernard Lyon 1

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Epidemiology

Sous l'égide de
Fondation
de
France

INTRODUCTION

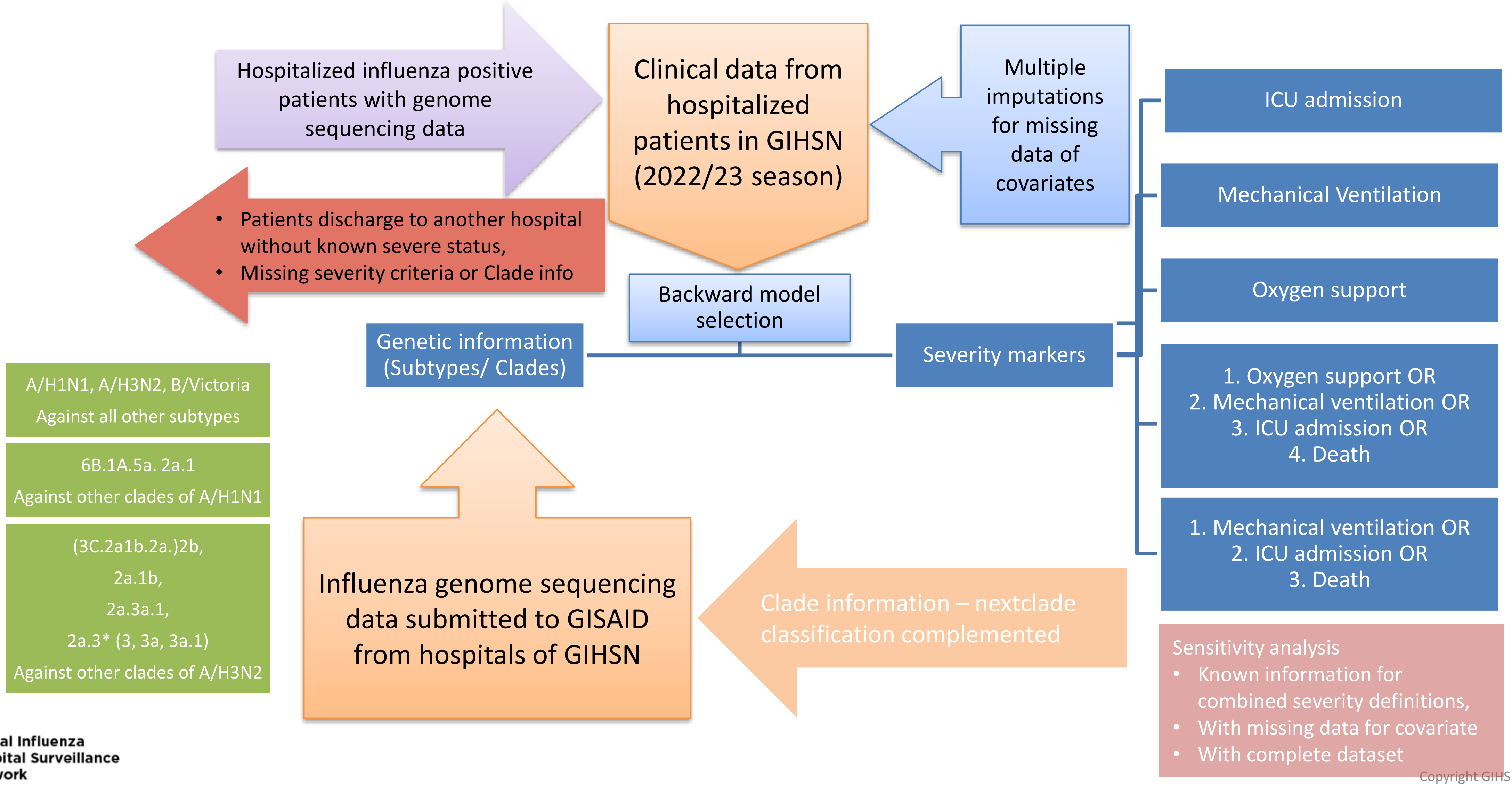
- Influenza - 54 million cases, 8.2 million severe cases, and 145,000 deaths globally in 2017 (Troeger et al., 2019).
- A/H3N2 subtypes - higher risk of hospitalization compared with A/H1N1 or influenza B (Rothman et al., 2023).
- A/H1N1 - more severe outcomes in hospitalized patients (Chagvardieff et al., 2018; Chaves et al., 2013; Delgado-Sanz et al., n.d.; Derqui et al., 2022; Lytras et al., 2020; Minney-Smith et al., 2019; Sumner et al., 2023), including in GIHSN hospitals (Cohen et al., 2023).
- Reassortant 3C.2a2 clade of A/H3N2 - more severe outcomes (Liu et al., 2024).

OBJECTIVE

To investigate the association of influenza viral genetic information and markers of clinical disease severity

Global Influenza
Hospital Surveillance
Network

MATERIALS AND METHOD



Hospitalized influenza positive patients with genome sequencing data

Clinical data from hospitalized patients in GIHSN (2022/23 season)

Multiple imputations for missing data of covariates

- Patients discharge to another hospital without known severe status,
- Missing severity criteria or Clade info

Backward model selection

Genetic information (Subtypes/ Clades)

Severity markers

ICU admission

Mechanical Ventilation

Oxygen support

1. Oxygen support OR
2. Mechanical ventilation OR
3. ICU admission OR
4. Death

1. Mechanical ventilation OR
2. ICU admission OR
3. Death

A/H1N1, A/H3N2, B/Victoria
Against all other subtypes

6B.1A.5a. 2a.1
Against other clades of A/H1N1

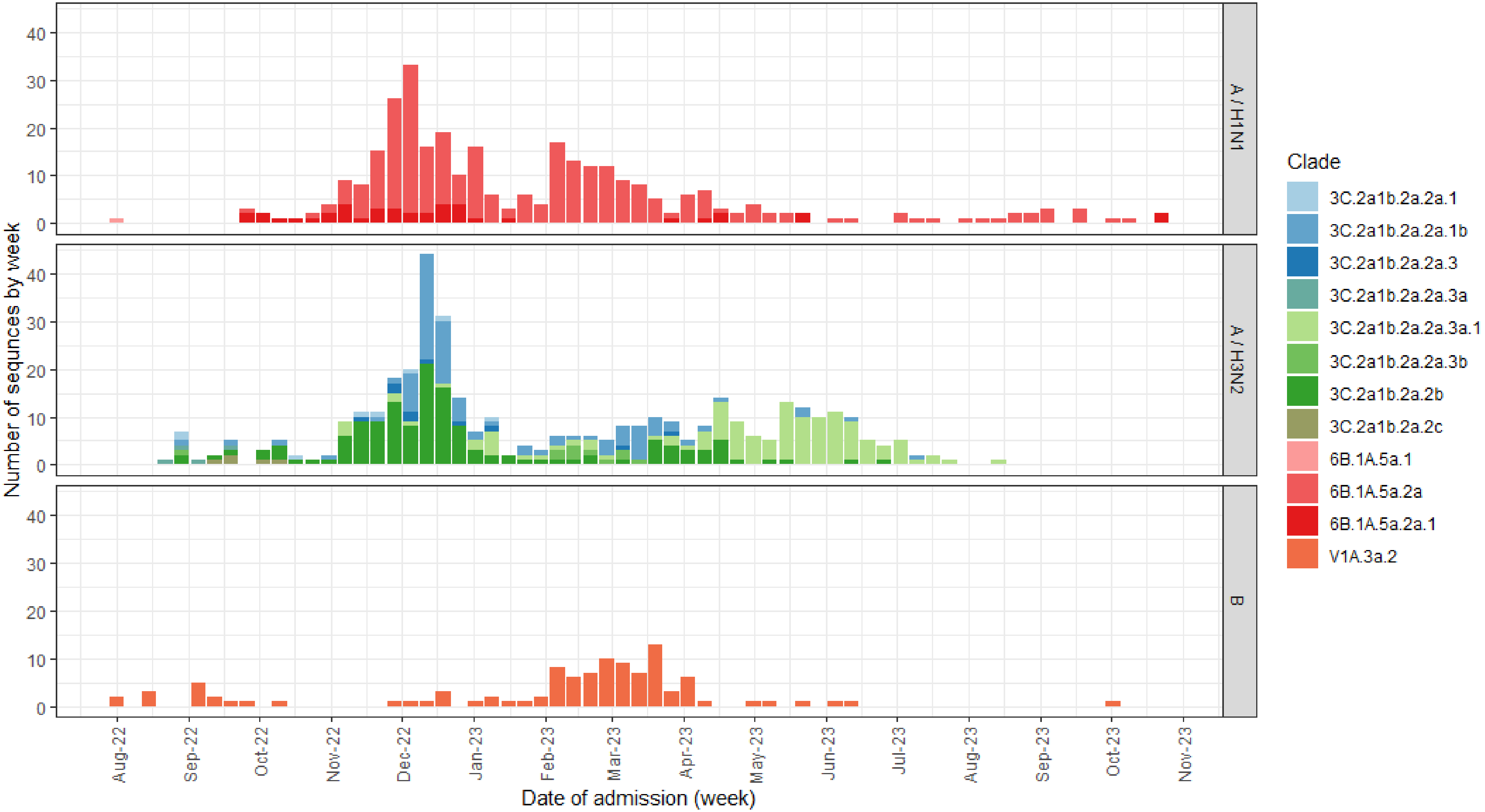
(3C.2a1b.2a.)2b,
2a.1b,
2a.3a.1,
2a.3* (3, 3a, 3a.1)
Against other clades of A/H3N2

Influenza genome sequencing data submitted to GISAID from hospitals of GIHSN

Clade information – nextclade classification complemented

Sensitivity analysis
- Known information for combined severity definitions,
- With missing data for covariate
- With complete dataset

RESULTS - SUBTYPES AND CLADES



A/H1N1 – 314
A/H3N2 – 394
B/Victoria – 104
Total - 812

A/H1N1:
5a.2a mainly
fewer 5a.2a.1

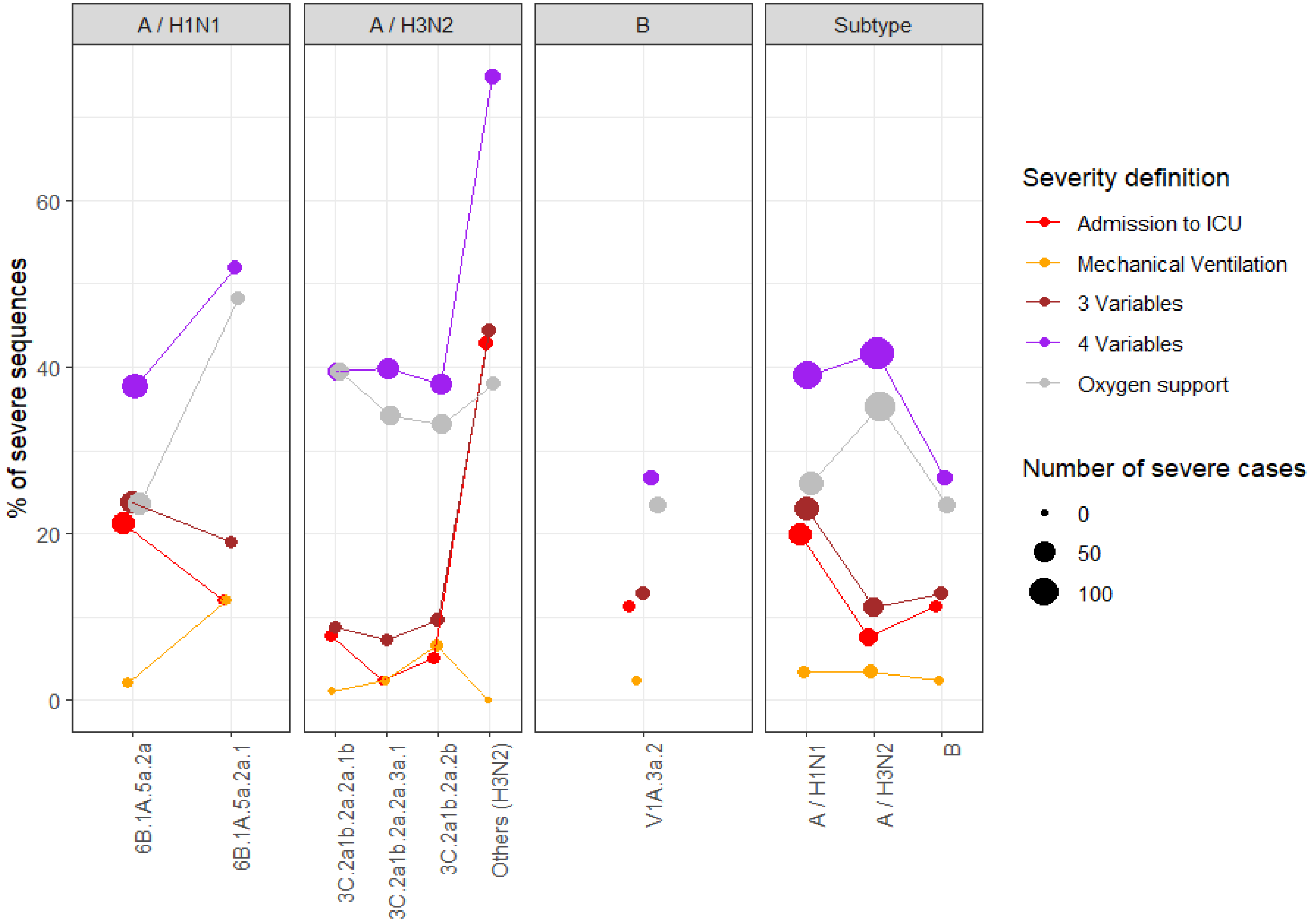
A/H3N2 – 2a.1b, 2a.2b, and 2a.3a.1 mainly

Global Influenza Hospital Surveillance Network

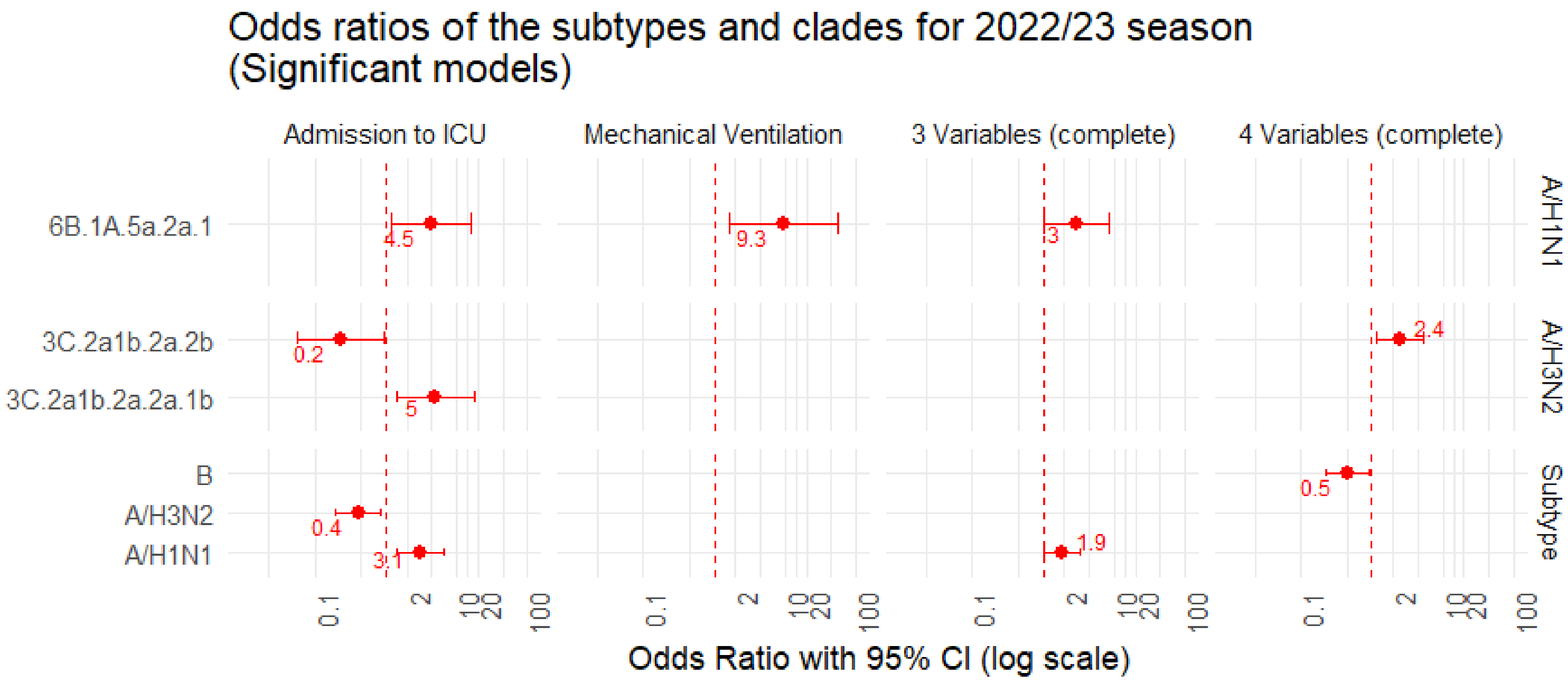
PATIENTS CHARACTERISTICS AMONG SUBTYPES AND CLADES

- Different age groups distribution
- Different proportion of antiviral usages
- Different proportion of antibiotics usages observed among subtypes, and clades within A/H1N1 and A/H3N2 subtypes.

NOTE: 10 of 11 patients with 3C.2a1b.2a.2a.3b needed ICU admission in 2022/23 (all from Pakistan), while all 11 patients reported in 2021/22 were not in ICU



RESULTS OF SIGNIFICANT ADJUSTED MODELS



Odds ratios of the subtypes and clades for 2022/23 season (Significant models)

Very wide confidence intervals for the clade comparisons for ICU admission and mechanical ventilation due to the low number of severe cases

P137S, T277A, E356D – mutations for 6B.1A.5a.2a.1
F79V and S156H - mutations for3C.2a1b.2a.2b

CONCLUSIONS

In the 2022/23 season

- Patients with A/H1N1 showed higher severity compared with other subtypes.
- Clades 6B.1A.5a.2.1 and 3C.2a1b.2a.2b were associated with more severe outcomes compared with other A/H1N1 and A/H3N2 clades, respectively.
- Future: to investigate the association of severity markers with A/H1N1 clade 6B.1A.5a.2.1 and the specific mutations of A/H3N2 clade 2a.2b.

Limitations

- Analyses conducted only among hospitalized patients with genome sequencing data and complete information for severity definitions.
- Different surveillance populations and settings by GIHSN site, including hospital type and sequencing capacity.

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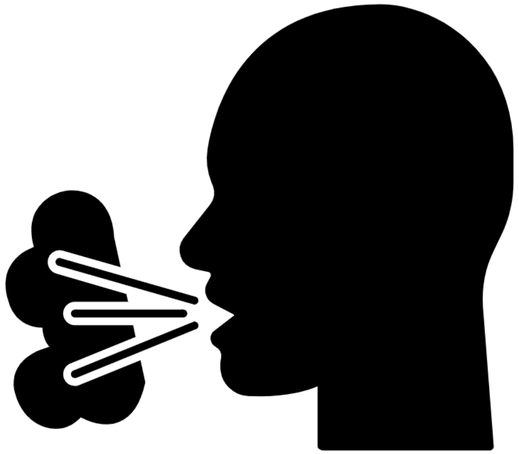
GIHSN ANNUAL MEETING, 25 NOVEMBER 2024

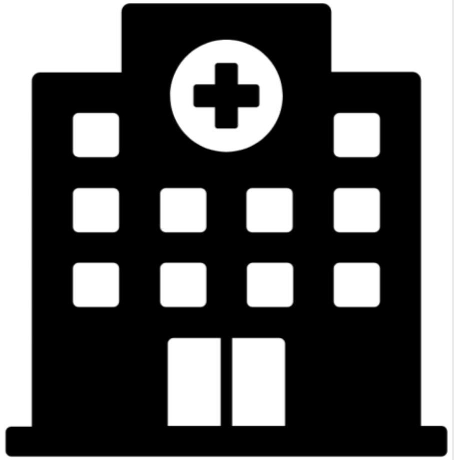
EV-D68 SURVEILLANCE: PROTOCOL OVERVIEW AND PROPOSED COLLABORATION WITH GIHSN

Miranda Delahoy, US Centers for Disease Control & Prevention

ENTEROVIRUS D68 (EV-D68) CAN CAUSE SERIOUS ILLNESS AND STRAIN HEALTHCARE CAPACITY



severe respiratory illness



strain healthcare capacity

acute flaccid myelitis

PRIMARY OBJECTIVES OF EV-D68 GLOBAL SURVEILLANCE

1. **Retrospectively describe EV-D68 detections** and percent positivity among hospitalized children previously enrolled in select GIHSN and Abbott Pandemic Defense Coalition (APDC) global sites and tested for EV-D68 during 2016–2024.

2. **Describe EV-D68 detections and percent positivity among all hospitalized children prospectively enrolled** in select GIHSN and APDC global sites beginning in 2025, including positivity by country and age.

3. **Describe clinical presentation & severity of illness among children hospitalized with EV-D68** enrolled in select GIHSN and APDC global sites and explore any geographic variations in clinical & demographic characteristics among patients hospitalized with EV-D68.

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)

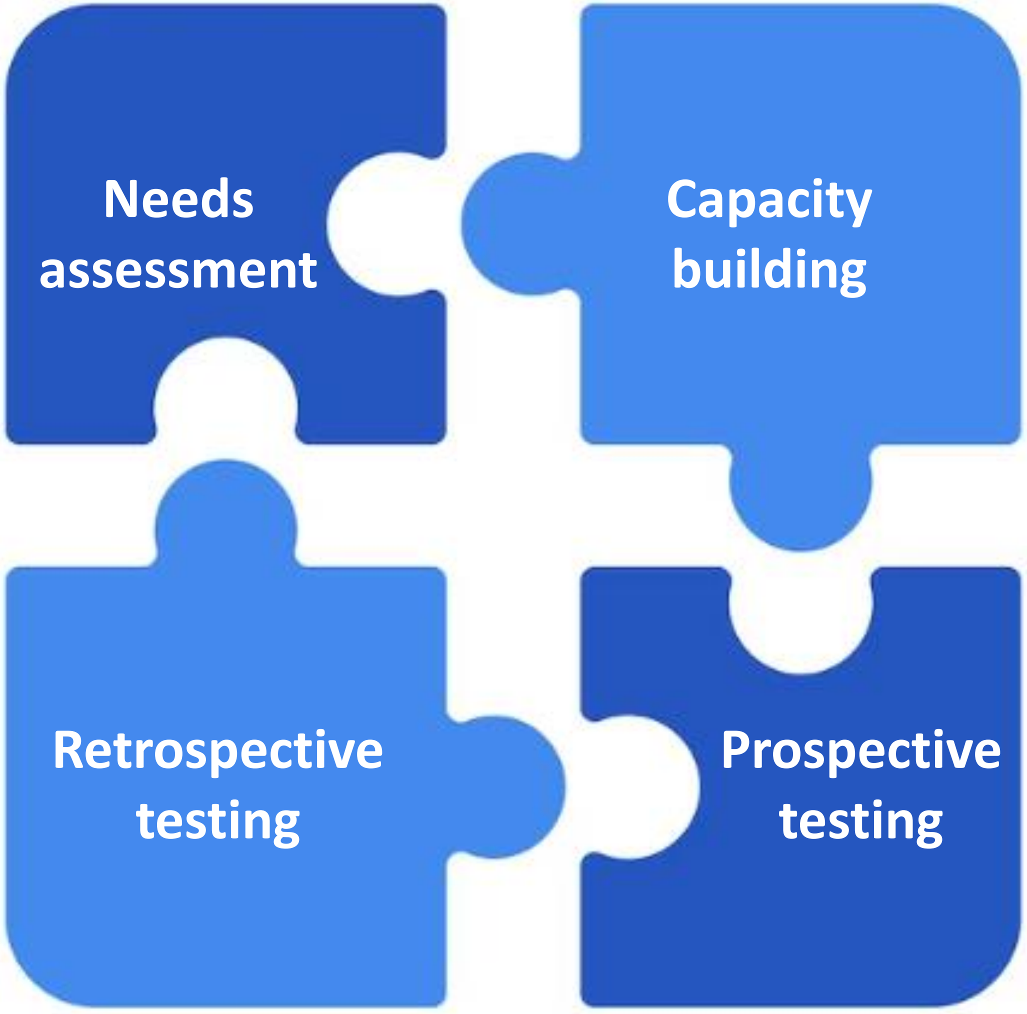
- Global network of sites collecting specimens for early detection & response to pandemic threats
- Laboratory expertise and resources (EV-D68 assay)

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 testing respiratory specimens for EV-D68 and providing technical assistance

EV-D68 GLOBAL SURVEILLANCE VISION



Needs assessment

Capacity building

Retrospective testing

Prospective testing

- **EV-D68 assay validation**
- Support for **growing testing capacity**
- EV-D68 **data compilation** and analysis

ASSAY VALIDATION AND EV-D68 RETROSPECTIVE DATA COMPILATION

- Sites already testing for EV-D68 will be invited to have their assays validated.
- CDC will create a panel of numbered samples (some positive, some negative for EV-D68) to conduct a blinded assay comparison.
- Panels will be tested at participating GIHSN site laboratories using their EV-D68 assays.
- CDC will provide technical assistance to investigate and understand any discrepancies.
- Sites using validated EV-D68 assays will be invited to share available EV-D68 results from specimens previously collected under the GIHSN protocol and tested during 2016–2024.

RETROSPECTIVE AND PROSPECTIVE EV-D68 TESTING

Retrospective EV-D68 testing

- Select sites with stored respiratory specimens (from 2016–2024) may participate in retrospective EV-D68 testing.

Prospective EV-D68 testing

- Sites with current capacity or interest in growing capacity for EV-D68 testing may participate.
- Certain sites may also ship specimens to APDC sites for testing.

POTENTIAL MECHANISMS FOR RETROSPECTIVE AND PROSPECTIVE EV-D68 TESTING

Potential testing mechanisms

- Sites conduct additional testing using their own validated assays.
- Local testing with reagents provided through CDC's International Reagent Resource (IRR).
- Sites with an Abbott m2000* may test locally with tests provided by Abbott.
- GIHSN sites with an APDC site in the same country may have testing conducted at the in-country APDC site.

Data compilation

- EV-D68 test results will be sent to Impact Healthcare monthly with a unique identifier to link to GIHSN surveillance data. GIHSN will send de-identified line-listed data to CDC.

*Abbott m2000 platform for research use only

GIHSN & APDC SITE LOCATIONS (2024–2025)

The CIRN (SOS) Network, Halifax, Canada 34

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

Instituto Nacional de Enfermedades Respiratorias, Mexico-City, Mexico 2

Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubiran: I, Mexico-City, Mexico 3

Fundacion para la Salud Integral de los Guatemaltecos, Coatepeque/Chiquirines, Guatemala 2

Universidad Nacional Mayor de San Marcos, Lima, Peru 4

Laboratorio UNIMOL, Universidad de Cartagena, Cartagena, Colombia 2

Hospital Pequeno Principe, Curitiba, Brazil 1

Laboratorio De Salud Publica De Antioquia, Medellin, Colombia 10

Fundação Ezequiel Dias (Funed), Belo Horizonte, Brazil 2

National Institute of Tuberculosis and Lung Diseases, Warsaw, Poland 4

ANRS-MIE, Paris, France 5

FISABIO-Public Health, Valencia, Spain 5

Institut Pasteur of Dakar, Dakar, Senegal 4

Nigeria Centre for Disease Control and Prevention, Abuja, Nigeria 12

INHP, Abidjan, Côte d'Ivoire 7

National Institute for Infectious Diseases, Bucharest, Romania 1

SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine, Kyiv, Ukraine 4

University of the Witwatersrand, Johannesburg, South Africa 1

Nelson Mandela Academic Clinical Research Unit, Mthatha, South Africa 6

KEMRI, Nairobi, Kenya 7

Makerere University Walter Reed Project, Kampala, Uganda 1

Smorodintsev Research Institute of Influenza, St-Petersburg, Russia 5

National Research Center of Epidemiology and Microbiology, Moscow, Russia 1

American University of Beirut, Beirut, Lebanon 6

The University of Hong Kong, Department of Microbiology, Hong Kong, China 1

National Institute of Health Islamabad Pakistan, Islamabad, Pakistan 8

The Chinese University of Hong Kong, Hong Kong, China 1

Institut Pasteur de Madagascar, Antananarivo, Madagascar 3

Institute of Environmental Science and Research, Wallaceville, New Zealand 2

○ APDC sites in the same country as GIHSN sites: USA, Mexico, Colombia, Peru, Brazil, Senegal, South Africa, Uganda, Pakistan

CONSIDERATIONS FOR PRIORITIZING SITES FOR PARTICIPATION

- Sites **enrolling higher numbers of children with ARI annually**
- **Ability and willingness to test & share data**
  - Additional support available for sites with Abbott m2000 platform* or APDC site in-country
- **General interest** in participating and able to meet project commitments
- **Geographic representativeness**, if relevant

*Abbott m2000 platform for research use only

SITE RESPONSIBILITIES (EV-D68 SURVEILLANCE)

- Share information on number of stored specimens.
- Coordinate and conduct local or in-country testing.
    - May involve shipping samples within the same country.
- Monthly EV-D68 laboratory results shared with GISHN network.
- Attend biannual and *ad hoc* EV-D68 surveillance meetings (virtual).
- Review reports and collaborate on potential publications.

BENEFITS OF COLLABORATION

share & publish information

EV-D68 assay validation

testing support

laboratory & epi collaboration

Note: participation is optional

FOR ADDITIONAL INFORMATION & TO EXPRESS INTEREST

- Please stop by the EV-D68 kiosk after this presentation!
- Contact—US CDC: Miranda Delahoy (vuo0@cdc.gov)
- Contact—Abbott: Mary Rodgers (mary.rodgers@abbott.com)

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

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

GIHSN & APDC PIs and site personnel

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

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CLOSING OF DAY 1

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Sous l'égide de
Fondation
de
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Coordination
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