Global Influenza Hospital Surveillance Network

www.gihsn.org

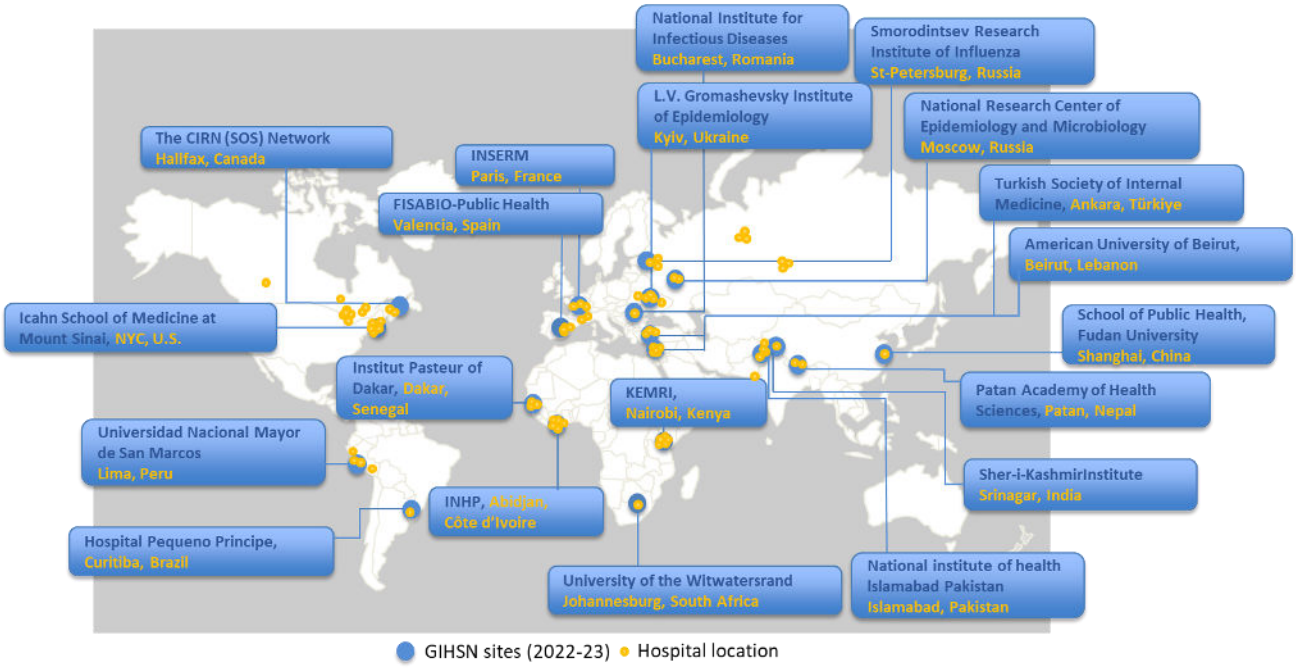
GIHSN report of activity prior to the WHO Consultation on the Composition of Influenza Virus Vaccines for use in the 2024 Southern Hemisphere Influenza Season.

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.

As reported by WHO, the number of virus detections in the southern hemisphere during the surveillance period between February and August 2023) was similar to that prior to the COVID-19 pandemic. Influenza activity in GIHSN was detected earlier than usual, as observed for the northern hemisphere season. Overall, influenza A (H3N2) has accounted for the majority of detections reported during this period, followed by A(H1N1)pdm09 viruses. Fewer influenza B/Victoria lineage virus detections have been reported and no B/Yamagata-like viruses have been detected.

This report is colliding the sequencing data from 13 sites: *Brazil (28), India (29), Côte d'Ivoire (9), Lebanon (45), Pakistan (62), Romania (140), Russia-Moscow (16), Russia-St Petersburg (48), South Africa (92), Spain (60), Türkiye (13), Ukraine (66) and USA-NYC (52).* All 660 sequences, from hospitalized cases only, have been uploaded in the GISAID database with a GIHSN tag. It includes viruses from the year-round surveillance, most sequenced isolates being collected form the Northern hemisphere surveillance. However, it is possible to analyze the distribution of the sequence of the viruses identified during the March to September surveillance period.

During this latter period, cases have been reported mainly from sites located in South Africa, Brazil, Peru and India.

2 - Description of the virus sequenced in the GIHSN

2 – 1 - Influenza A viruses

A(H1N1)pdm09 viruses (Fig 2)

No specific lineage or clade could be associated with severity

Of the A(H1N1)pdm09 viruses that have been detected in the network since February 2023, phylogenetic analysis of their HA genes were all belonging to clade 6B.1A.5a derivatives. The HA gene had previously been reported to diversify into 5a.1 or 5a.2 subclades, with decreasing numbers in the 5a.1. For the viruses detected in the GIHSN during this period of surveillance, all viruses belonged to HA subclade 5a.2a. As reported by the WHO, HA from this clade showed continued genetic diversification, with a minor circulation of 5a.2a.1 HA subclade viruses, some of these being detected recently in the southern hemisphere and in the intertropical zone (Figure 2c).

No specific lineage or clade could be associated with severity, according to the relative proportion of cases with O2 requirement

A(H3N2) viruses (Fig 3)

A(H3N2) viruses were detected in most parts of the world since September 2022. The HA genes of all viruses belonged to 3C.2a1b.2a.2 [defined by HA1 substitutions Y159N, T160I (resulting in the loss of a glycosylation site), L164Q, G186D, D190N, F193S and Y195F] with A/Darwin/6/2021 and A/Darwin/9/2021 as reference viruses. There continued to be further diversification in this 2a.2 subclade into 2a.2a and 2a.2b, with further diversification in the 2a.2a subclade (2a.2a.1 with subsclades 2a.2a.1a and 2a.2a.1b; 2a.2a.2 ;and 2a.2a.3 with 2a.2a.3a and 2a.2a.3b). Representatives of these different clades have been detected in the network, with all lineages reported. However, after March, no viruses of the HA 2a.2a.1 or 2a.2a.1b HA subclades have been detected (figure 3A).

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).

2 – 2 - Influenza B viruses

B/Victoria Lineage (Fig 4)

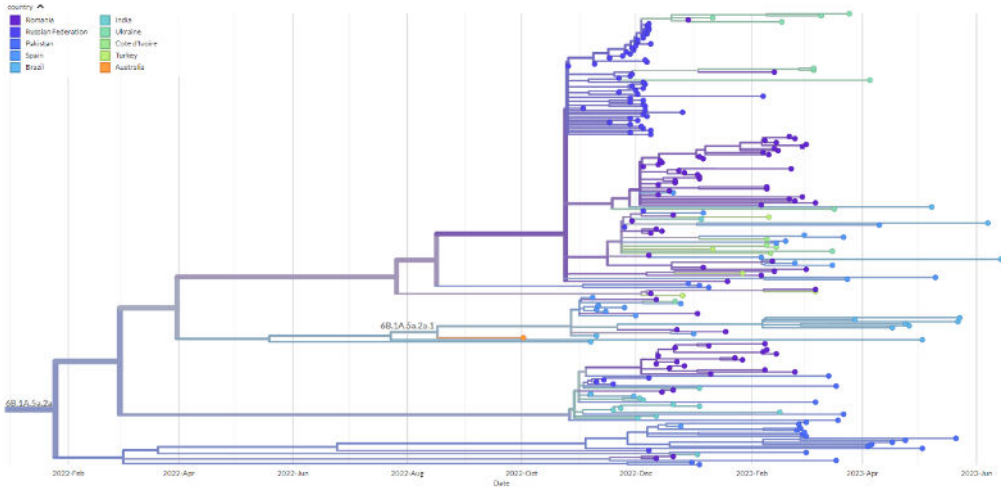
The very limited influenza B/Victoria/2/87 lineage viruses collected since September 2022 belonged to clade 1A.3 with an amino acid deletion of three residues (162-164) in HA1 and a K136E HA1 substitution. Viruses from subclade 1A.3a.2 have predominated in countries where B/Victoria lineage viruses were detected and subjected to sequencing. Only very few viruses have been reported since March 2023.

No specific lineage or clade could be associated with severity (limited data available)

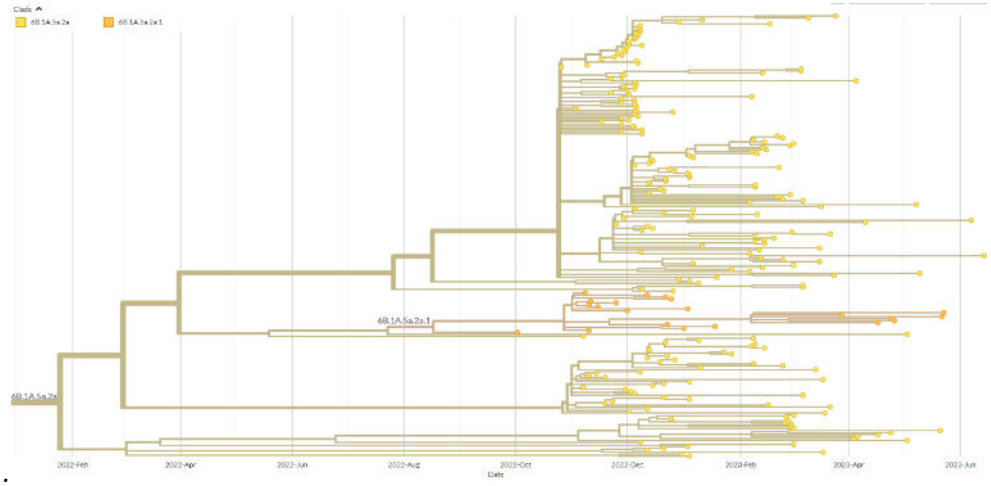
B/Yamagata Lineage

No B/Yamagata-like viruses have been detected during this surveillance.

Fig 2: Phylogenetic tree of the H1N1pdm09 viruses analyzed between September 2022 and September 2023 2A – Geographic distribution, 2B – Clade distribution 2C – Cases requiring Oxygen supplementation.

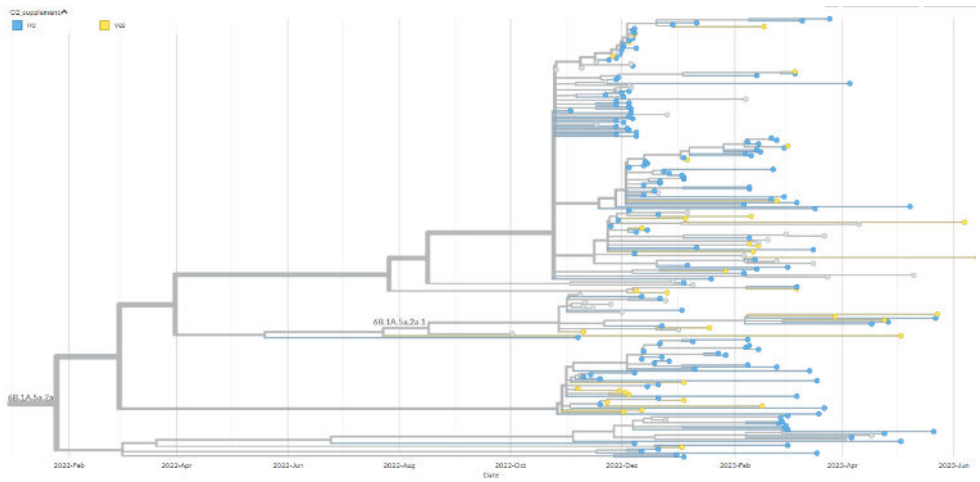


2A – Geographic distribution



.

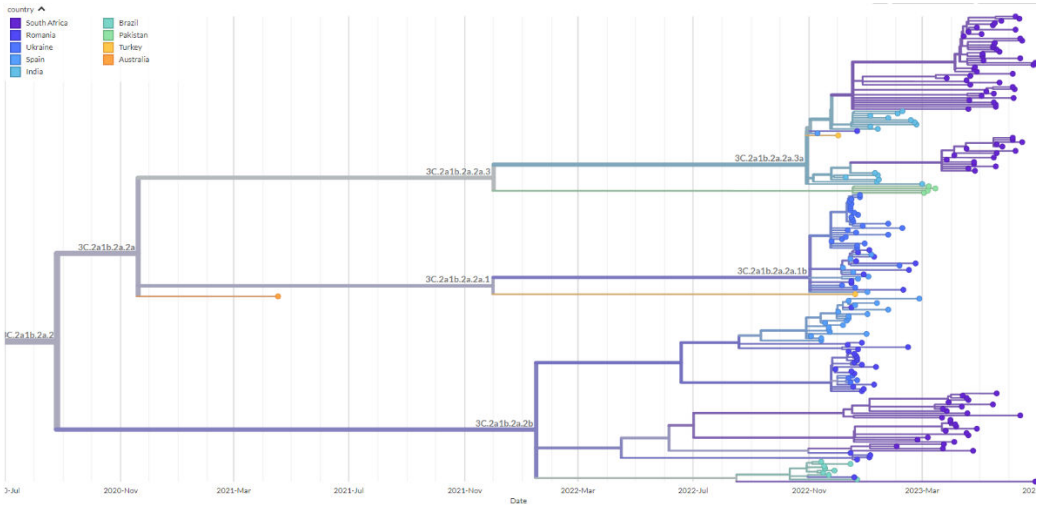
2B – Clade distribution



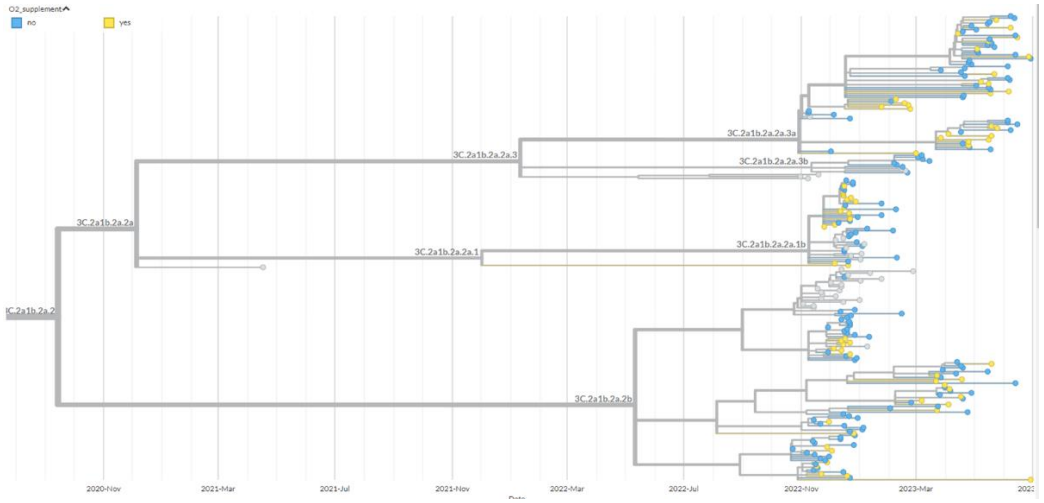
2C – Cases requiring Oxygen supplementation in yellow

Fig 3: Phylogenetic tree of the H3N2 viruses analyzed between September 2022 and September 2023

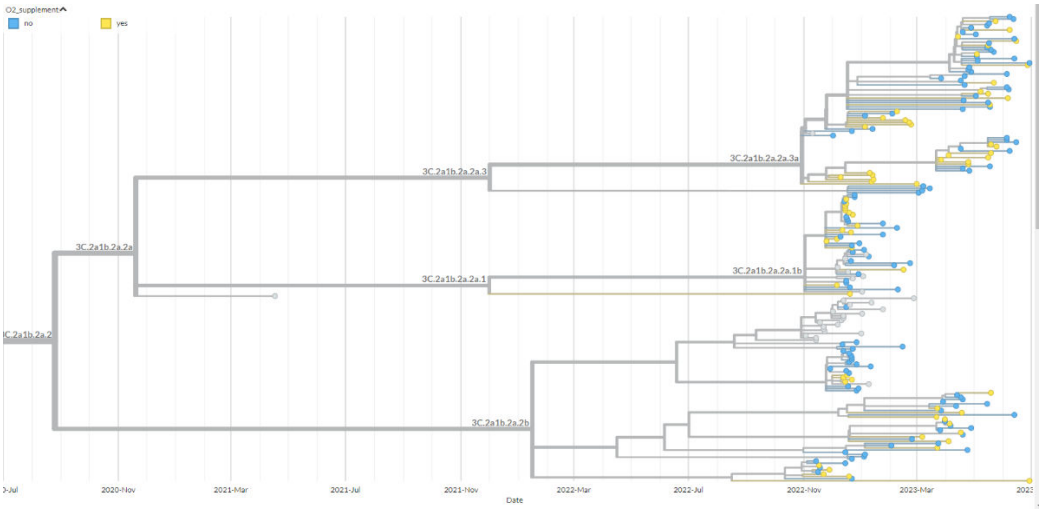
3A – Geographic distribution, 3B – Clade distribution 3C: Cases requiring Oxygen supplementation.



3A – Geographic distribution



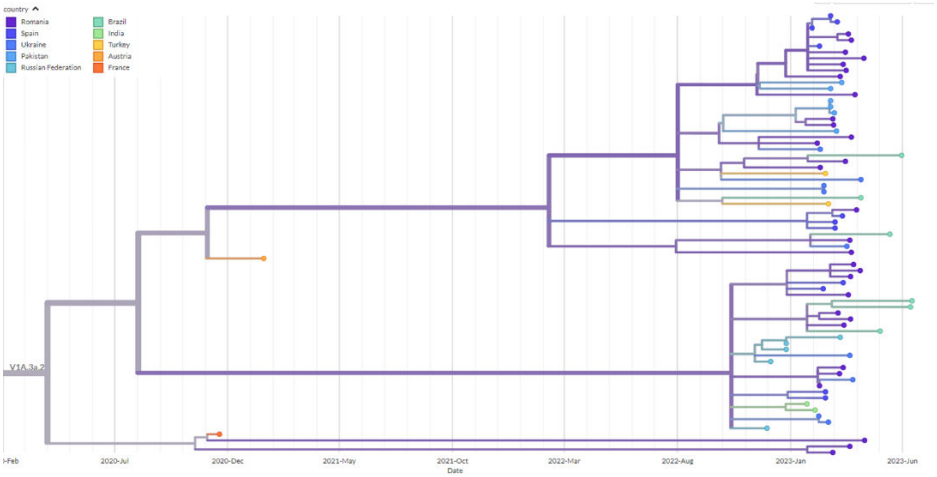
3B – Clade distribution



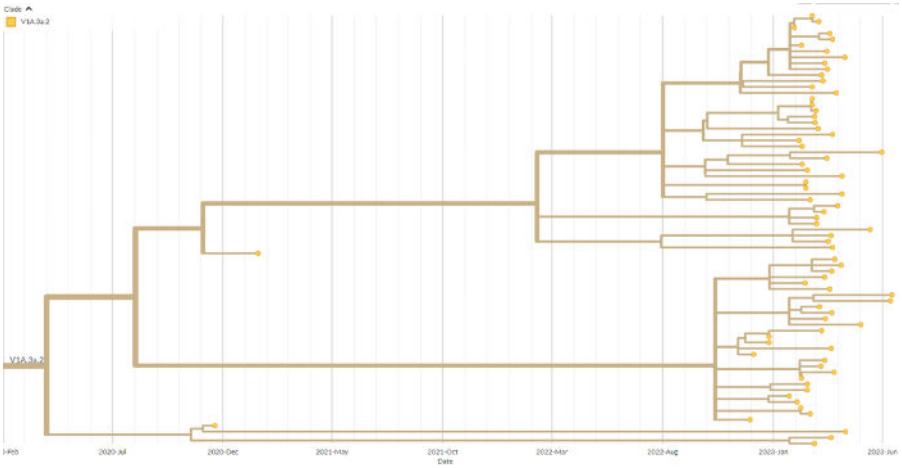
3C – Oxygen supplementation

Fig 4 : Phylogenetic tree of the B viruses analyzed between September 2022 and September 2023.

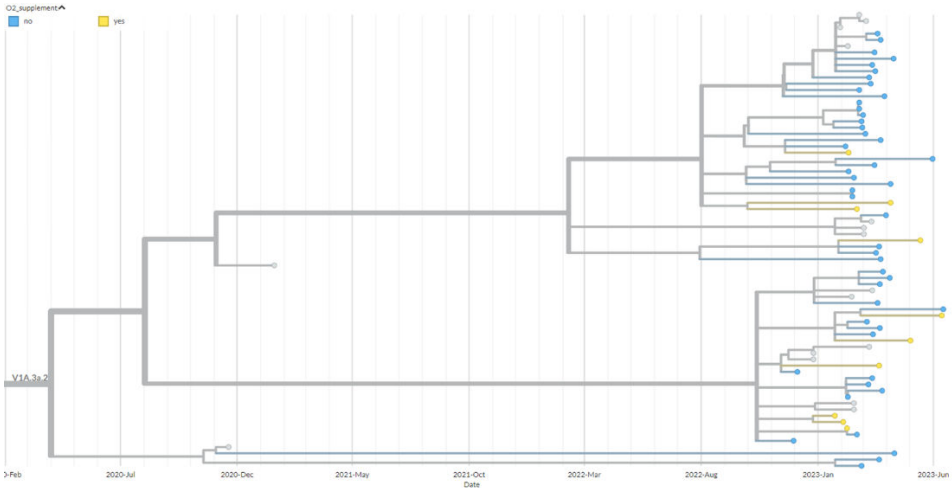
4A – Geographic distribution, 4B – Clade distribution 4C – Cases requiring Oxygen supplementation.



4A – Geographic distribution,



4B – Clade distribution



4C – Oxygen supplementation in yellow