GISHN 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.

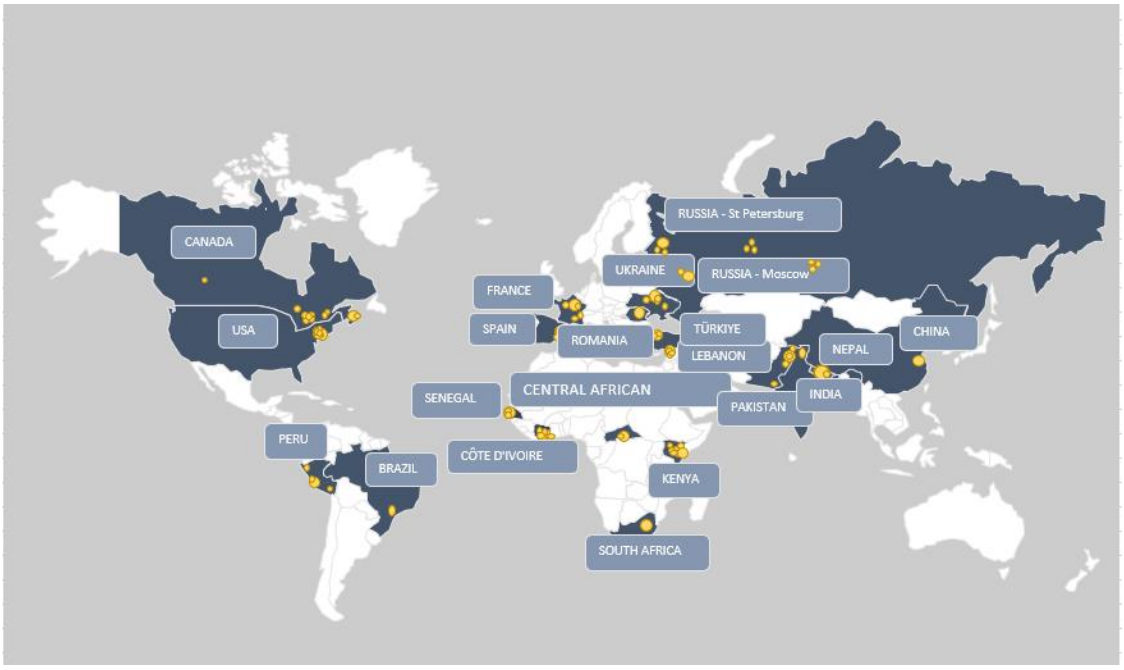
GIHSN is collecting clinical and virological information from hospitalized cases through a network of sites located in different regions of the world (figure1). This combined clinical and virological surveillance allows the identification of viruses responsible for severe influenza. This severity is 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.



Influenza A viruses

A(H1N1)pdm09 viruses (Fig 2)

A limited number of A(H1N1)pdm09 viruses have been detected globally since September 2022. Sequencing results indicated that globally, the majority of these viruses had HA genes belonging to 6B.1A subclade 5a.2a close to references strains A/Victoria/2570/2019 and A/Sydney/5/2021, defined by additional HA1 substitutions K130N, N156K, L161I, V250A); only very few subclade 5a.1 viruses (close to reference strain A/Guangdong-Maonan/SWL1536/2019) were detected. In 2022, further diversification in Subclade 5a.2 viruses has been reported, with additional HA1 amino acid substitutions (K54Q, A186T, Q189E, E224A, R259K and K308R), some of which are located in antigenic site Sb. Some genetic diversity was noted amongst recent viruses in the 5a.2 subclade.

Viruses sharing HA substitutions of P137S, K142R, D260E, T227A, E356D and N451H have predominated in Europe and North America. A new nomenclature for the H1pdm09 HA subclades has been developed to address this emerging diversity. This is now available on Nextstrain and Nextclade.

No specific lineage or clade could be associated with severity

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 subclade 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 3 main groups defined by additional HA1 substitutions; H156S with D53N (plus other substitutions), H156S with D53G (plus other substitutions) and one with E50K, F79V and I140K (lacking H156S). A small number of viruses belonging to 3C.2a1b subclade 2a.1 (substitutions of G186S, F193S, Y195F and S198P) e.g. A/Cambodia/e0826860/2020, were detected. A new nomenclature for the H3N2 HA subclades has been developed to address the emerging diversity. This is now available on Nextstrain and Nextclade can be used to classify viruses if desired.

No specific lineage or clade could be associated with severity

Influenza B viruses

B/Victoria Lineage (Fig 4)

The 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 close to B/Austria/1359417/2021 reference virus [HA1 substitutions of A127T, P144L, N150K, G184E, N197D (resulting in the loss of an N-linked glycosylation motif), K203R, R297K] have predominated in countries where B/Victoria lineage viruses were detected and subjected to sequencing. Several countries have reported ongoing outbreaks of influenza B; sequencing of submitted viruses is ongoing.

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

B/Yamagata/16/88 viruses

No B/Yamagata/16/88 viruses have been detected.

Fig 2: Phylogenetic tree of the H1N1pdm09 viruses analyzed between 1st of September 2022 and 1st of February 2023. Cases requiring Oxygen supplementation are in yellow.

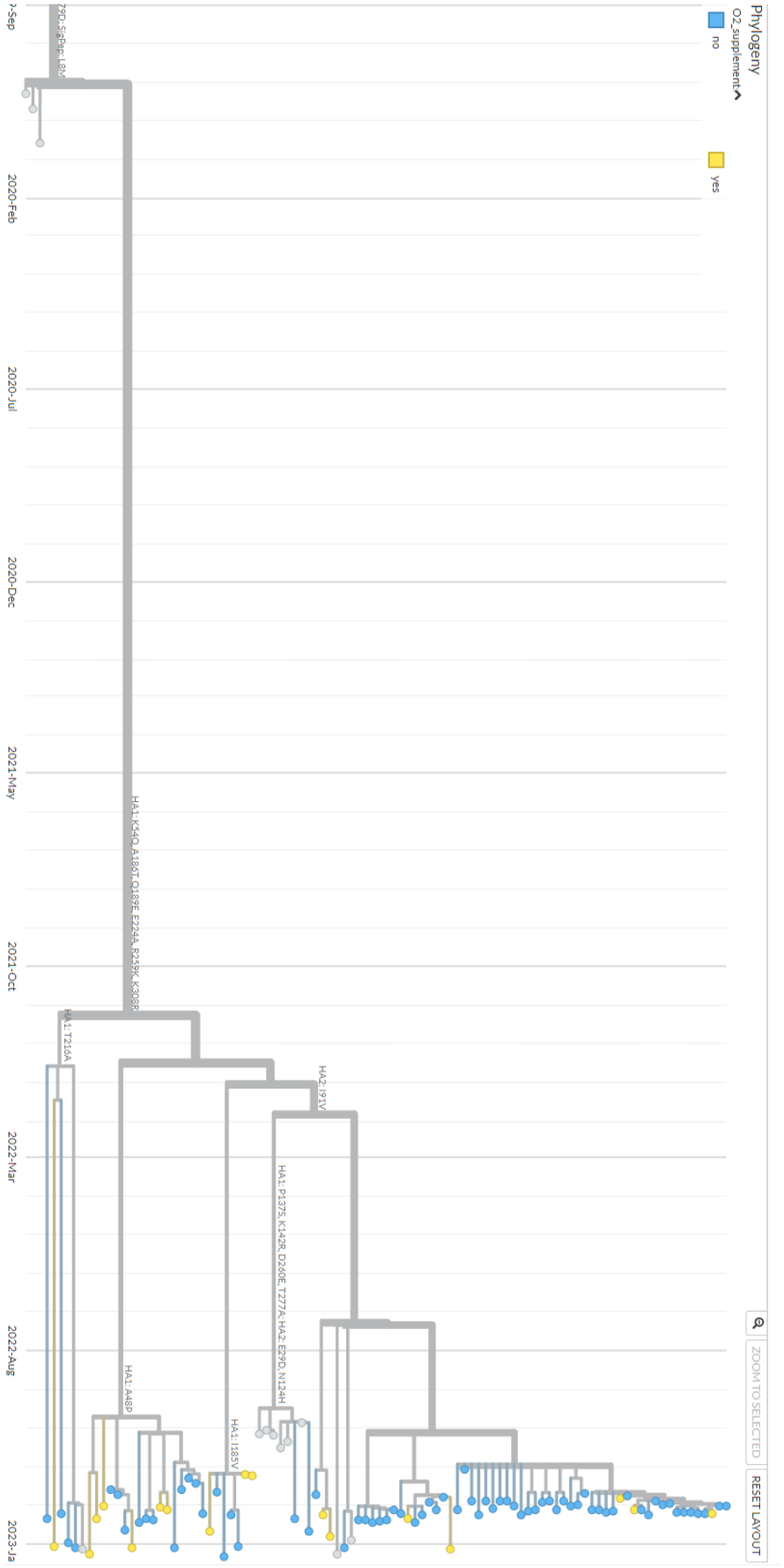


Fig 3: Phylogenetic tree of the H3N2 viruses analyzed between 1st of September 2022 and 1st of February 2023. Cases requiring Oxygen supplementation are in yellow.

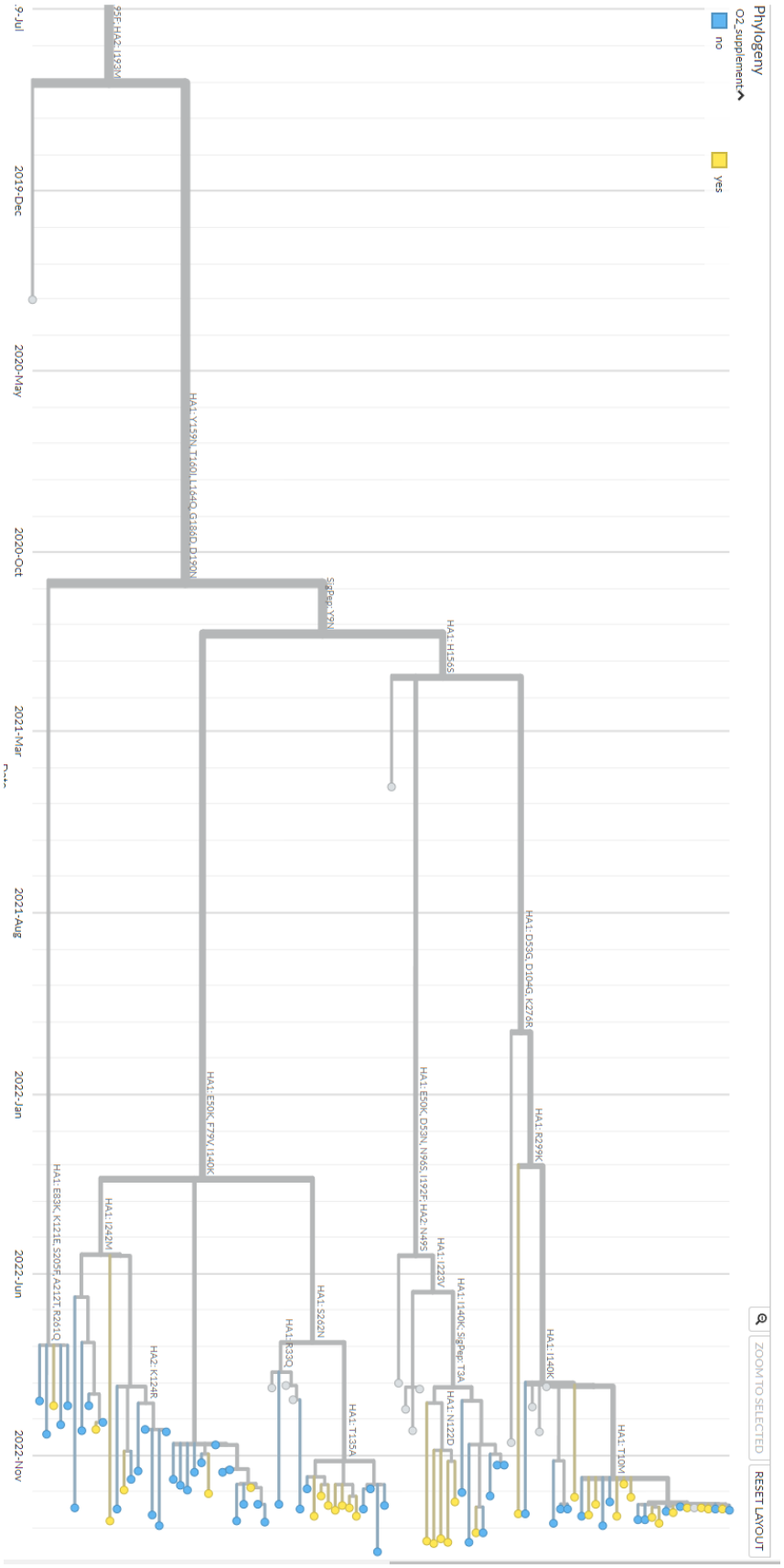


Fig 3 : Phylogenetic tree of the B viruses analyzed between 1st of September 2022 and 1st of February 2023. Cases requiring Oxygen supplementation are in yellow.