Global Influenza Hospital Surveillance Network

GIHSN report of activity prior to the WHO Consultation on the Composition of Influenza Virus Vaccines for use in the 2026-27 Northern Hemisphere Influenza Season.

Report prepared the 4th of February 2026

1 - Description of the network

GIHSN is collecting clinical and virological information from hospitalized cases through a network of sites located in different regions of the world (**Fig. 1**). 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 in the phylogenetic trees provided, to determine if specific lineages or clades are associated with more frequent severe presentation.

This report collates the sequencing data of hospitalized patients from 21 sites in 19 countries reporting 1,013 sequences passing quality filters and available in the GISAID database on 2026-02-03: *Brazil (1), Canada (7), Colombia (40), Cote d'Ivoire (44), Guatemala (25), Hong Kong (65), Kenya (17), Lebanon (77), Madagascar (21), Mexico (34), New Zealand (2), Pakistan (67), Peru (10), Romania (38), Russian Federation (353), Senegal (11), Spain (107), Ukraine (26), United States (68).*

Samples were collected between 2025-09-01 and 2026-01-19. During this period, A/H3N2 virus dominated (n=843), followed by A/H1N1 viruses (n=157) and rare detections of B viruses (n=13). Note that one A/H5N2 virus was detected in Mexico City in September 2025 but is not described in this report.

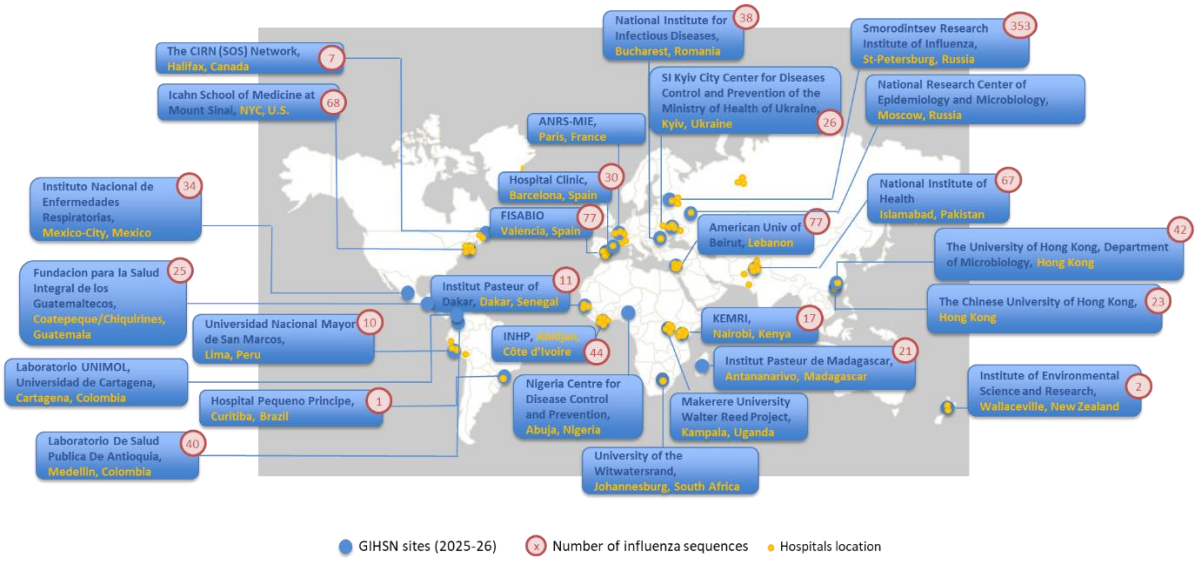

Fig. 1 *Map showing the repartition of the participating countries, between September 2025 and February 2026, with the number of influenza sequences shared by sites.*

2 - Description of the virus sequenced in the GIHSN

2.1 - Influenza A viruses

A(H1N1)pdm09 viruses

A(H1N1)pdm09 viruses were reported in most countries (15/19) participating in the GIHSN network in 2025, with a total of 157 sequences reported (**Fig. 2**).

Sequencing results indicated that most of these viruses (125/157, 80%) belonged to 6B.1A.**5a.2a.1** clade represented by the 2023–25 northern hemisphere (NH) vaccine strain A/Victoria/4897/2022, while 20% (32/157) belonged to 6B.1A.**5a.2a** clade.

Among 5a.2a clade, 10 viruses belonged to **C.1** subclade, 9 viruses carried the HA1:T120A and K169Q additional substitutions that defines subclade **C.1.9**, and 13 viruses belonged to **C.1.9.3** subclade characterized by the additional HA1:S83P substitution.

All of the 5a.2a.1 viruses carried HA1:T120A in comparison with A/Victoria/4897/2022 and belonged to subclade D.3, with 34% (43/125) further characterized into subclade **D.3.1** represented by the 2026 southern hemisphere (SH) vaccine strain A/Missouri/11/2025. A majority of 5a.2a.1 viruses (82/125, 66%) were further characterized into subclade **D.3.1.1** defined by the additional HA1:K302E substitution.

Using a binomial logistic regression model, we observed a **significantly higher odds of requiring respiratory support among patients infected with the D.3.1 subclade** (19/24 patients with available oxygen data, 79%) compared to those infected with the D.3.1.1 subclade, taken as the reference (14/73 patients with available oxygen data, 19%) (OR = 5.34, 95% CI [2.22–13.36], $p < 0.05$). This signal was no longer observed after adding region as a covariate in the model. Due to the limited sample size, we could not further adjust for important potential confounding factors such as age, date of collection or selection bias. Therefore, these findings should be interpreted with caution. Other A(H1N1)pdm09 subclades did not show statistical significance after adjustment, likely due to limited sample sizes.

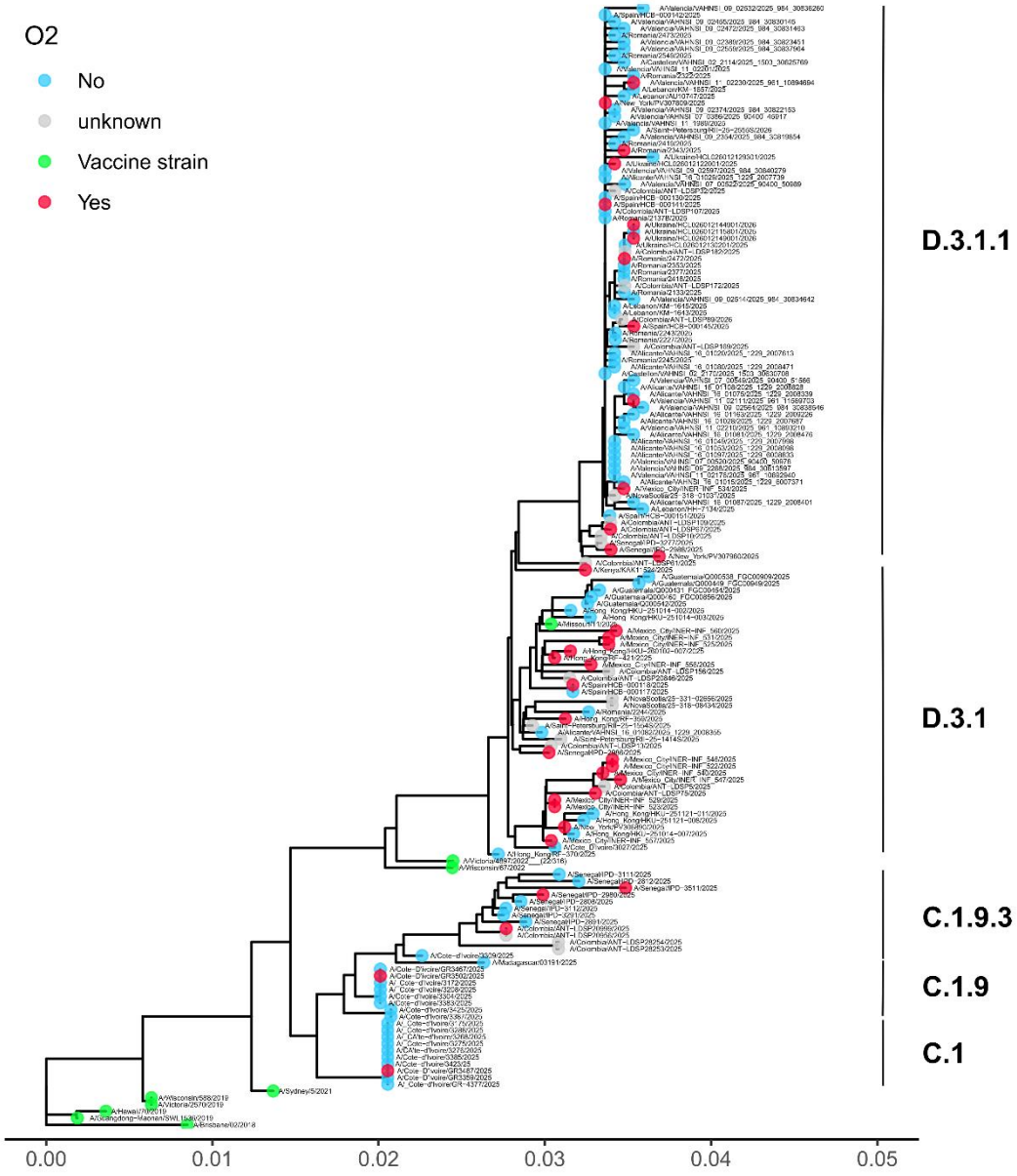

Fig 2: Phylogenetic tree of the A(H1N1) viruses analyzed between September 2025 and February 2026. The phylogeny has been inferred using a Neighbor Joining approach (Seaview). Visualization was displayed using ggtree in R. Tips (samples) colors correspond to Oxygen supplementation (yes: red; no:blue) with vaccine reference strains displayed in green.

A(H3N2) viruses

A(H3N2) viruses were reported in most countries (16/19) participating in the GIHSN network in 2025, with a total of 843 sequences reported (**Fig. 3**).

All viruses belonged to 3C.2a1b.2a.**2a.3a.1** clade, with all but one virus falling into subclade **J.2*** characterized by the HA1:N122D and K276E substitutions and represented by NH 2025-26 vaccine strain A/Croatia/10136RV/2023.

Additional diversification on the J.2 branch occurred with 6% of viruses (47/842) evolving into subclade **J.2.2**, 4% (36/842) into **J.2.3**, 5% (39/842) to **J.2.4**. and 81% (678/842) to **K** (J.2.4.1 subclade).

Subclade K viruses are characterized by J.2.4 subclade defining mutations HA1:T135K and K189R present in the SH 2026 vaccine strain A/Sydney/1359/2024, as well as additional ones including HA1:K2N, S144N, N158D, I160K, Q173R, T328A and S378N.

Using a binomial logistic regression model, we observed a **significantly higher odds of requiring respiratory support among patients infected with the J.2.3 subclade** (19/24 patients with available oxygen data, 79%) compared to those infected with the K subclade, taken as the reference (94/406 patients with available oxygen data, 23%) (OR = 12.61, 95% CI [4.92–38.87], $p < 0.05$). **J.2.4 was also associated with higher odds of requiring respiratory support compared with K subclade**, although the association was weaker (OR = 2.82, 95% CI [1.41–5.61], $p<0.05$). When the model was adjusted for region, these higher odds remained significant for J.2.3 (OR = 5.95, 95% CI [1.96–20.8], $p < 0.05$) and J.2.4 (OR = 3.26, 95% CI [1.29–8.24], $p < 0.05$). However, these findings should be interpreted with caution, as the analysis did not account for potential covariates such as age, collection date, and selection bias, which could represent important confounders.

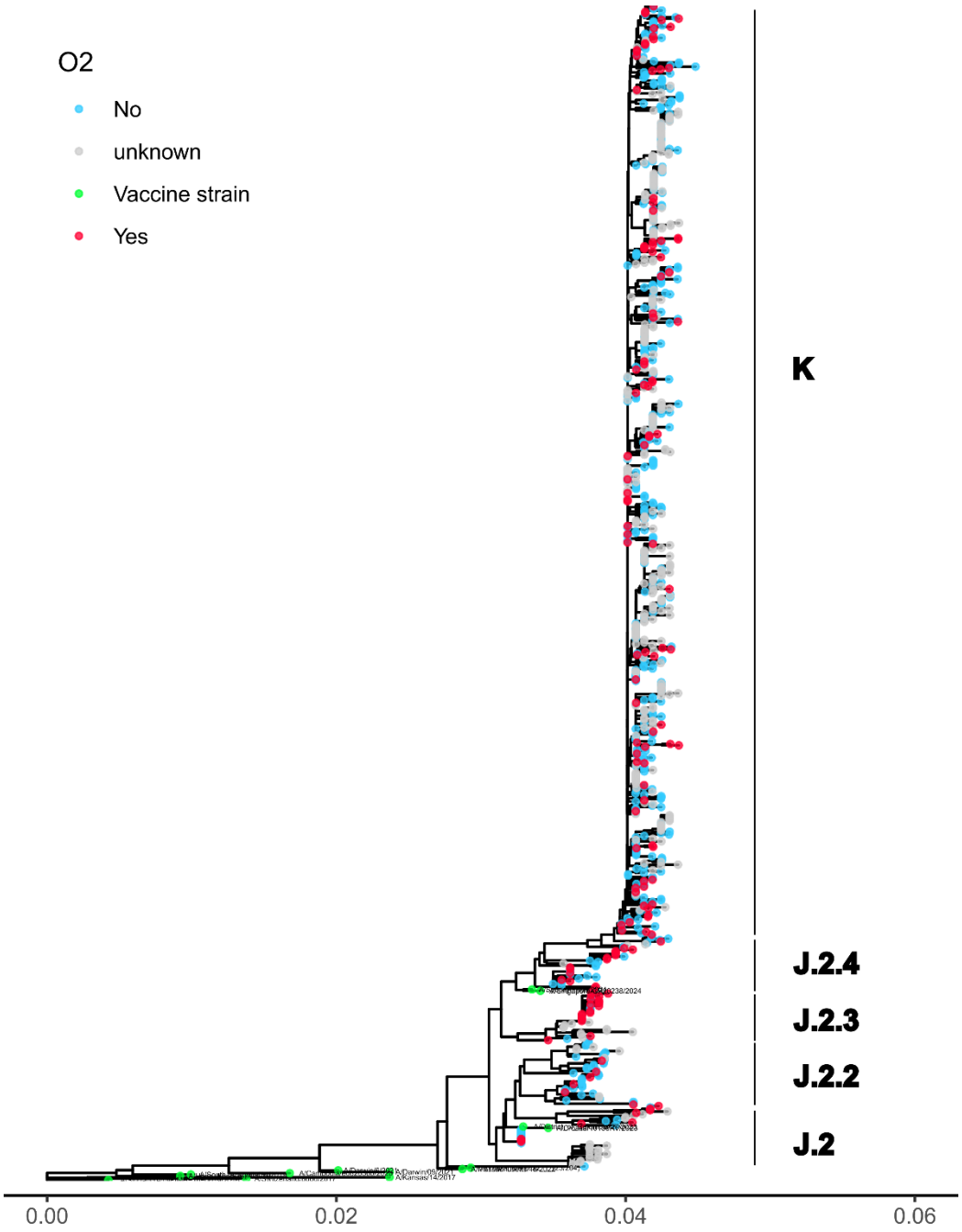

Fig 3: Phylogenetic tree of the A(H3N2) viruses analyzed between September 2025 and February 2026. The phylogeny has been inferred using a Neighbor Joining approach (Seaview). Visualization was displayed using ggtree in R. Tips (samples) colors correspond to Oxygen supplementation (yes: red; no:blue) with vaccine reference strains displayed in green.

2.2 - Influenza B viruses

B/Victoria Lineage

Influenza B/Victoria lineage was reported in 5 countries from the GIHSN network, with only 13 sequences reported (**Fig. 4**).

All Influenza B viruses sequenced belonged to clade **V1A.3a.2** subclade C, with B/Austria/1359417/2021 as reference virus.

All viruses fell into C.5.* subclades characterized by HA1:N197E substitution compared with B/Austria/1359417/2021 reference strain, with a majority of the viruses (9/13, 69%) evolving into **C.5.6** subclade including 2 viruses further diversified into **C.5.6.1** subclade.

Other C.5 viruses fell into **C.5.7** subclade (2 viruses) and **C.5.1** subclade (2 viruses).

Due to the very limited sample size, no statistical analysis was performed to investigate the association between subclades of the B/Victoria lineage and the need for oxygen support.

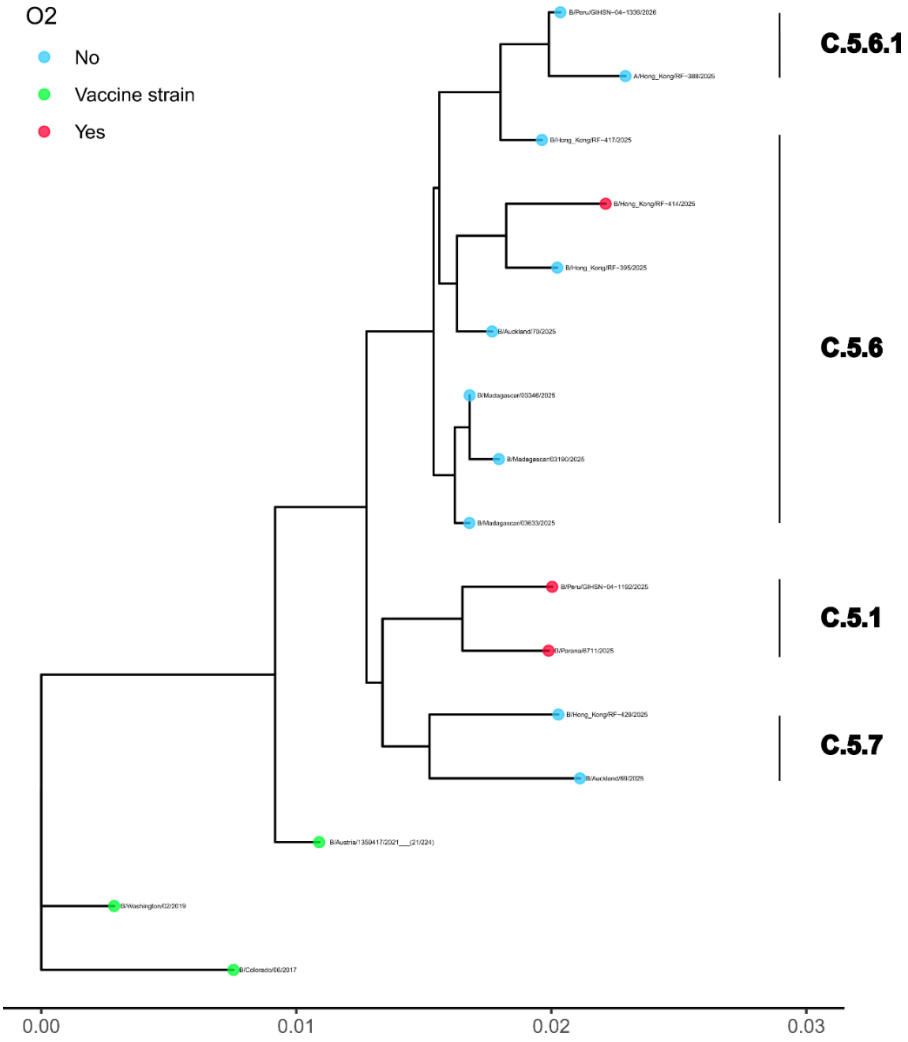

Fig 4: Phylogenetic tree of the B/Victoria viruses analyzed between September 2025 and February 2026. The phylogeny has been inferred using a Neighbor Joining approach (Seaview). Visualization was displayed using ggtree in R. Tips (samples) colors correspond to Oxygen supplementation (yes: red; no:blue) with vaccine reference strains displayed in green.

B/Yamagata viruses

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

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