

GIHSN report of activity prior to the WHO Consultation on the Composition of Influenza Virus Vaccines for use in the 2027 Southern Hemisphere Influenza Season.

Report prepared on 7 September 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. Severe clinical outcomes included supplemental oxygen use (collected at admission), intensive care unit (ICU) admission, mechanical ventilation, and death during hospitalization. In this report, viruses detected and sequenced from severe cases 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 19 sites in 18 countries reporting 551 sequences passing quality filters (detailed in the Methods section) and available in the GISAID database on 2026-08-31: *Brazil (16), Canada (11), Colombia (50), Cote d'Ivoire (3), France (5), Guatemala (51), Hong Kong (61), Kenya (11), Lebanon (5), Madagascar (32), Mexico (18), Pakistan (34), Peru (32), Russian Federation (64), Senegal (1), South Africa (103), Ukraine (42), United States (12).*

Samples were collected between 2nd February (week 6) to 1st August 2026 (week 31). During this period, the most frequently detected viruses were A(H3N2) (n=336), followed by A(H1N1) viruses (n=137) and B viruses (n=78) ([Fig. 1](#)). Influenza A viruses predominated in most GIHSN sites, with the exception of Pakistan, Côte d'Ivoire and Brazil. Among influenza A viruses, A(H3N2) predominated except in Russia, the USA and France. [Table 1](#) and [Fig. 2](#) provide a descriptive analysis of the cases' demographics and clinical data.

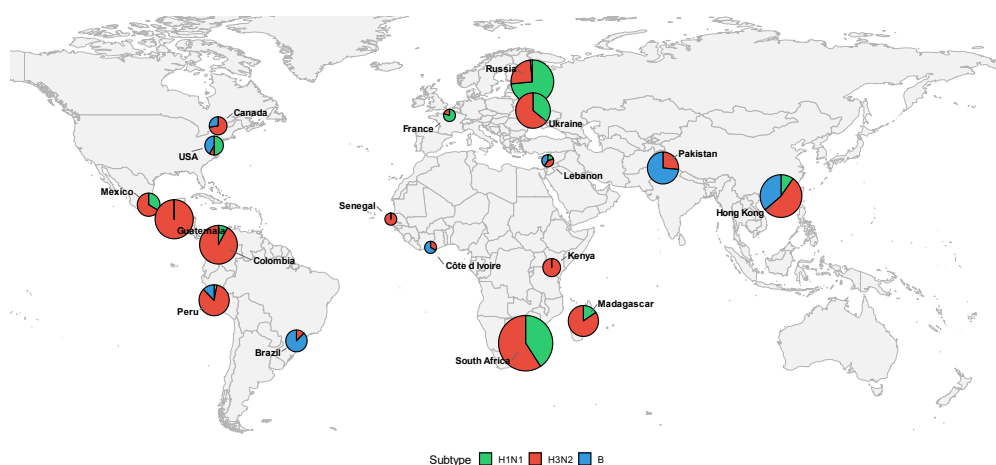


Figure 1. Map showing the distribution of influenza type/subtype sequenced by the participating countries, between February 2026 and August 2026.



Table 1. Patient characteristics by subtype and subclade.

Descriptive analysis 2026												
		B					H1N1			H3N2		
		Total	C.3.1	C.5.6	C.5.6.1	Other subclades	D.3.1.1	D.3.1	Other subclades	K	J.2.4.2	Other subclades
N total		551	42	17	11	8	94	42	1	250	54	32
Age	<5 years	258	17	3	2	0	22	37	0	134	31	12
	5-17 years	94	17	1	3	1	16	3	0	31	15	7
	18-64 years	90	7	8	4	6	23	1	0	29	5	7
	+ 65 years	109	1	5	2	1	33	1	1	56	3	6
Site	Brazil	16	13	0	1	0	0	0	0	2	0	0
	Canada	11	1	1	0	1	0	0	0	8	0	0
	Colombia	50	0	0	0	0	1	2	1	30	10	6
	Côte d'Ivoire	3	0	2	0	0	0	0	0	1	0	0
	France	5	0	0	0	0	4	0	0	1	0	0
	Guatemala	51	0	0	0	0	0	0	0	7	37	7
	Hong Kong	61	0	11	4	7	6	0	0	33	0	0
	Kenya	11	0	0	0	0	0	0	0	11	0	0
	Lebanon	5	0	2	0	0	1	0	0	2	0	0
	Madagascar	32	0	0	0	0	5	0	0	27	0	0
	Mexico	18	0	0	0	0	5	1	0	9	0	3
	Pakistan	34	25	0	0	0	0	0	0	9	0	0
	Peru	32	0	0	4	0	1	0	0	18	4	5
	Russia	64	0	1	0	0	44	3	0	11	0	5
	Senegal	1	0	0	0	0	0	0	0	1	0	0
	South Africa	103	0	0	0	0	6	36	0	61	0	0
	Ukraine	42	0	0	0	0	15	0	0	18	3	6
	USA	12	3	0	2	0	6	0	0	1	0	0
O2 supplementation		143/506 (28.3%)	5/41 (12.2%)	2/16 (12.5%)	2/11 (18.2%)	0/7 (0%)	27/83 (32.5%)	16/41 (39%)	0/1 (0%)	69/231 (29.9%)	14/49 (28.6%)	8/26 (30.8%)
Mechanical ventilation		18/534 (3.4%)	1/42 (2.4%)	0/17 (0%)	0/11 (0%)	0/8 (0%)	4/87 (4.6%)	1/41 (2.4%)	0/1 (0%)	7/244 (2.9%)	4/53 (7.5%)	1/30 (3.3%)
ICU admission		47/540 (8.7%)	4/42 (9.5%)	0/16 (0%)	1/11 (9.1%)	0/8 (0%)	12/94 (12.8%)	1/41 (2.4%)	0/1 (0%)	21/244 (8.6%)	6/53 (11.3%)	2/30 (6.7%)
Death		15/545 (2.8%)	0/42 (0%)	0/17 (0%)	0/11 (0%)	0/8 (0%)	7/91 (7.7%)	1/42 (2.4%)	0/1 (0%)	3/247 (1.2%)	3/54 (5.6%)	1/32 (3.1%)

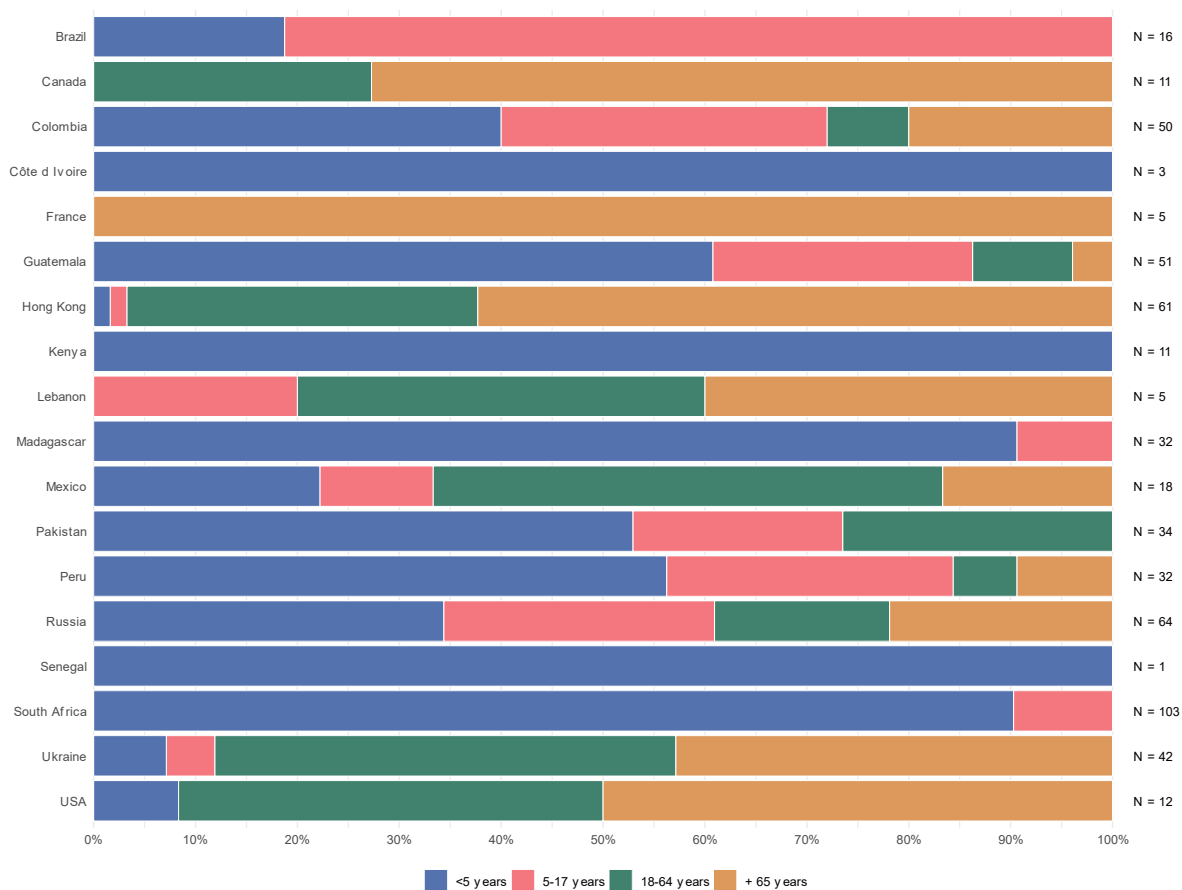


Figure 2. Age distribution of cases per country

2 - Description of the viruses sequenced in the GIHSN

2.1 - Influenza A viruses

A(H1N1)pdm09 viruses

A(H1N1)pdm09 viruses were reported in most countries (11/18) participating in the GIHSN network in 2026, with a total of 137 sequences reported ([Table 1](#)).

Phylogenetic analysis showed that 136 of 137 viruses belonged to clade 6B.1A.5a.2a.1, while a single sequence from Colombia belonged to clade 6B.1A.5a.2a, subclade C.1.9.3 ([Fig. 3](#)).

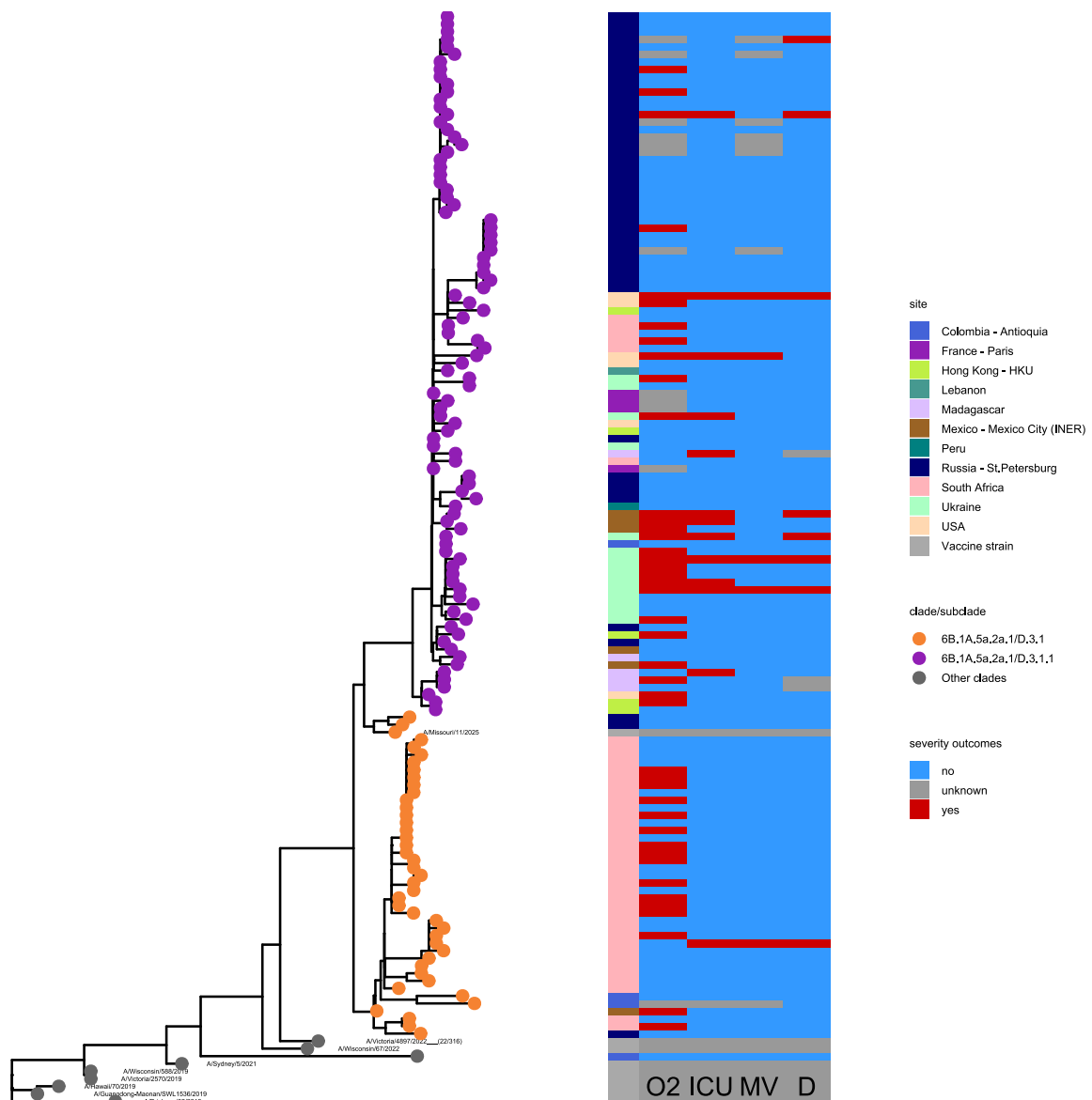


Figure 3. Phylogenetic tree of the A(H1N1) viruses analyzed between February 2026 and August 2026. Tips are coloured according to viral subclade. Vaccine reference strains are labelled. The heatmap indicates study site and clinical severity outcomes (yes: red, blue: no) for supplemental oxygen at admission (O2), intensive care unit admission (ICU), mechanical ventilation (MV), and death (D).

Within clade 6B.1A.5a.2a.1, subclade D.3.1.1 predominated (94/136, 69%), with most viruses detected in the Northern Hemisphere between February and April 2026. Subclade D.3.1 accounted for 42/136 (31%) sequences and was detected predominantly in South Africa in May–June 2026 ([Fig. 4](#)). D.3.1 viruses were predominantly detected in children aged <5 years (37/42, 88%), whereas D.3.1.1 viruses were mainly detected in adults (56/94, 60%). This distribution may partly reflect, at least in part, differences in the age composition of participating cohorts and the regional circulation of the respective subclades, with the South African cohort comprising predominantly children <5 years (90%) ([Fig. 2](#)).



Figure 4. Subclade distribution by country and month of collection.

Using a binomial logistic regression model, we observed a trend toward lower odds of ICU admission/death among patients infected with the D.3.1 subclade compared to those infected with the D.3.1.1 subclade, taken as the reference (OR = 0.15, 95% CI [0.01-0.80], $p = 0.07$) ([Fig. 5](#)). This signal was no longer observed after adjusting for age and considering the site as random effect in the model. There were no association between oxygen supplementation or mechanical ventilation and subclade.

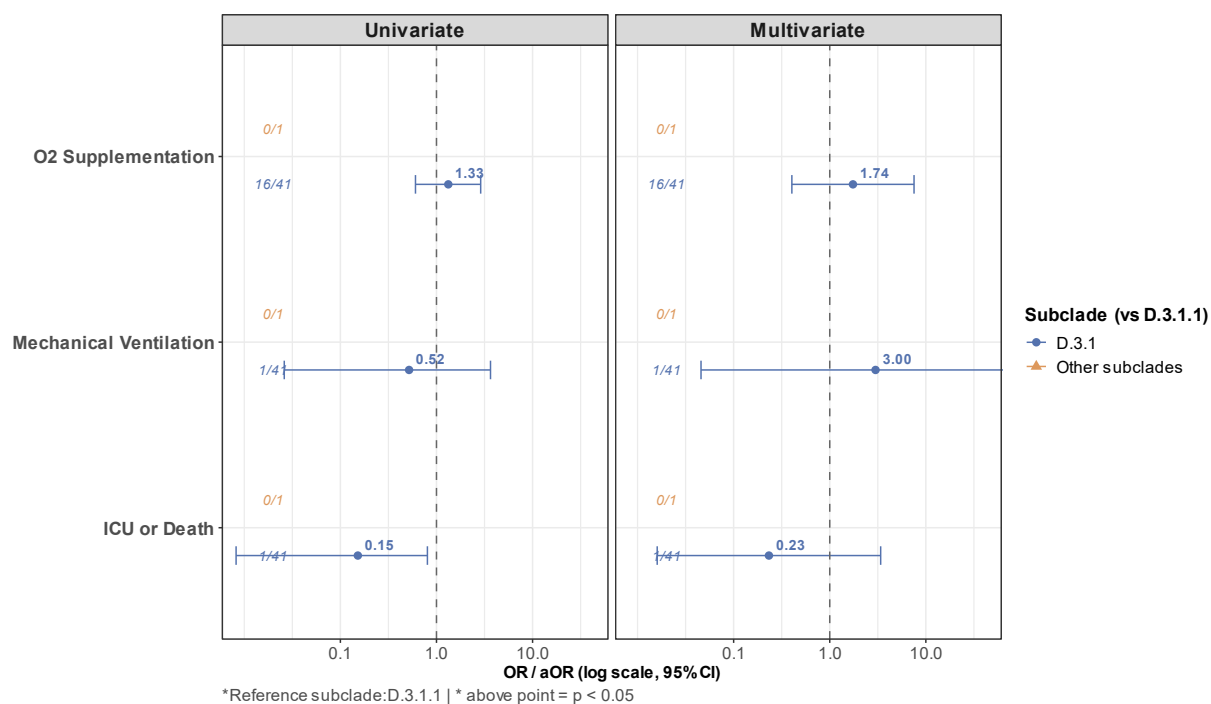


Figure 5. Association between A(H1N1) subclades and severity outcomes. OR: odd ratio. aOR: adjusted odd ratio. ICU: intensive care unit. * - Statistically significant results (p value < 0.05).

A(H3N2) viruses

A(H3N2) viruses were reported in all the countries participating in the GIHSN network in 2026, with a total of 336 sequences reported ([Table 1](#)).

All viruses belonged to 3C.2a1b.2a.2a.3a.1 clade, subclade J.2* ([Fig. 6](#)). Subclade K was predominant (250/336, 74%) in all regions, except in Guatemala, where J.2.4.2 predominated ([Fig. 7](#)). Other J.2* subclades included: J.2.4.2 (54/336, 16%) characterized by HA1:F79V, J.2.3 (9/336, 3%), J.2.2 (9/336, 3%), J.2 (9/336, 3%) and J.2.4 (5/336, 1.5%).

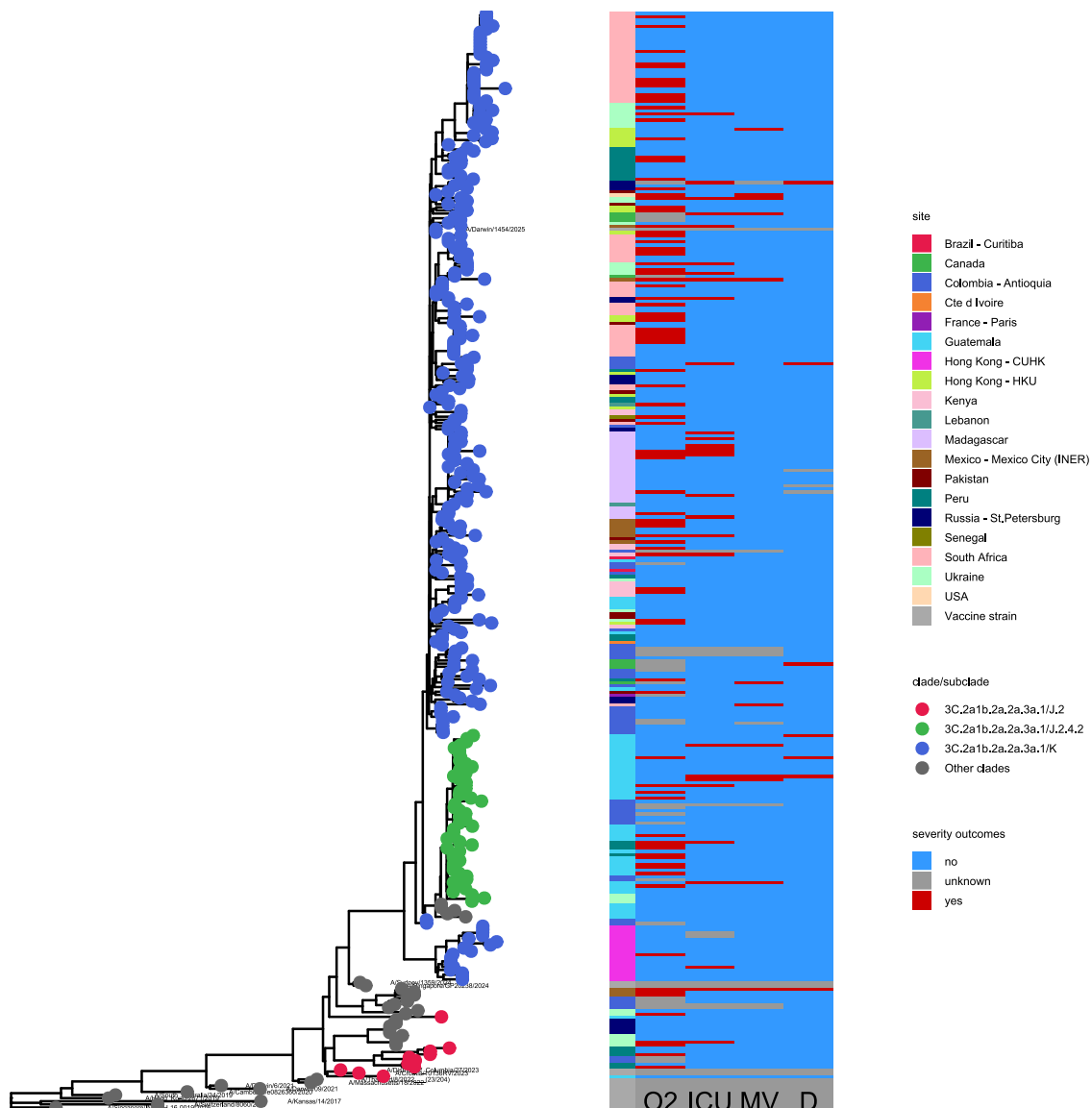


Figure 6. Phylogenetic tree of the A(H3N2) viruses analyzed between February 2026 and August 2026. Tips are coloured according to viral subclade. Vaccine reference strains are labelled. The heatmap indicates study site and clinical severity outcomes (yes: red, blue: no) for supplemental oxygen at admission (O2), intensive care unit admission (ICU), mechanical ventilation (MV), and death (D).

Cases infected with K viruses included a higher proportion of individuals aged >65 years than those infected with J.2.4.2 viruses (Fisher's exact test, $p=0.004$). This difference may partly reflect differences in the age composition of the study populations across sites, as only 3.9% of the Guatemalan cohort were aged >65 years (Fig. 2).

Continued diversification was observed within subclade K, including geographically associated sequence clusters (Fig. 6). A cluster carrying the HA1:D122N reversion was identified among sequences from CUHK, Hong Kong, while the HA1:I214T substitution was observed among sequences from Madagascar.

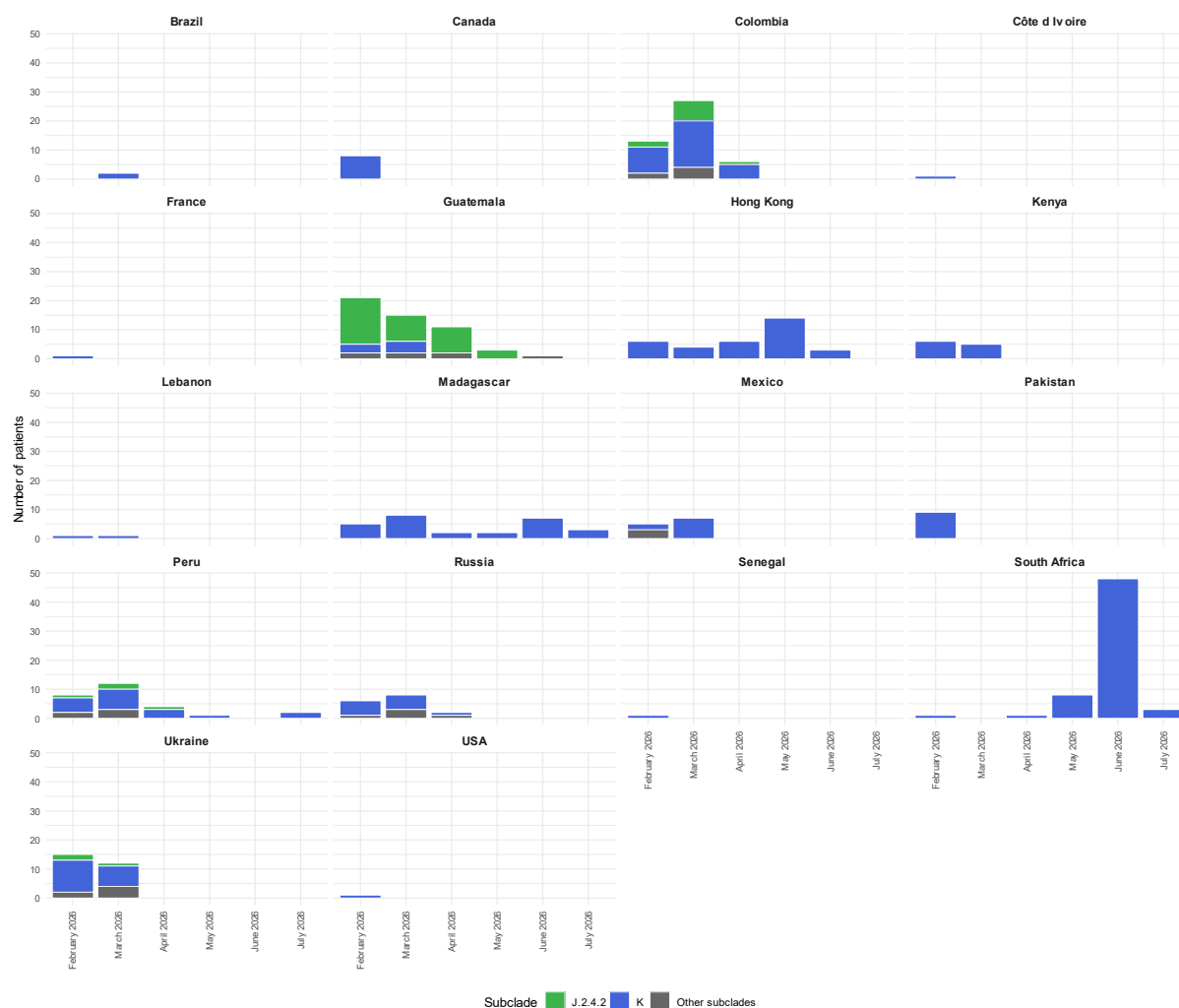


Figure 7. Subclade distribution by country and month of collection.

In univariate analyses, no significant association was observed between viral subclade and disease severity (**Fig. 8**). After adjusting for age and considering site as a random effect in the model, we observed a significantly higher odds of requiring supplemental oxygen at admission and mechanical ventilation during hospitalization among patients infected with the J.2.4.2 subclade compared to those infected with the K subclade, taken as the reference (OR for supplemental oxygen = 3.71, 95% CI [1.07-12.89]; OR for mechanical ventilation = 4.63, 95% CI [1.17-18.25]). These associations should be interpreted with caution, as J.2.4.2 viruses accounted for >50% of sequences in a single country (Guatemala), and subclade and country effects may therefore be confounded. Furthermore, the models did not account for other potential confounders, including sampling date, underlying conditions and vaccination status.

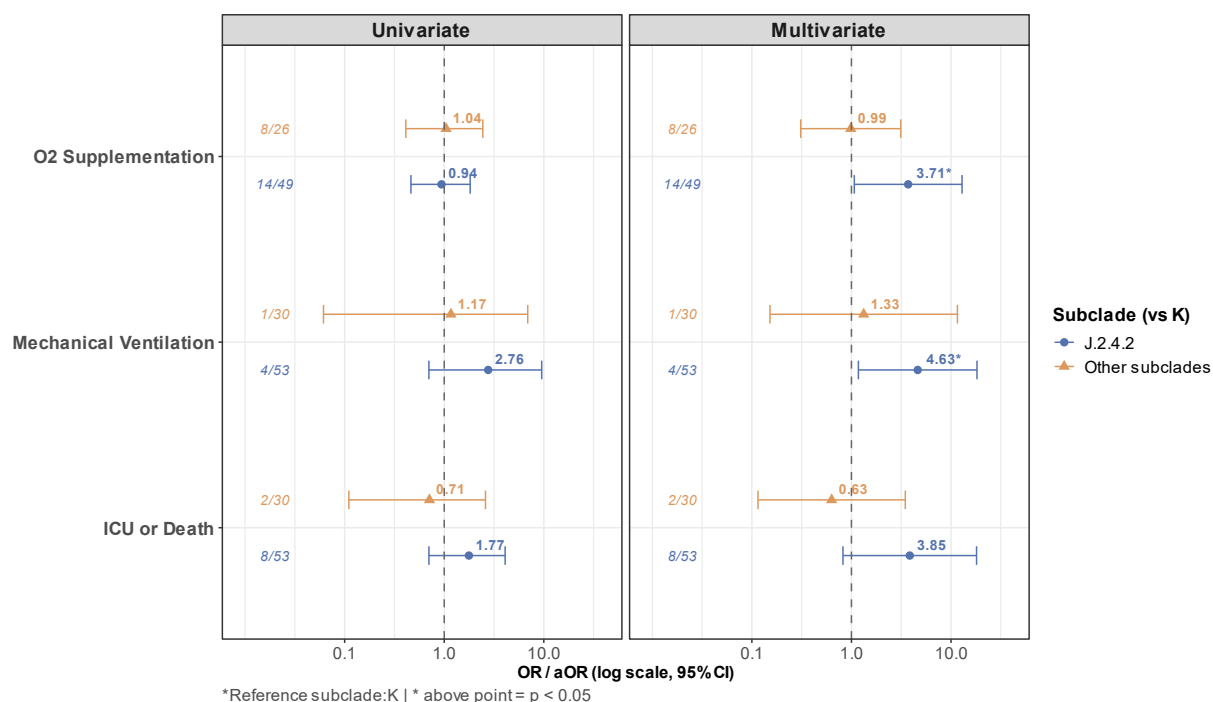


Figure 8. Association between A(H3N2) subclades and severity outcomes. OR: odd ratio. aOR: adjusted odd ratio. ICU: intensive care unit. * - Statistically significant results (p value <0.05).

2.2 - Influenza B viruses

B/Victoria Lineage

Influenza B/Victoria lineage was reported in half of the countries (9/18) participating in the GIHSN network in 2026, with a total of 75 sequences reported ([Table 1](#)).

All sequenced Influenza B viruses belonged to clade V1A.3a.2 subclade C*, with a majority of the viruses (42/75, 56%) classified as C.3.1 subclade, followed by C.5.6 (17/75, 23%), C.5.6.1 (11/75, 15%), C.3.3 (6/75, 8%), C.5 (1/75) and C.5.1 (1/75) ([Fig. 9](#)). C.3.1 viruses were predominantly detected in Pakistan and Brazil, whereas C.5.6* viruses were mainly reported from Hong Kong ([Fig. 10](#)).

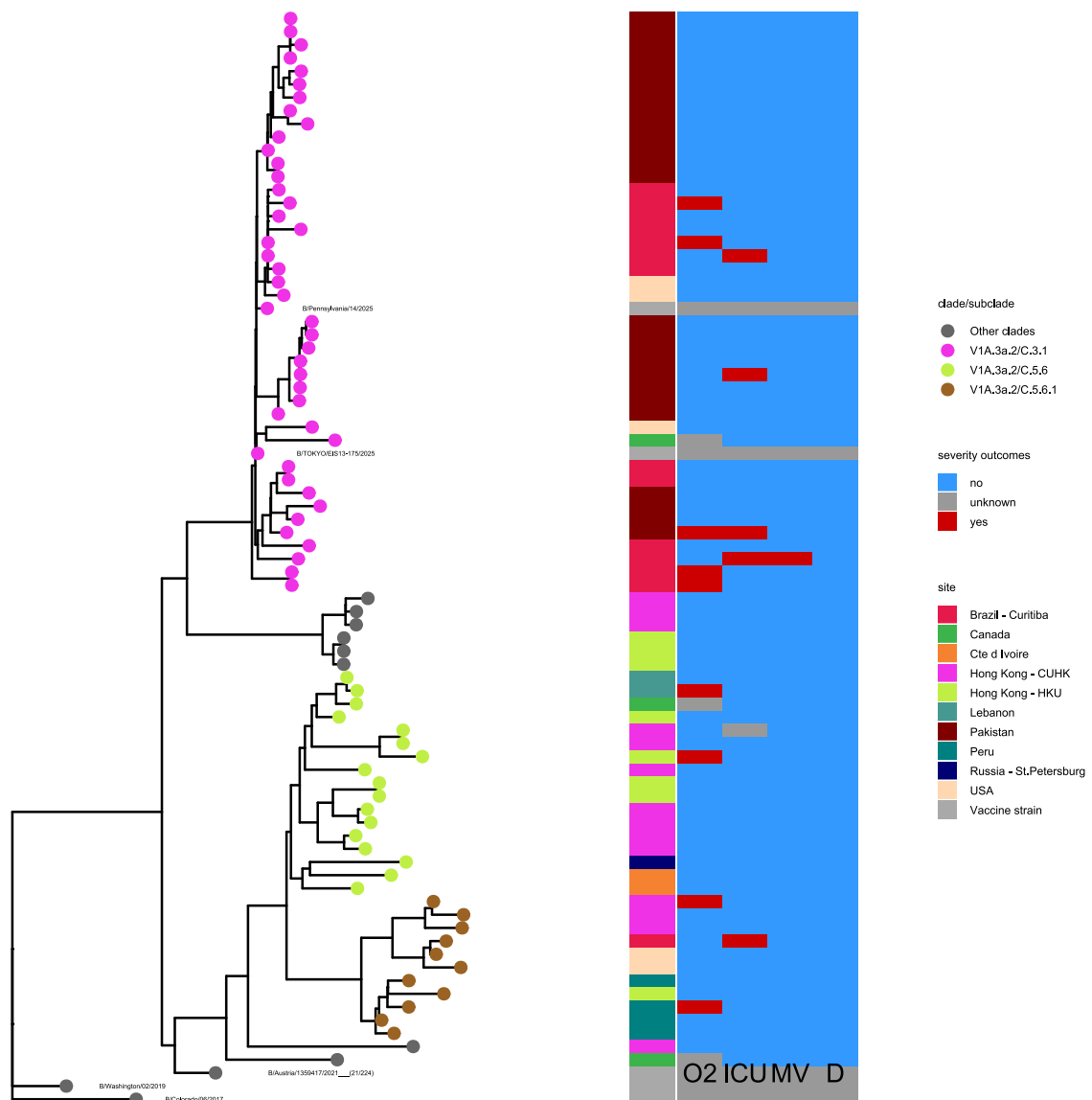


Figure 9. Phylogenetic tree of the B/Victoria viruses analyzed between February 2026 and August 2026. Tips are coloured according to viral clade. Vaccine reference strains are labelled. The heatmap indicates study site and clinical severity outcomes (yes: red, blue: no) for supplemental oxygen at admission (O2), intensive care unit admission (ICU), mechanical ventilation (MV), and death (D).

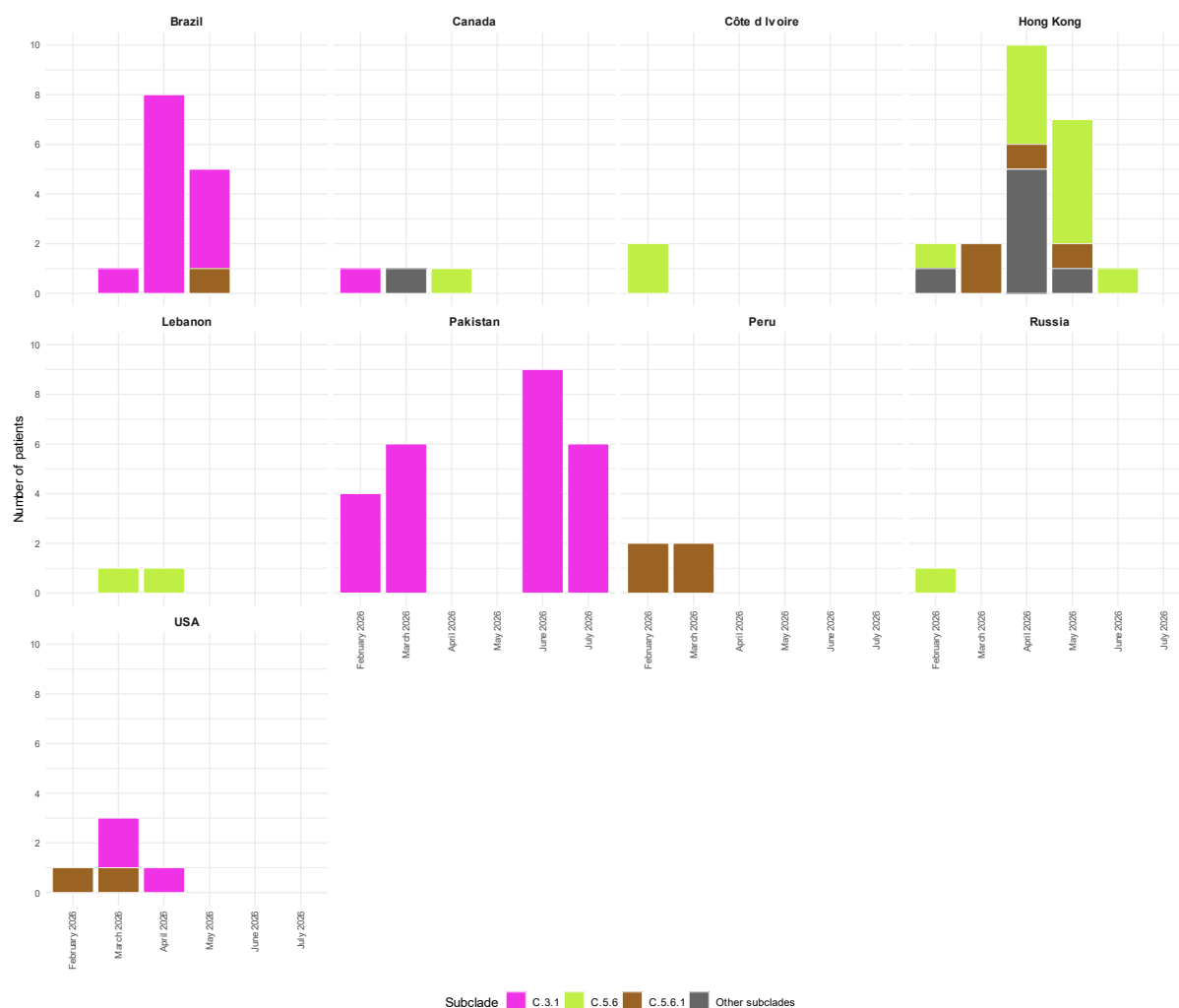


Figure 10. Subclade distribution by country and month of collection.

There were few severe cases among patients infected with influenza B viruses ([Table 1](#)). Neither univariate nor multivariate analyses identified a significant association between viral subclade and disease severity ([Fig. 11](#)).

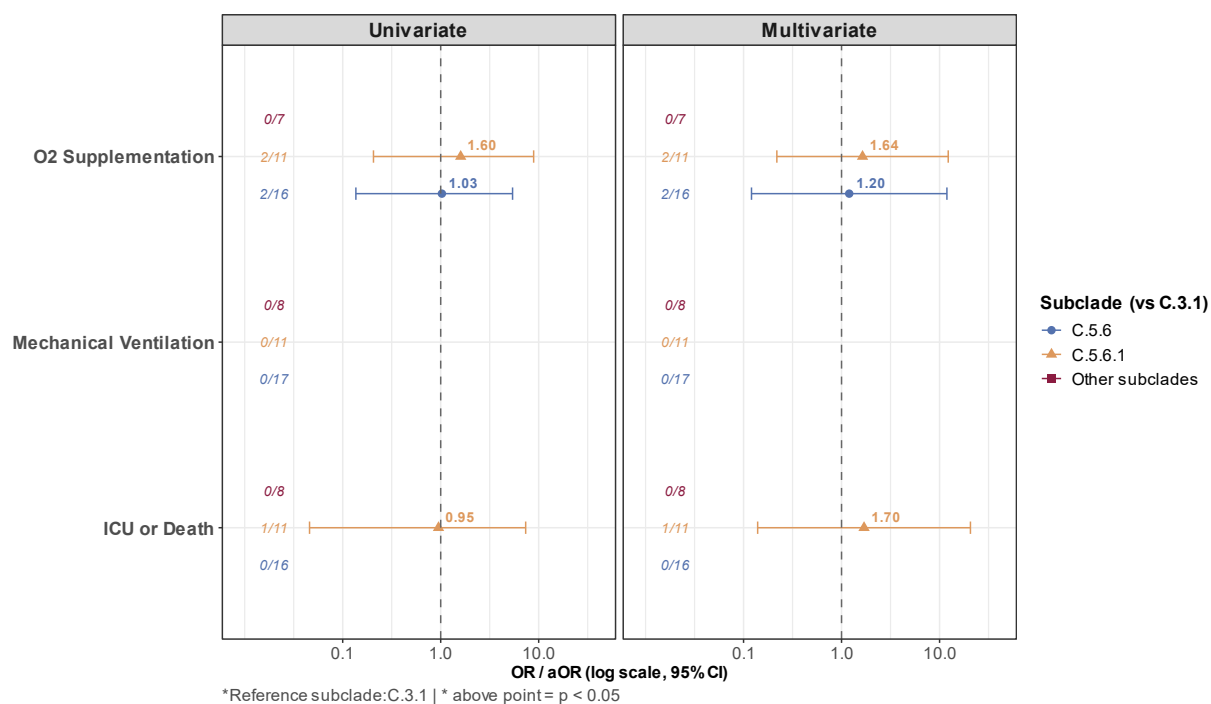


Figure 11. Association between B subclades and severity outcomes. OR: odd ratio. aOR: adjusted odd ratio. ICU: intensive care unit. * - Statistically significant results (p value < 0.05).

B/Yamagata viruses

No B/Yamagata lineage viruses have been detected.

3. Methods

Study population

The GIHSN enrolled patients admitted to hospital for at least one night due to acute respiratory illness or symptoms suggestive of a recent respiratory infection. The present analysis included GIHSN participants who tested positive for influenza between 2nd February to 1st August 2026 and for whom viral genomic sequences were available on GISAID. Patients with missing or duplicate GISAID entries or with <90% HA sequence coverage were excluded.

Clinical severity analysis

Associations between viral subclade and clinical severity were assessed for three outcomes: supplemental oxygen at admission, mechanical ventilation during hospitalization, and a composite outcome of intensive care unit admission or death during hospitalization. For each influenza subtype (A(H1N1)pdm09, A(H3N2) and B/Victoria), the most prevalent subclade was used as the reference.

Univariable odds ratios (ORs) and 95% confidence intervals (CIs) were estimated using logistic regression, with viral subclade as the sole predictor. Subclades with no events resulted in non-finite or highly imprecise estimates due to zero-cell counts. These estimates were considered non-interpretable, and corresponding event counts (n/N) were reported on the forest plots.

To account for potential confounding and the multicentre structure of the data, subtype-specific generalized linear mixed models (GLMMs) with a binomial distribution were fitted. Adjusted ORs (aORs) were estimated with viral subclade and age group as fixed effects and country as a random intercept. As in the univariable analyses, zero-event subclades could result in non-finite estimates or model non-convergence due to separation and were considered non-interpretable.

Phylogenetic analysis

For each influenza subtype, sequences were aligned using MAFFT. Phylogenetic trees were inferred using the neighbour-joining method and rooted using the oldest available vaccine strain. Clade and subclade assignments were performed using the latest available Nextclade datasets at the time of analysis.

This report was prepared by the National Influenza Center in Lyon, France: Bruno Lina, Antonin Bal, Nathalie Bergaud, Gwendolyne Burfin, Hadrien Règue, Inès Yous, Laurence Josset and the GENEPII platform.

Acknowledgments to sites which contributed sequences:

Brazil: Hospital Pequeno Principe, Curitiba (Sonia M Raboni; Heloïsa I G Giamberardino);

Canada: Canadian Serious Outcomes Surveillance Network Halifax, Nova Scotia (Shelly A. McNeil; Melissa K. Andrew);

Colombia: Laboratorio de Salud Publica de Antioquia, Medellin (Idabely Betancur Ortiz);

Côte d'Ivoire : Institut National d'Hygiène Publique (INHP), Abidjan (Daouda Coulibaly) ;

France : ANRS-MIE, Paris (Liem Luong, Odile Launay) ;

Guatemala: Fundacion para la Salud Integral de los Guatemaltecos, calletera de Coatepeque a Chiquirines (Daniel Olson);

Hong Kong: The Chinese University of Hong Kong (Lai Koon Chi Christopher);

Hong Kong: The University of Hong Kong, Department of Microbiology (Kelvin To);

Kenya: Kenya Medical Research Institute (KEMRI), Nairobi (Nancy A. Otieno);

Lebanon: Center for Infectious Diseases Research (CIDR), American University of Beirut (Ghassan Dbaibo);

Madagascar: Institut Pasteur de Madagascar (IPM), Antananarivo (Norosoa Razanazatoivo ; Jean-Michel Heraud);

Mexico: Instituto Nacional de Enfermedades Respiratorias, Mexico City (Joel Armando Vazquez-Perez);

Pakistan: National Institute of Health, Islamabad, (Muhammad Salman; Nazish Badar);

Peru: Instituto de Medicina Tropical Universidad San Marcos Lima PeruLima (Victor Alberto Laguna-Torres);

Russia St-Petersburg: Smorodintsev Research Institute of Influenza, St-Petersburg (Anna Sominina; Daria Danilenko);

Senegal: Institut Pasteur of Dakar (IPD), Dakar (Ndongo Dia);

South Africa: Respiratory and Meningeal Pathogens Research Unit, Johannesburg (Vickie Baillie);

Spain: Fisabio-Public Health, Valencia (Alejandro Orrico Sanchez; Ainara Mira Iglesias);

Ukraine: SI Kyiv City Center for Diseases Control and Prevention of the Ministry of Health of Ukraine (Alla Mironenko; Nataliia Teteriuk);

USA: Icahn School of Medicine at Mount Sinai, NYC (Viviana Simon; Harm van Bakel; Emilia Sordillo).



Based on data extracted from the GIHSN database for patients admitted between 2nd february to 1st august 2026, with the support of Impact Healthcare, Catherine Commaille-Chapus and Camille Hunsinger, and of the Foundation for Influenza Epidemiology, Cédric Mahé, Sandra Chavez and Laurence Pagnon.