PHF Science

RECOMMENDATION FOR SEASONAL INFLUENZA VACCINE COMPOSITION FOR NEW ZEALAND FOR 2026

This report is compiled by WHO National Influenza Centre and Health Intelligence Team, Institute of Environmental Science and Research, New Zealand

TABLE OF CONTENTS

1. RECOMMENDATION

The Australian Influenza Vaccine Committee (AIVC) met with a New Zealand representative in Canberra on 8 October 2025 to consult on the influenza vaccine composition for 2026 for New Zealand, Australia and South Africa (Table 1).

Egg-based influenza vaccines:

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Singapore/GP20238/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage) - like virus.

Cell-based or recombinant-based or nucleic acid-based influenza vaccines:

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Sydney/1359/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

The continued absence of confirmed detection of naturally occurring B/Yamagata lineage viruses after March 2020 is indicative of a very low risk of infection by B/Yamagata lineage viruses. Consistent with previous four WHO recommendations since September 2023, it remains the opinion of the WHO influenza vaccine composition advisory committee that inclusion of a B/Yamagata lineage antigen is no longer warranted. **There will no longer be updated recommendations for the B/Yamagata lineage component.** The AIVC noted this position and supports the WHO committee's views.

Quadrivalent vaccines, where the transition to trivalent vaccines is not yet complete, contain a 4th component – a B/Yamagata lineage virus.

Table 0. Influenza vaccine recommendations for New Zealand, 1994–2025

Decision		Use	A H3N2	A H1N1	B (Trivalent)	B (Quadrivalent)
NZ & WHO*	2025	2026	A/Singapore/GP20238/2024	A/Missouri/11/2025	B/Austria/1359417/2021	B/Phuket/3073/2013
NZ & WHO*	2024	2025	A/Croatia/10136RV/2023	A/Victoria/4897/2022	B/Austria/1359417/2021	B/Phuket/3073/2013
NZ & WHO*	2023	2024	A/Thailand/8/2022	A/Victoria/4897/2022	B/Austria/1359417/2021	B/Phuket/3073/2013
NZ & WHO*	2022	2023	A/Darwin/9/2021	A/Sydney/5/2021	B/Austria/1359417/2021	B/Phuket/3073/2013
NZ & WHO*	2021	2022	A/Darwin/9/2021	A/Victoria/2570/2019	B/Austria/1359417/2021	B/Phuket/3073/2013
NZ & WHO*	2020	2021	A/Hong Kong/2671/2019	A/Victoria/2570/2019	B/Washington/02/2019	B/Phuket/3073/2013
NZ & WHO*	2019	2020	A/South Australia/34/2019	A/Brisbane/02/2018	B/Phuket/3073/2013	B/Washington/02/2019
NZ & WHO*	2018	2019	A/Switzerland/8060/2017	A/Michigan/45/2015	B/Phuket/3073/2013	B/Colorado/06/2017
NZ & WHO*	2017	2018	A/Singapore/INFIMH-16-0019/2016	A/Michigan/45/2015	B/Phuket/3073/2013	B/Brisbane/60/2008
NZ & WHO*	2016	2017	A/Hong Kong/4801/2014	A/Michigan/45/2015	B/Brisbane/60/2008	B/Phuket/3073/2013
NZ & WHO*	2015	2016	A/Hong Kong/4801/2014	A/California/7/2009	B/Brisbane/60/2008	B/Phuket/3073/2013
NZ & WHO*	2014	2015	A/Switzerland/9715293/2013	A/California/7/2009	B/Phuket/3073/2013	B/Brisbane/60/2008
NZ & WHO*	2013	2014	A/Texas/50/2012	A/California/7/2009	B/Massachusetts/2/2012	B/Brisbane/60/2008
NZ & WHO*	2012	2013	A/Victoria/361/2011	A/California/7/2009	B/Wisconsin/1/2010	
NZ & WHO*	2011	2012	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2010	2011	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2009	2010	A/Perth/16/2009	A/California/7/2009	B/Brisbane/60/2008	
NZ & WHO*	2008	2009	A/Brisbane/10/2007	A/Brisbane/59/2007	B/Florida/4/2006	
NZ & WHO*	2007	2008	A/Brisbane/10/2007	A/Solomon Islands/3/20[illegible]	B/Florida/4/2006	
NZ & WHO*	2006	2007	A/Wisconsin/67/2005	A/New Caledonia/20/99	B/Malaysia/2506/2004	
NZ & WHO*	2005	2006	A/California/7/2004	A/New Caledonia/20/99	B/Malaysia/2506/2004	
NZ & WHO*	2004	2005	A/Wellington/1/2004	A/New Caledonia/20/99	B/Shanghai/361/2002	
NZ & WHO*	2003	2004	A/Fujian/411/2002	A/New Caledonia/20/99	B/Hong Kong/330/2001	
NZ & WHO*	2002	2003	A/Moscow/10/99	A/New Caledonia/20/99	B/Hong Kong/330/2001	
NZ & WHO*	2001	2002	A/Moscow/10/99	A/New Caledonia/20/99	B/Sichuan/379/99	
NZ	2000	2001	A/Sydney/5/97	A/New Caledonia/20/99	B/Beijing/184/93	
WHO*	2000	2001	A/Moscow/10/99	A/New Caledonia/20/99	B/Beijing/184/93	
NZ & WHO*	1999	2000	A/Sydney/5/97	A/Beijing/262/95	B/Beijing/184/93	
NZ	1998	1999	A/Sydney/5/97	A/Bayern/7/95	B/Beijing/184/93	
WHO**	1997–98		A/Wuhan/359/95	A/Bayern/7/95	B/Beijing/184/93	
NZ	1997	1998	A/Wuhan/359/95	A/Texas/36/91	B/Beijing/184/93	
WHO**	1996–97		A/Wuhan/359/95	A/Singapore/6/86***	B/Beijing/184/93	
NZ	1996	1997	A/Johannesburg/33/94	A/Texas/36/91	B/Beijing/184/93	
WHO**	1995-96		A/Johannesburg/33/94	A/Singapore/6/86	B/Beijing/184/93	
NZ	1995	1996	A/Guangdong/25/93	A/Texas/36/91	B/Panama/45/90	
WHO**	1994–95		A/Shangdong/9/93	A/Singapore/6/86	B/Beijing/184/93	
NZ	1994	1995	A/Beijing/32/92	A/Texas/36/91	B/Panama/45/90	

* WHO recommendations are for the Southern Hemisphere winter; * * WHO recommendations are for the Northern Hemisphere winter

2. SUMMARY

In 2025, influenza activity in New Zealand is described at a moderate level. Overall impact on healthcare use in hospitals was moderate as measured by influenza-associated severe acute respiratory illness (SARI). Seriousness of disease (i.e. clinical severity) that indicates the extent to which individuals get sick when infected with the influenza virus was moderate as measured by the ratio of influenza-associated SARI admitted in ICU over influenza-associated SARI hospitalization. Virus transmissibility which reflects the ease of movements of the influenza virus between individuals and communities was moderate as measured by influenza-associated acute respiratory illness among the SHIVERS community cohort participants.

The hospital-based severe acute respiratory illness was moderate in 2025. Influenza–associated SARI hospitalizations were higher in both young children (0–4 years) and elderly (≥65) compared to other age groups; also higher in Pacific Peoples and Māori ethnic groups compared to other ethnic groups.

The community cohort-based acute respiratory illness (ARI) was moderate to high in 2025, higher than 2023 & 2024 but lower than 2022. Influenza-associated ARI was lower than 2024 but higher than 2023. The influenza-associated ARI disease burden was higher in children aged 0–19 years compared to other age groups; also higher in Māori and Pacific peoples compared to Asians and Europeans ethnic groups.

The laboratory-based influenza surveillance tested samples from various surveillance systems as well as samples ordered by clinicians during routine hospital diagnosis. A total of 5887 influenza viruses were detected and reported through this system. Of them, influenza A represented 63.6% (3743) and influenza B 36.4% (2144) of all influenza viruses. Among 2011 subtyped and lineage-typed influenza viruses, 1230 (61.2%) were A(H1N1)pdm09, 321(16.0%) were A(H3N2), 460 (22.9%) were influenza B/Victoria lineage viruses.

WHO National Influenza Centre (NIC) at the New Zealand Institute of Public Health and Forensic Science (formerly ESR) conducted antigenic/genetic typing: 1) 49 influenza A(H1N1)pdm09 viruses were antigenically closely related to the vaccine strain A/Victoria/4897/2022(H1N1)pdm09-like virus. Genetically most of influenza A(H1N1)pdm09 viruses fell into group 6B.1A.5a.2a; 2) Two influenza A(H3N2) viruses were antigenically closely related to the vaccine strain A/Croatia/10136RV/2023 (H3N2)-like virus. Genetically most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2a.3a.1. 3) 149 (99.3%) influenza B/Victoria-lineage viruses were antigenically closely related to the vaccine strain B/Austria/1359417/2021-like virus. One (0.7%) influenza B/Victoria-lineage virus was antigenically drifted away from the vaccine strain. Genetically, influenza B/Victoria lineage viruses fell into group V1.3a.2.

For influenza-confirmed SARI cases among acutely admitted hospital patients, the estimated adjusted vaccine effectiveness (VE) was 69.5% (95% CI: 58.2, 78.0). For influenza-confirmed ILI cases among GP consultation patients, the estimated adjusted vaccine effectiveness (VE) was 72.8% (95% CI: 59.3, 82.4). For influenza-confirmed ARI among community cohort participants, the estimated adjusted vaccine effectiveness (VE) was 56.8% (95% CI: 41.6, 68.1).

3. EPIDEMIOLOGY - NEW ZEALAND INFLUENZA SEASON IN 2025

The national influenza surveillance system in New Zealand is an essential public health tool for assessing and implementing strategies to control influenza. The surveillance system includes hospital-based surveillance (hospital-based SARI surveillance and Ministry of Health data on publicly funded hospital discharges). Additionally, the surveillance system includes community-based surveillance (community-based longitudinal cohort surveillance and sentinel GP based virological surveillance). Furthermore, the surveillance includes laboratory-based surveillance for testing ordered by clinicians for hospital in-patients and outpatients during routine viral diagnosis as well as testing for public health surveillance.

3.1 HOSPITAL-BASED SURVEILLANCE

3.1.1 Hospital-based Severe Acute Respiratory Illness (SARI) surveillance

Inpatients with suspected respiratory infections admitted overnight to any of the four hospitals (Auckland City Hospital and the associated Starship Children's Hospital, Middlemore Hospital and the associated Kidz First Children's Hospital) in the Auckland District Health Board (ADHB) and Counties Manukau DHB, were screened by research nurses each day. Overnight admission is defined as: "*A patient who is admitted under a medical team, and to a hospital ward or assessment unit*". Case ascertainment followed a surveillance algorithm. The presence of the components of the case definition was determined through a combination of reviewing the clinician's admission diagnoses and by interviewing patients about their presenting symptoms. Records of all patients admitted overnight to medical wards were reviewed daily to identify anyone with a suspected respiratory infection. These patients were categorised into one of ten admission diagnostic syndrome groups. Research nurses then interviewed the patients and documented the components of the case definition of severe acute respiratory illness (SARI) that were present and ascertain the patients whether meeting the SARI case definition.

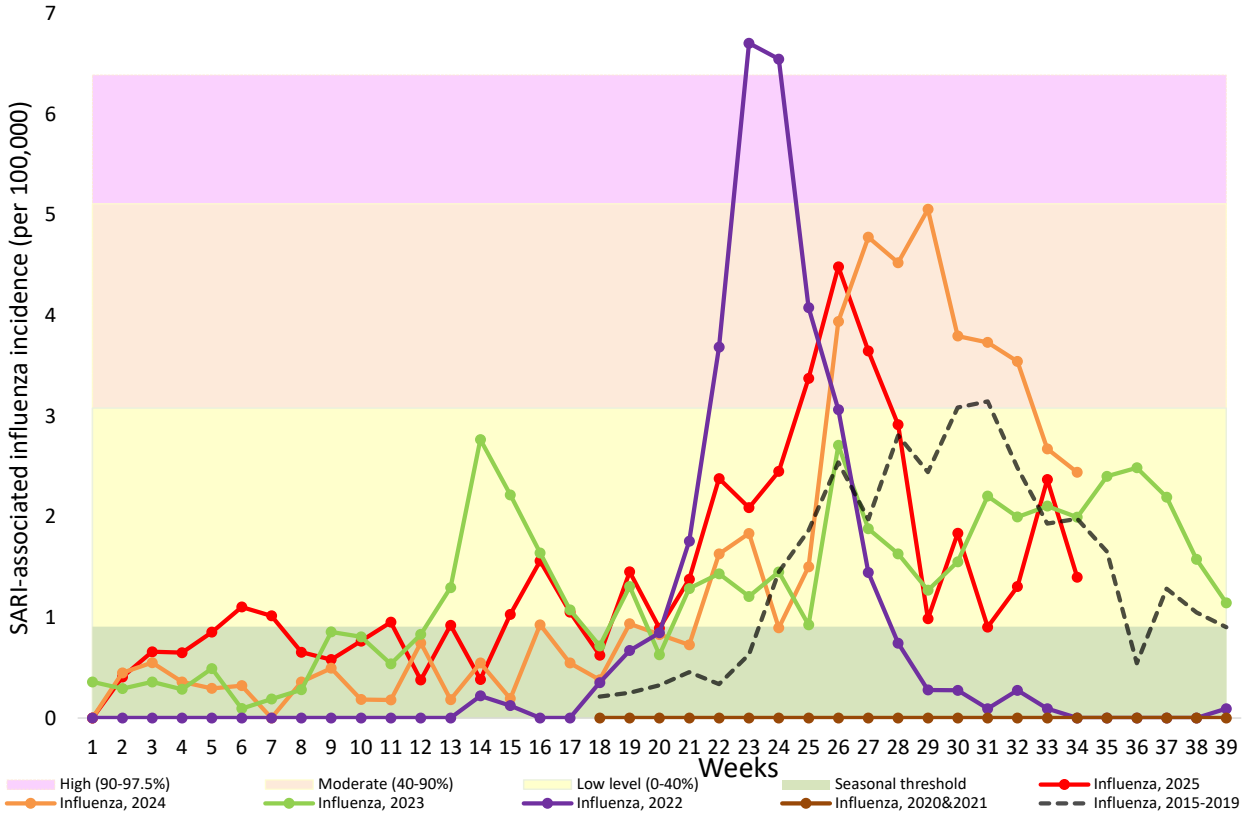
The case definition being used is the World Health Organisation (WHO) SARI case definition: *"an acute respiratory illness with a history of fever or measured fever of ≥38°C, and cough, and onset within the past 10 days, and requiring inpatient hospitalisation"*. If a patient with suspected respiratory infection met the SARI case definition, a respiratory sample was collected to test for influenza and other respiratory pathogens. In addition, patient information was captured via a case report form which included patient demographics, presenting symptoms and illness, pre-hospital healthcare, medication usage, influenza vaccination history, co-morbidities, disease course and outcome, including major treatments, ICU admission and mortality, epidemiologic risk factors and laboratory results.

The total numbers of all new hospital inpatient acute admissions and newly assessed and tested patients, including ICU admissions and deaths were collected. This allowed calculation of population-based incidence for SARI and associated influenza cases overall and stratified by age, sex, ethnicity and socio-economic status among the ADHB and CMDHB resident population (from the census data). Incidence rates were calculated along with 95% confidence intervals (95%CI). In addition, this allowed the calculation of the proportion of SARI and associated influenza cases, including ICU admissions and deaths, by overall and stratified patients, among all acute admissions regardless of residence status. An acute admission is defined as an unplanned admission on the day of presentation at the admitting health care facility. Admission may have been from the

emergency or outpatient departments of the health care facility, a transfer from another facility or a referral from primary care.

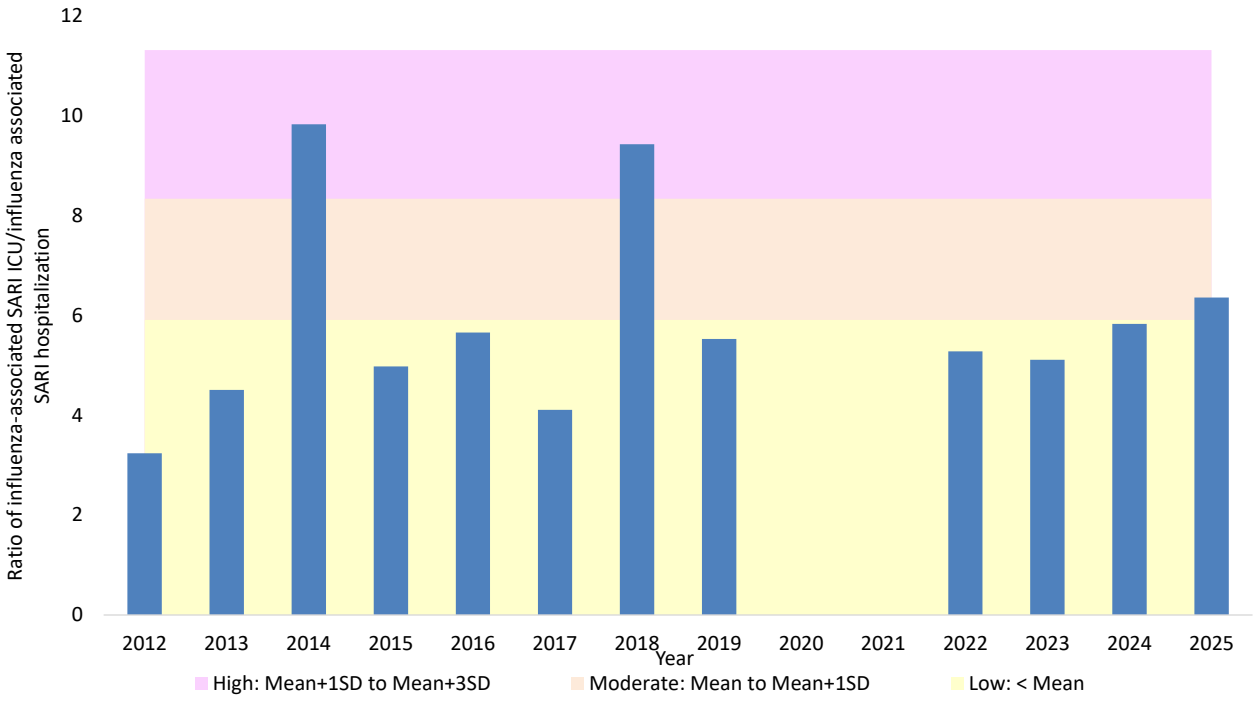
Overall impact on healthcare use is measured by influenza-associated severe acute respiratory illness (SARI) hospitalizations. During the study period from week 1 (commencing 1 January 2025) to week 34 (ending 24 August 2025), influenza-associated SARI hospitalizations were at moderate level in 2025 (Figure 1). Influenza hospitalizations peaked at week 26.

Figure 1. Influenza-associated SARI hospitalizations in 2025 compared to pre-pandemic 2015-2019, and during pandemic 2020-2024



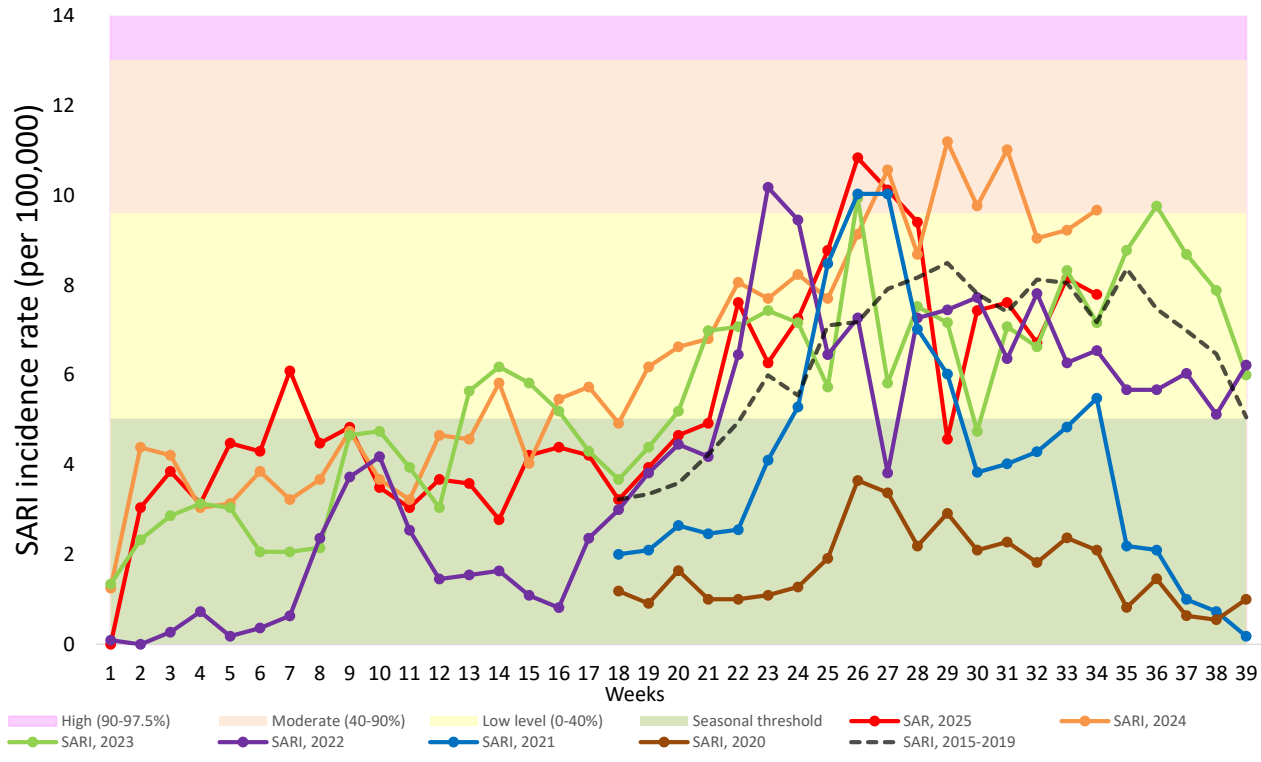
Seriousness of disease (i.e. clinical severity) that indicates the extent to which individuals get sick when infected with the influenza virus as measured by the ratio of influenza-associated SARI ICU admission over influenza-associated SARI hospitalization. Seriousness of disease was moderate in 2025 (Figure 2).

Figure 2. Seriousness of disease indicator in 2025 compared to 2012–2024



SARI hospitalization was moderate. It was below baseline during weeks 1-21, then increased to low level in week 22, and peaked at week 26 and then declined gradually (Figure 3).

Figure 3. Weekly hospitalisation rates for SARI in 2025 compared to 2012-2024



From 1 January to 24 August 2025, there were 48476 acute admissions to CMDHB hospital (Table 1). A total of 3079 patients with suspected respiratory infections were assessed in CMDHB hospital. Of these, 1273 (41%) patients met the SARI case definition, giving a proportion of SARI among acutely admitted hospital patients as 26.3 per 1000 patients. Among both CMDHB and ADHB acutely admitted patients, a total of 5481 residents were assessed and 2269 met SARI case definitions and 565 influenza cases. Among ADHB and CMDHB residents who were acutely admitted in hospitals, 2057 were SARI cases, giving the SARI incidence rate of 186.4 per 100 000 population (214.2 per 100 000 in 2024). Among the SARI cases who were ADHB and CMDHB residents, 520 had positive influenza virus results. This gives influenza-associated SARI incidence of 47.1 per 100 000 population, slightly lower than 48.6 per 100 000 in 2024, higher than 42.3 per 100,000 in 2023.

Influenza–associated SARI hospitalizations were higher in both young children (0–4 years) and elderly (≥65) groups compared to other age groups; also higher in Pacific Peoples and Māori ethnic groups compared to other ethnic groups.

Table 1. Demographic characteristics of SARI & influenza cases, weeks 1-34, 2025

Characteristics	SARI & influenza in CMDHB hospital				SARI & influenza in ADHB and CMDHB hospitals			SARI & influenza cases among ADHB & CMDHB residents					
	Admissions	Assessed	SARI	SARI per 1000 patients	Assessed	SARI Cases	Influenza positive	SARI cases	SARI incidence (per 100 000)	Influenza-associated SARI	Influenza-SARI incidence (per 100 000)	Influenza cases (SARI & non SARI)	Influenza incidence (SARI & non SARI) (per 100 000)
Overall	**48476**	**3079**	**1273**	**26.3**	**5481**	**2269**	**565**	**2057**	**186.4**	**520**	**47.1**	**828**	**75.0**
Age group (years)													
<1	760	435	185	243.4	904	355	46	326	2429.2	43	320.4	61	454.5
1–4	3,869	370	208	53.8	1000	560	116	479	943.3	102	200.9	133	261.9
5–19	4,514	260	152	33.7	510	249	97	202	94.3	82	38.3	117	54.6
20–34	8,056	142	77	9.6	227	101	37	93	32.8	35	12.3	44	15.5
35–49	8,292	224	107	12.9	353	176	54	166	75.6	54	24.6	83	37.8
50–64	8,464	450	181	21.4	700	279	77	268	143.5	77	41.2	120	64.3
65–79	8,922	686	235	26.3	1048	346	94	324	310.8	86	82.5	166	159.2
>80	5,599	512	128	22.9	739	203	44	199	634.6	41	130.7	104	331.6
Unknown	0	0	0	-	0	0	0	0	0.0	0	0.0	0	0.0
Ethnicity													
Māori	8,717	770	304	34.9	1200	459	102	420	294.3	93	65.2	155	108.6
Pacific peoples	15,044	1082	507	33.7	1600	750	221	717	370.9	215	111.2	307	158.8
Asian	9,011	306	134	14.9	651	298	73	270	75.8	66	18.5	103	28.9
European and Other	15,327	921	328	21.4	1970	625	129	530	128.8	110	26.7	219	53.2
Unknown	377	0	0	-	60	137	40	120		36		44	
DHB of Residence													
ADHB					1735	765	163	765	153.9	163	32.8	237	47.7
CMDHB	48476	3079	1273	26.3	3242	1292	357	1292	213.0	357	58.9	591	97.4
Other				-	504		45						
Sex													
Female	24,817	1479	615	24.8	2609	1085	279	993	179.4	258	46.6	422	76.3
Male	23,649	1600	658	27.8	2872	1184	286	1064	193.4	262	47.6	406	73.8
Unknown	10	0	0	-	0	0	0						

From 1 January to 24 August 2025, 2119 SARI specimens have been tested and 565 (26.7%) were positive for influenza viruses (Table 2). Of the 339 specimens collected from ICU admitted patients with acute respiratory illness (SARI and non-SARI), 60 (17.7%) were positive for influenza viruses. Of the 99 specimens collected from fatal cases with acute respiratory illness (SARI and non-SARI), 16 were positive for influenza A viruses. Influenza A(H1N1)pdm09 and B/Victoria lineage viruses were two predominant strains.

Additionally, 2436 SARI specimens were tested for non-influenza respiratory viruses (Table 2).

Table 2. Influenza and non-influenza respiratory viruses among SARI cases, 2025

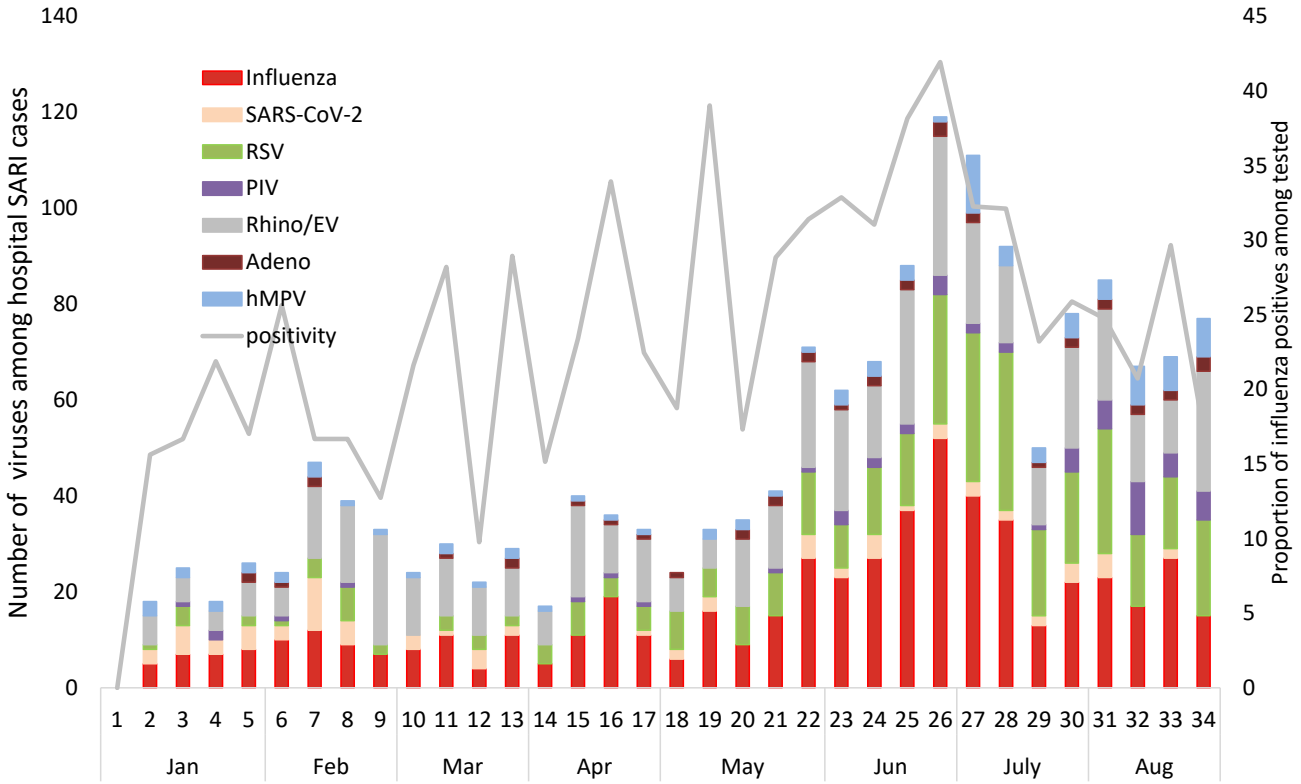
Influenza viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2119	339	99
No. of positive specimens (%)[1]	565 (26.7)	60 (17.7)	16 (16.2)
Influenza A	387	46	15
A (not subtyped)	108	18	5
A(H1N1)pdm09			
A(H1N1)pdm09 by PCR	264	26	10
A/Victoria/4897/2022 (H1N1)pdm09-like	4	1	
A(H3N2)			
A(H3N2) by PCR	11	1	
A/Croatia/10136RV/2023 (H3N2)-like			
Influenza B	178	14	1
B (lineage not determined)	126	13	1
B/Yamagata lineage			
B/Yamagata lineage by PCR			
B/Phuket/3073/2013-like			
B/Victoria lineage			
B/Victoria lineage by PCR	45	1	
B/Austria/1359417/2021-like	7		
Influenza and non-influenza co-detection (%+ve)	43 (7.6)	7 (11.7)	0 (-)

Non-Influenza respiratory viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2119	339	99
No. of positive specimens (%)[1]	903 (42.6)	193 (56.9)	13 (13.2)
Respiratory syncytial virus (RSV)	368	41	2
Parainfluenza (PIV)	53	12	0
Rhinovirus (RV) /Enterovirus	408	135	4
Adenovirus (AdV)	36	7	0
Human metapneumovirus (hMPV)	78	10	0
SARS-Cov-2	94	12	7
Single virus detection (% of positives)	773 (85.6)	166 (86.0)	13 (100)
Multiple virus detection (% of positives)	130(14.4)	27 (14.0)	0 (0.0)

[1]Number of specimens positive for at least one of the listed viruses; note a specimen may be positive for more than one virus

The temporal distribution of the number of influenza and non-influenza respiratory viruses is shown in Figure 4a. Influenza was the dominant virus among all common respiratory viruses in 2025.

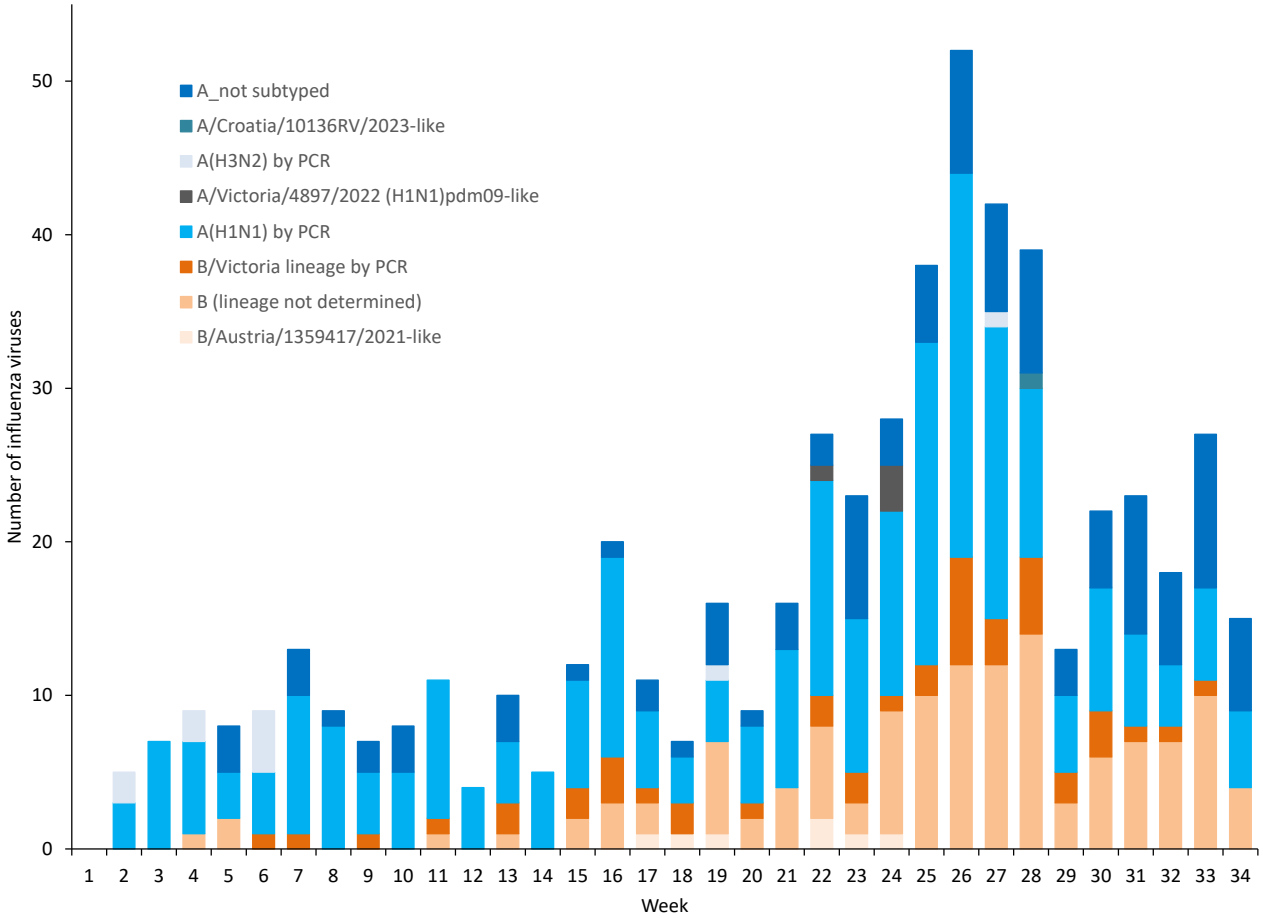
Figure 4a. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1] in 2025



[1]Numbers for recent weeks will be underestimates due to time lag in receiving laboratory test results

The temporal distribution of the number of influenza is shown in Figure 4b. Influenza A(H1N1)pdm09 and influenza B/Victoria lineage viruses were two main predominant viruses among SARI patients in 2025.

Figure 4b. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1] in 2025



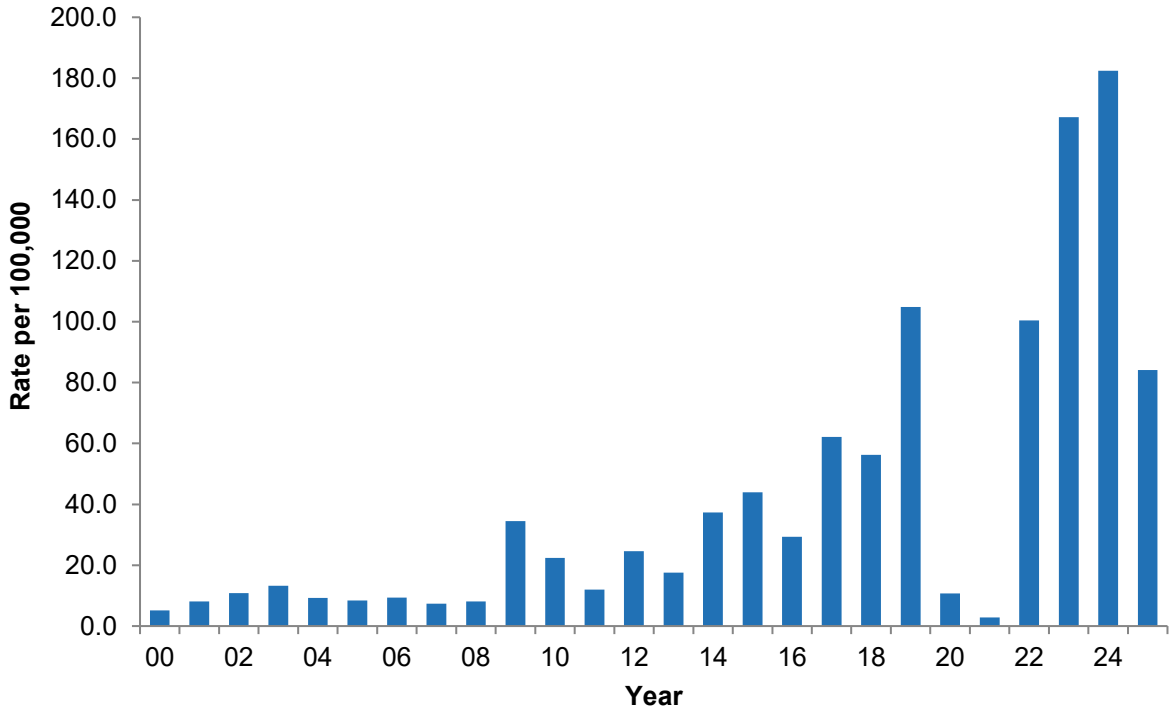
[1]Numbers for recent weeks will be underestimates due to time lag in receiving laboratory test results

3.1.2 Ministry of Health data on publicly funded hospital discharges

Hospitalisation data for influenza (ICD-9-CMA-II code 487) for 2025 which correlate with previous versions of ICD-10AM codes J10-J11, were extracted from the New Zealand Ministry of Health's NMDS (by discharge date). In this dataset, people who received less than 1 day of hospital treatment in hospital emergency departments were excluded from any time series analysis of influenza hospitalisations during 2000–2025. Influenza-related hospitalisations were conservatively taken to include only those cases where influenza was the principal diagnosis. Repeat admissions were included, as infections with another influenza A subtype or B virus are possible.

From 1 January to 19 August 2025, there were a total of 4490 hospitalisations (84.1 per 100,000) for influenza (Figure 5). Influenza hospitalisation coding has not been completed for the year. This data only captured a proportion of influenza-coded cases for the winter season of 2025.

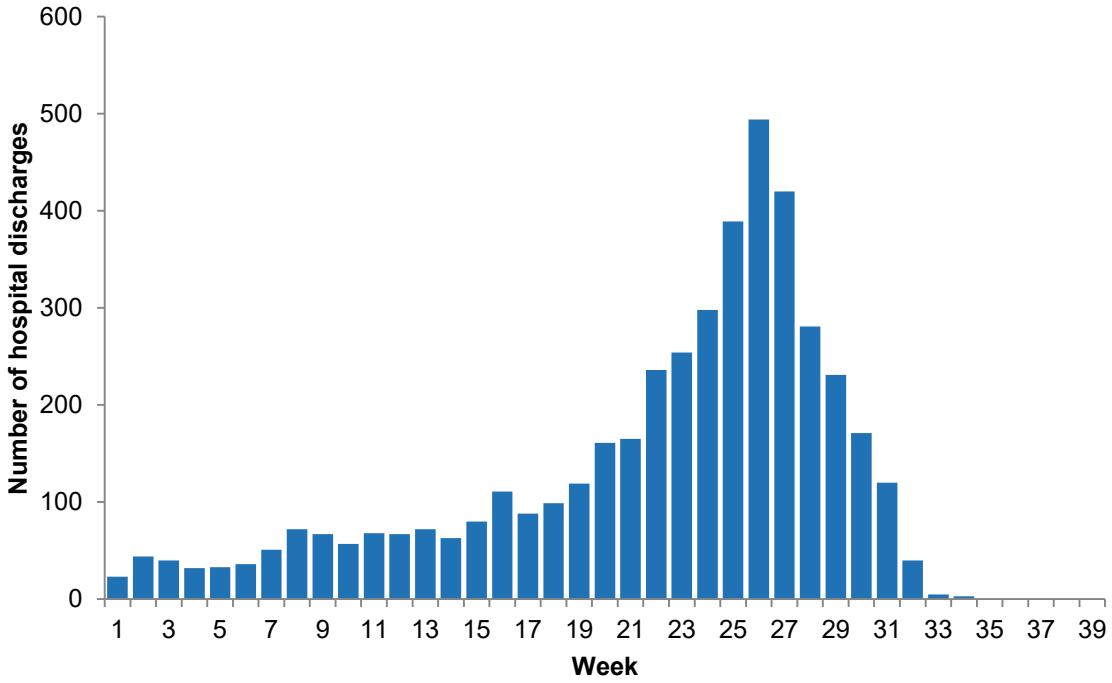
Figure 5. Influenza hospital discharge rates, 2000–2025*



*2025 preliminary data from 1 Jan to 19 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

Figure 6 shows influenza hospitalisations by week discharged. The highest number of hospitalisations (494) occurred in week 26 (week ending 29 June 2025).

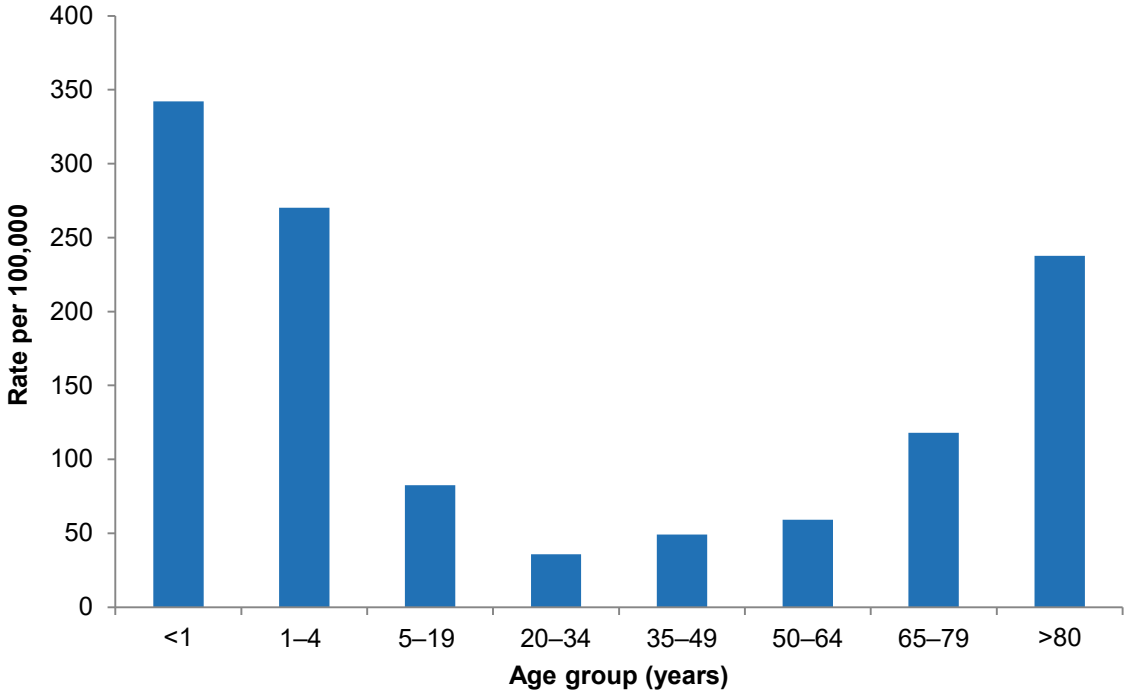
Figure 6. Influenza hospital discharges by week, 2025*



*2025 preliminary data from 1 Jan to 19 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

From 1 January to 19 August 2025, the highest influenza hospitalisation rates were recorded among infants <1 year (342.1 per 100,000) followed by young children aged 1–4 years (270.2 per 100,000) (Figure 7).

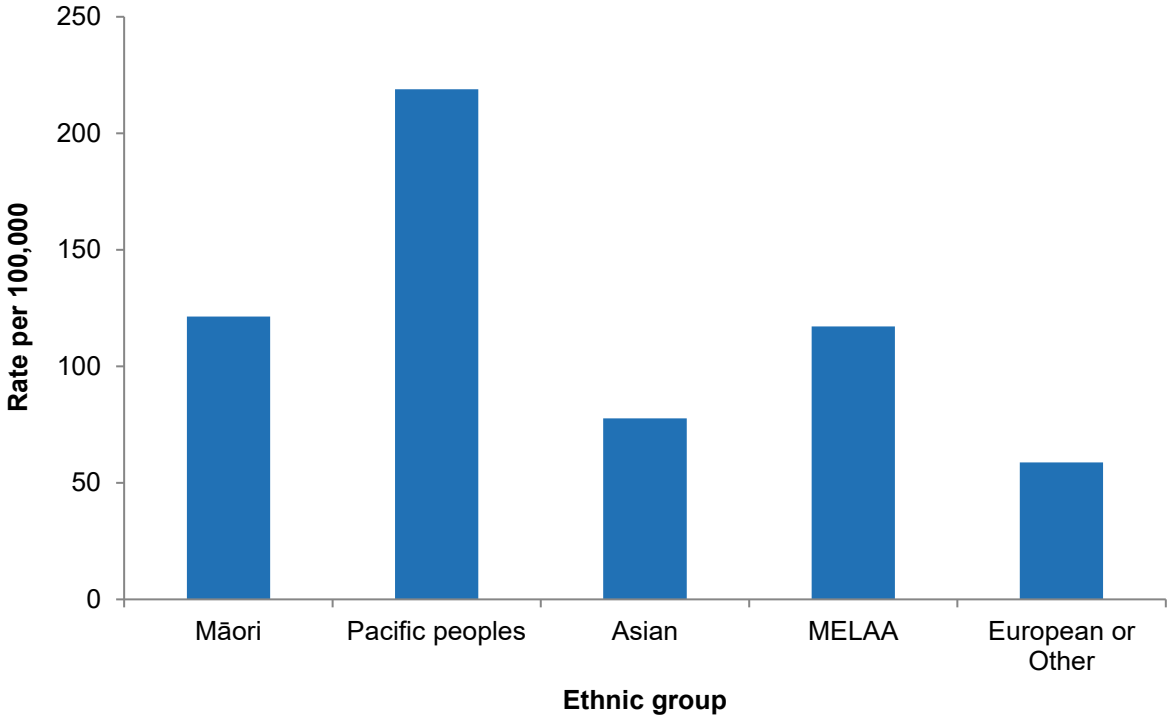
Figure 7. Influenza hospital discharge rates by age group, 2025*



*2025 preliminary data from 1 Jan to 19 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

The ethnic distribution of influenza hospitalisations in 2025 is shown in Figure 8. Pacific peoples had the highest hospitalisation rate (218.9 per 100,000) followed by Māori (121.4 per 100,000), MELAA (117.1 per 100,000), Asian (77.7 per 100,000), and European or Other (58.7 per 100,000) ethnic groups had the lowest rates of hospitalisations.

Figure 8. Hospital discharge rates by prioritised ethnic group, 2025*



*2025 preliminary data from 1 Jan to 19 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

MELAA – Middle Eastern/Latin American/African

3.2 COMMUNITY-BASED SURVEILLANCE

3.2.1 Community-based longitudinal cohort study

SHIVERS-II (the second iteration of the Southern Hemisphere Influenza and Vaccine Effectiveness Research and Surveillance programme) is a prospective adult cohort study in Wellington, NZ. The cohort study is also called WellKiwis Adult study and has been in operation since 2018 enrolling individuals aged 20-69 years, randomly selected from those healthy individuals listed in the general practice's primary care management system. In 2025, SHIVERS-II study staff followed these participants (~800) and monitored their ILIs and acute respiratory illness (ARI)s.

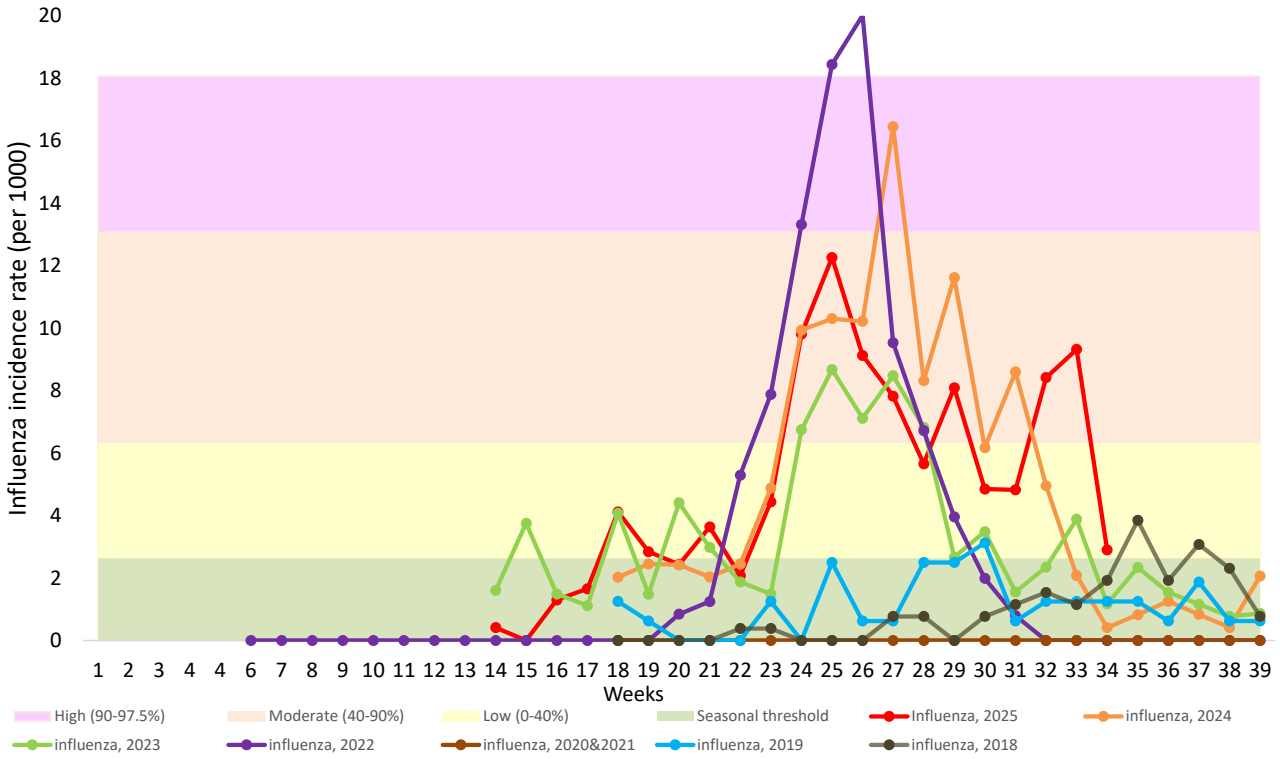
SHIVERS-III (i.e. WellKiwis Infant) is a prospective Wellington infant cohort aiming to recruit 600 infant-mother pairs from Oct 2019-Sept 2022 (200 pairs a year) and follow them until 2026. In 2025, the study staff followed up ~700 infants and monitored their ILIs and ARIs.

SHIVERS-IV (i.e. WellKiwis Household) is a prospective Wellington household cohort in Wellington, NZ. Households with at least one child aged 19 years or younger are invited to participate from SHIVERS-II and III participants and individuals randomly selected from participating general practice's patient list. Enrolled participants are to be followed for 7 years during 2021-2028. In 2025, the study staff followed up ~1500 household members and monitored their ILIs and ARIs.

During 31-March (week 14) to 24-August (week 34) 2025, the study staff sent weekly surveys to participants regarding their respiratory illness. The ARI case definition was: "acute respiratory illness with fever or feverishness and/or one of following symptoms (cough, running nose, wheezing, sore throat, shortness of breath, loss of sense of smell/taste) with onset in the past 10 days." The case definition for ILI was: "acute respiratory illness with cough and fever/measured fever of ≥38°C and onset within the past 10 days". For those participants who met the case definition for ILI/ARI, research nurses guided the participant to take a nasal swab to test for influenza, SARS-CoV-2, RSV, rhinovirus, parainfluenza virus types 1-3, human metapneumovirus, adenovirus and enterovirus.

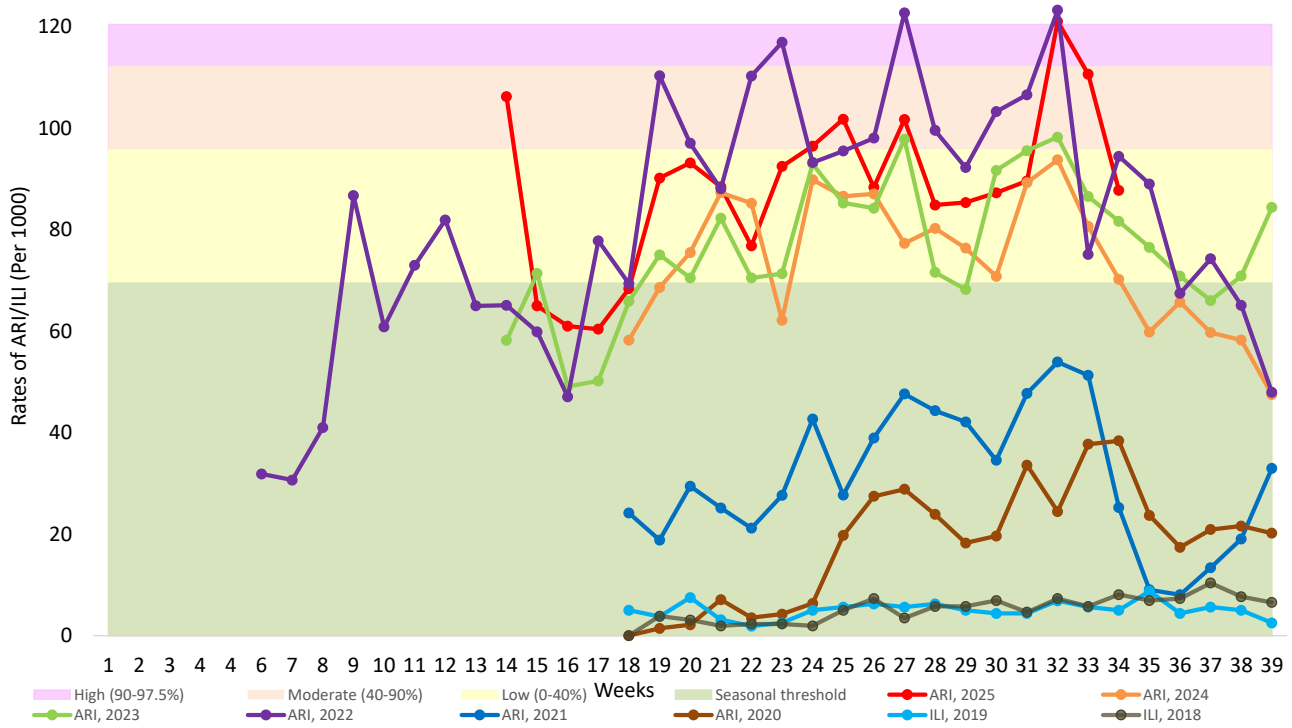
Virus transmissibility reflects the ease of movements of the influenza virus between individuals and communities, and it is measured by influenza-associated ARI. In 2025, the influenza-associated ARI was at a moderate level, its peak was lower than 2024 and 2022, but higher than other years (Figure 9).

Figure 9. Weekly influenza associated ARI rates in 2025, compared to 2018–2024



The ARI rates in 2025 was at a moderate to high level. It is higher than 2024, but lower than 2022 (Figure 10).

Figure 10. Weekly ARI/ILI incidence rates in 2025, compared to 2018–2024



From 31-March to 24-August 2025, a total of 5988 participants with acute respiratory illness (ARI) were reported, giving the ARI incidence rate of 196.9 per 100 population (107.3 per 100 in 2024) (Table 3). Of the ARI cases, 260 had positive influenza virus results. This gave the influenza-associated ARI incidence of 8.5 per 100, slightly higher than 8.4 per 100 in 2024.

The influenza-associated ARI disease burden was higher in children aged 0–19 years compared to other age groups. Influenza–associated ARI were higher in Māori and Pacific peoples than Asians and Europeans ethnic groups.

Table 3. Demographic characteristics of ARI cases and related influenza cases, during 31 March to 24 August, 2025

Characteristics	ARI cases among WellKiwis participants		Influenza cases among WellKiwis participants	
	ARI Cases	ARI incidence (per 100)	Influenza Cases	Influenza incidence (per 100)
Overall	**5988**	**196.9 (192.2, 201.7)**	**260**	**8.5 (7.5, 9.7)**
Age group (years)				
<1	356	1186.7 (1103.2, 1268.8)	9	30.0 (13.8, 56.6)
1–4	2101	273.6 (262.7, 284.7)	84	10.9 (8.7, 13.5)
5–19	817	188.2 (176.1, 201.0)	71	16.4 (12.8, 20.6)
20–34	463	180.2 (164.7, 196.5)	8	3.1 (1.3, 6.1)
35–49	1587	206.1 (196.6, 216.0)	66	8.6 (6.6, 10.9)
50–64	464	91.0 (83.0, 99.4)	14	2.7 (1.5, 4.6)
≥65	200	73.5 (63.8, 84.2)	8	2.9 (1.3, 5.8)
Ethnicity				
Māori	599	202.4 (187.2, 218.3)	33	11.1 (7.7, 15.6)
Pacific peoples	217	188.7 (165.4, 214.1)	10	8.7 (4.2, 16.0)
Asian	558	206.7 (190.6, 223.6)	23	8.5 (5.4, 12.8)
European and Other	4614	195.5 (190.2, 201.0)	194	8.2 (7.1, 9.5)
Sex				
Female	3342	194.0 (187.7, 200.3)	139	8.1 (6.8, 9.5)
Male	2631	200.8 (193.6, 208.3)	119	9.1 (7.5, 10.9)
Other	15	187.5 (106.8, 300.3)	2	25.0 (3.0, 88.9)

From 31-March to 24-August 2025, 2877 respiratory specimens have been tested and 260 (9.0%) were positive for influenza viruses. Of which, A(H1N1)pdm09 (125) was the predominant strain. Influenza B/Victoria lineage (112) co-circulated throughout this period (Table 4). Additionally, 2875 specimens were tested for non-influenza respiratory viruses.

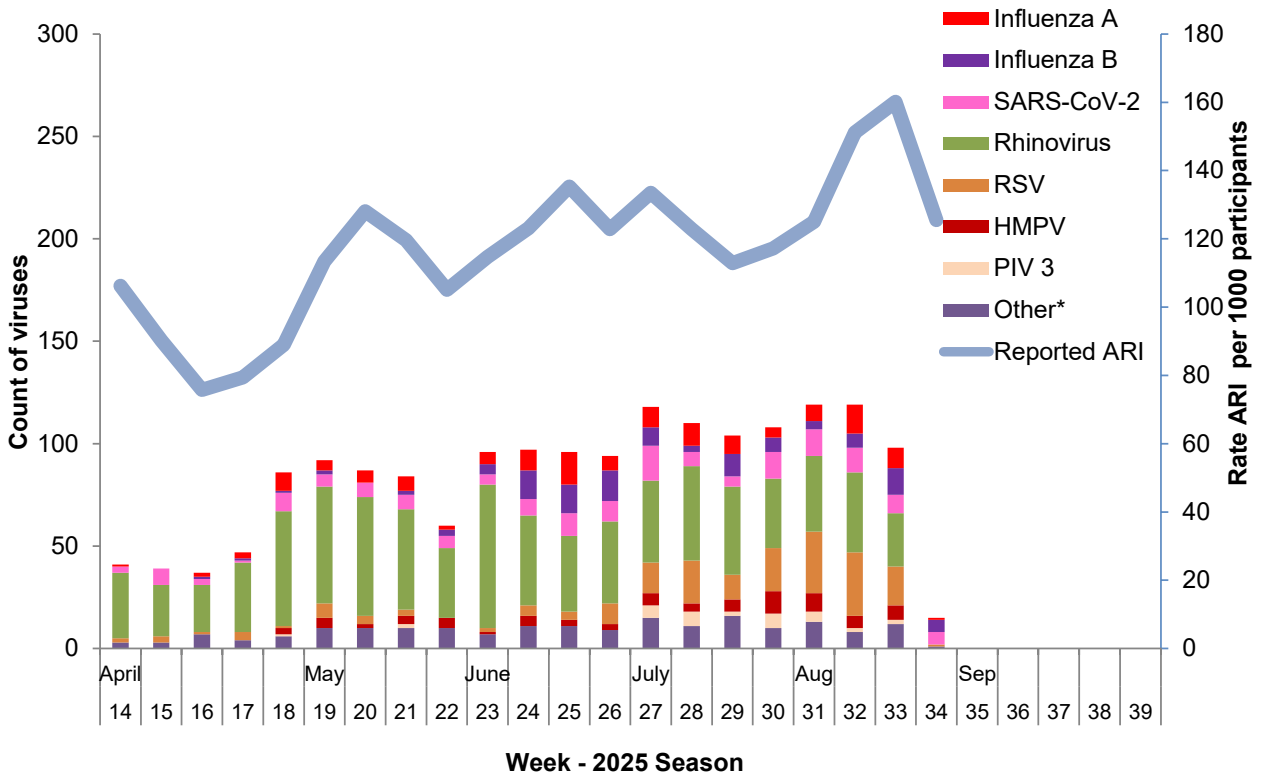
Table 4 Influenza and Non-influenza respiratory viruses among ARI cases, 31 March to 24 August 2025

Influenza viruses	WellKiwis Households	Wellkiwis Adults	WellKiwis Infants	Total
No. of specimens tested	**1617**	**269**	**991**	**2877**
No. of positive specimens (%)[1]	156 (9.6)	23 (8.6)	81 (8.2)	260 (9.0)
Influenza A	72	20	50	142
A (not subtyped)	9	4	1	14
A(H1N1)pdm09	63	16	46	125
A(H1N1)pdm09 by PCR	63	16	46	125
A/Victoria/4897/2022 (H1N1)pdm09 - like	0	0	0	0
A(H3N2)	0	0	3	3
A(H3N2) by PCR	0	0	3	3
A/Croatia/10136RV/2023 (H3N2)-like	0	0	0	0
Influenza B	84	3	31	118
B (lineage not determined)	5	0	1	6
B/Yamagata lineage	0	0	0	0
B/Yamagata lineage by PCR	0	0	0	0
B/Phuket/3073/2013 - like	0	0	0	0
B/Victoria lineage	79	3	30	112
B/Victoria lineage by PCR	79	3	30	112
B/Austria/1359417/2021-like virus	0	0	0	0
Influenza and non-influenza co-detection (% +ve)	7 (4.5)	1 (4.3)	6 (7.4)	14 (5.4)

Non-influenza respiratory viruses	WellKiwis Households	Wellkiwis Adults	WellKiwis Infants	Total
No. of specimens tested	**1616**	**269**	**990**	**2875**
No. of positive specimens (%)[1]	716 (44.3)	125 (46.5)	530 (53.5)	1371 (47.7)
Respiratory syncytial virus (RSV)	78	12	106	196
Parainfluenza 1 (PIV1)	2	0	11	13
Parainfluenza 2 (PIV2)	16	0	17	33
Parainfluenza 3 (PIV3)	19	2	13	34
Rhinovirus (RV)	431	72	321	824
Adenovirus (AdV)	40	1	47	88
Human metapneumovirus (hMPV)	39	4	37	80
Enterovirus	37	3	13	53
SARS-CoV-2	104	33	29	166
Single virus detection (% of positives)	671 (93.7)	123 (98.4)	468 (88.3)	1262 (92.0)
Multiple virus detection (% of positives)	45 (6.3)	2 (1.6)	62 (11.7)	109 (8.0)

Figure 11 shows the weekly rate of acute respiratory illness (ARI) and associated viruses detected among the SHIVERS-II, III, IV cohort participants during the active surveillance period in 2025.

Figure 11. Weekly incidence rate of acute respiratory illness and associated viruses in 2025



Note: other viruses include enterovirus, adenovirus and parainfluenza virus types 1 and 2. The left axis indicates number of respiratory viruses detected among participants each week. The different coloured bars on the graph represent the count of the different respiratory viruses detected. The right axis shows weekly ARI rates - the blue line is the weekly rate of ILI reported by participants (per 1000). (Note: The case definition[1] in 2020–2025 has been widened compared to previous years, 2018–2019. This is to increase the sensitivity to detecting influenza as well as SARS-CoV-2 that causes COVID-19 infection). X-axis is based on the date of symptom onset.

3.2.2 Community-based virological surveillance

Virological surveillance at sentinel GP sites provides insight into the prevalence of respiratory viruses circulating in the community at any one time. GPs that participate in virological ILI surveillance take a nasopharyngeal or throat swab from some of the ILI patients they see each week. The samples are sent to PHF Science and tested for influenza, SARS-CoV-2, RSV and other respiratory viruses.

In 2025, 43 sentinel general practices participated in this surveillance. Between 1 January to 24 August 2025, a total of 1417 ILI specimens were tested for influenza viruses (Table 5) and 386 (27%) were positive, with 179 influenza A and 207 influenza B viruses detected. Influenza A(H1N1)pdm09 (154) and B/Victoria lineage (196) were two main predominant viruses.

Additionally, a total of 1417 ILI specimens were tested for non-influenza viruses and 421 (30%) were positive with non-influenza viruses.

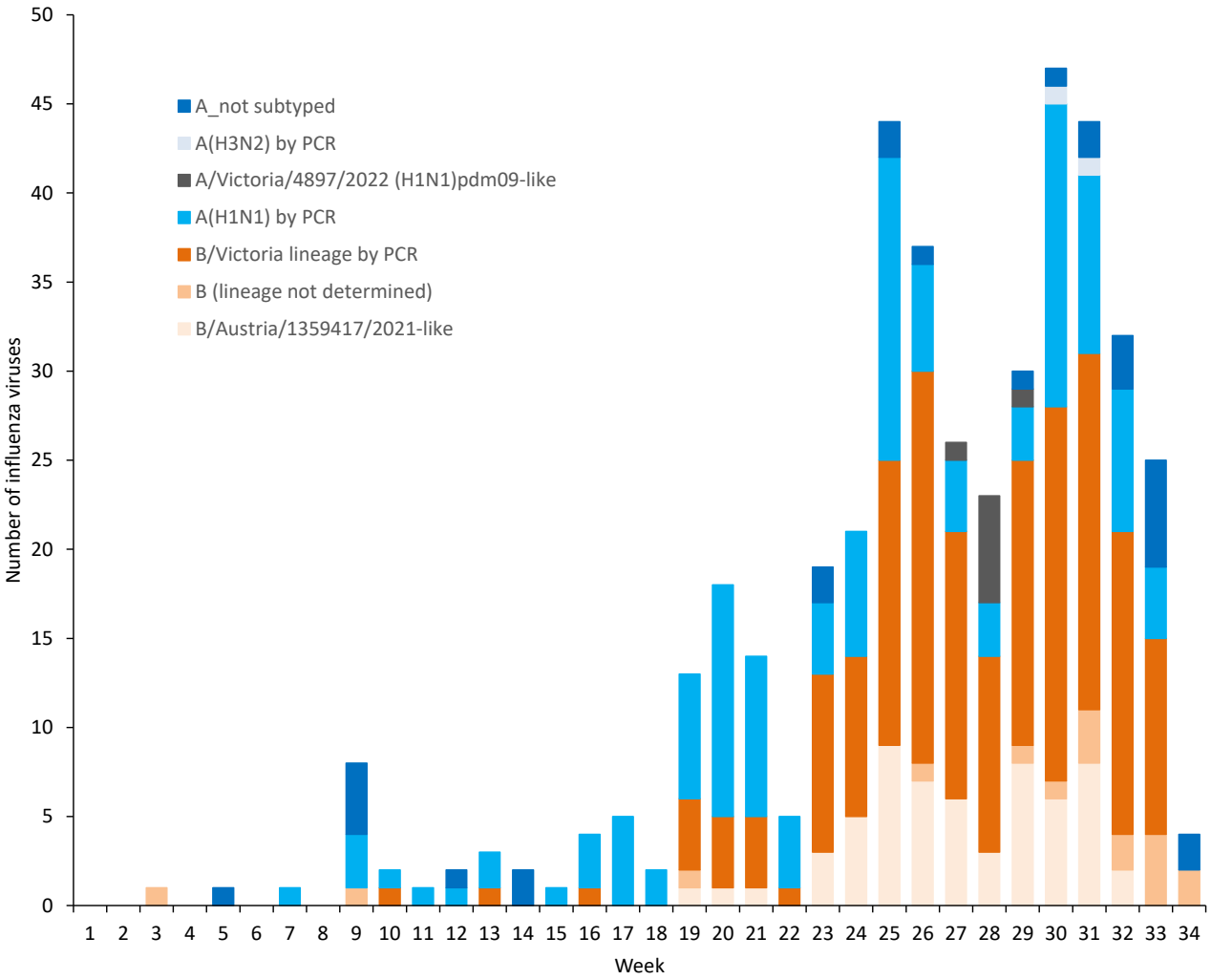
Table 5. Influenza and non-influenza respiratory viruses among ILI cases, 1 January to 24 August, 2025

Influenza viruses	ILI Cases (%)
No. of specimens tested	1417
No. of positive specimens (%)[1]	386 (27.2)
Influenza A	179
A (not subtyped)	22
A(H1N1)pdm09	154
A(H1N1)pdm09 by PCR	146
A/Victoria/4897/2022 (H1N1)pdm09-like	8
A(H3N2)	3
A(H3N2) by PCR	3
A/Croatia/10136RV/2023 (H3N2)-like	
Influenza B	207
B (lineage not determined)	11
B/Yamagata lineage	
B/Yamagata lineage by PCR	
B/Phuket/3073/2013-like	
B/Victoria lineage	196
B/Victoria lineage by PCR	136
B/Austria/1359417/2021-like	60

Non-Influenza respiratory viruses	ILI Cases (%)
No. of specimens tested	1417
No. of positive specimens (%)[1]	421 (29.7)
Respiratory syncytial virus (RSV)	93
Parainfluenza (PIV)	34
Rhinovirus (RV) /Enterovirus	93
Adenovirus (AdV)	28
Human metapneumovirus (hMPV)	67
SARS-Cov-2	39

The temporal distribution of the number and proportion of the influenza viruses from 1 January to 24 August 2025, is shown in Figure 12. Influenza A(H1N1)pdm09 and influenza B/Victoria lineage viruses were the two main predominant strains co-circulating with A(H1N1)pdm09 circulated predominant in early winter followed by B/Victoria viruses predominant since the end of June (week 26).

Figure 12. Temporal distribution of the number and proportion of influenza viruses from ILI specimens, by type and week, 2025



4. RECENT STRAIN CHARACTERISATIONS

The laboratory-based surveillance for influenza is carried out all-year-around by the New Zealand virus laboratory network consisting of the WHO National Influenza Centre (NIC) at PHF Science and six hospital laboratories at Auckland, Waikato, Wellington, Christchurch and Dunedin, serving nearly 70% of the NZ population. This laboratory network tests specimens ordered by clinicians for hospital in-patient and outpatients during routine viral diagnosis. In addition, this laboratory network conducts testing for public health surveillance including hospital-based SARI and sentinel GP-based surveillance and SHIVERS research.

The WHO National Influenza Centre at PHF Science receives samples from local hospital laboratories for further typing from active surveillance (sentinel ILI and SARI) as well as passive surveillance (i.e. mainly hospital in-patient and outpatients during routine viral diagnosis).

4.1 CIRCULATING STRAINS IN 2025

During 1-Jan to 24-August-2025, a total of 5887 influenza viruses were detected and reported through any surveillance system, with influenza A representing 63.6%% (3743/5887) and influenza B 36.4% (2144/5887) of all influenza viruses (Table 6). Among 2011 subtyped and lineage-typed viruses, 61.1% (1230/2011) were A(H1N1)pdm09 viruses, 16.0% (321/2011) were A(H3N2) viruses, and 22.9% (460/2011) were B/Victoria lineage viruses.

Table 6. Influenza virus identifications by type and sub-type and lineage-typed, 2025

Viruses	All viruses		Sub-typed and lineage-typed	
	N.	Col%	N.	%
Influenza virus	**5887**	**100.0**	**2011**	**100.0**
Influenza A	3743	63.6	1551	77.1
Influenza A (not sub-typed)	2192	37.2		
Influenza A(H1N1)pdm09	1230	20.9	1230	61.1
A(H1N1)pdm09 by PCR	1181	20.1		
A/Victoria/4897/2022 (H1N1)pdm09-like	49	0.8		
Influenza A(H3N2)	321	5.5	321	16.0
A(H3N2) by PCR	319	5.4		
A/Croatia/10136RV/2023 (H3N2)-like	2	0.0		
Influenza B	2144	36.4	460	22.9
Influenza B (not lineage-typed)	1684	28.6		
B/Victoria lineage	460	7.8	460	
B/Victoria lineage by PCR	312	5.3		
B/Austria/1359417/2021-like	148	2.5		
B/Yamagata lineage	0	0.0	0	
B/Yamagata lineage by PCR	0	0.0		
B/Phuket/3073/2013-like	0	0.0		

Figure 13 shows the influenza virus identifications by type and sub-type and lineage for each week throughout 2025. A(H1N1)pdm09 and influenza B/Victoria lineage were two main viruses cocirculating throughout the season and both with intensity from late June to August.

Figure 13. Total influenza A and B viruses by week specimen taken, 2025

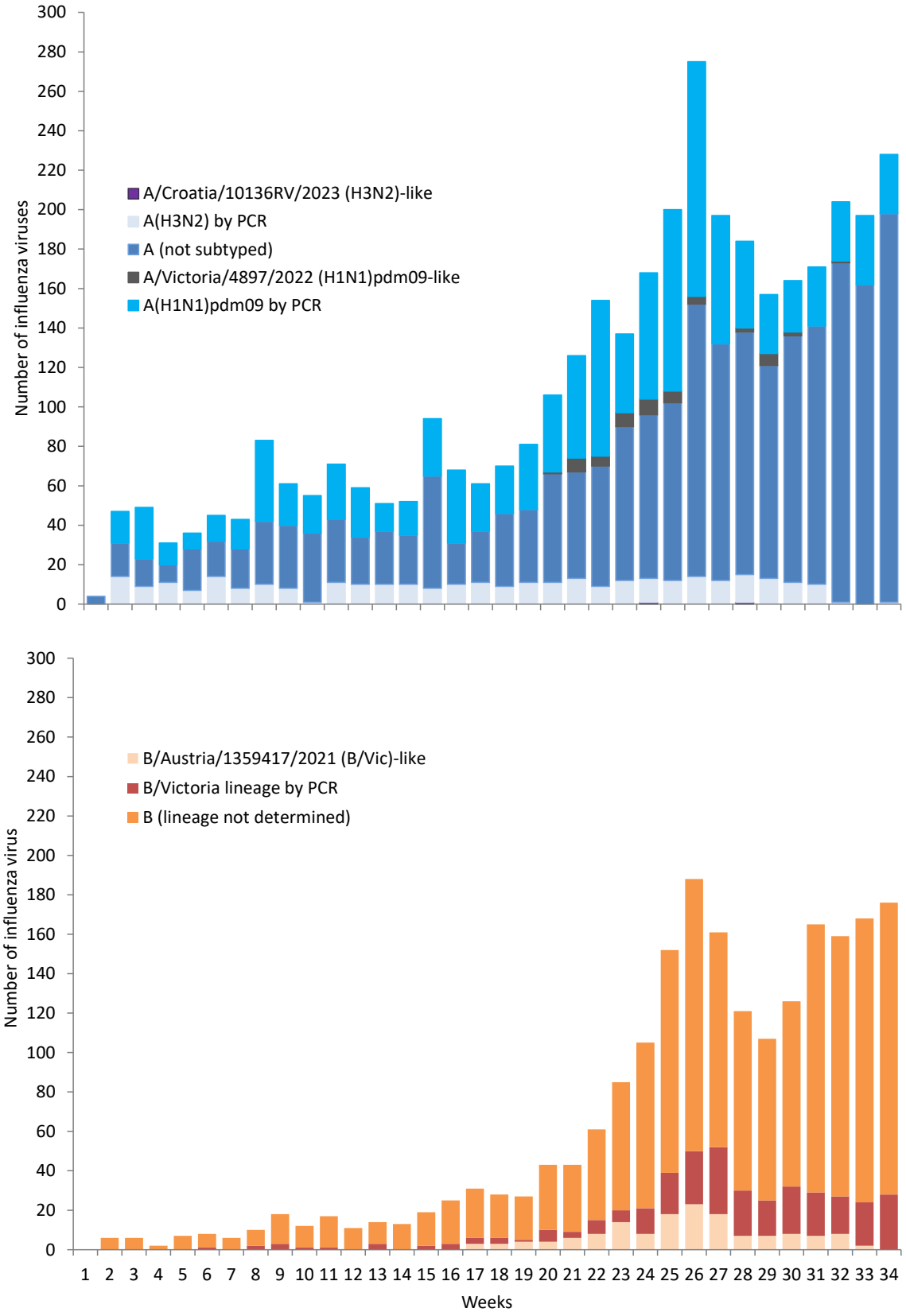
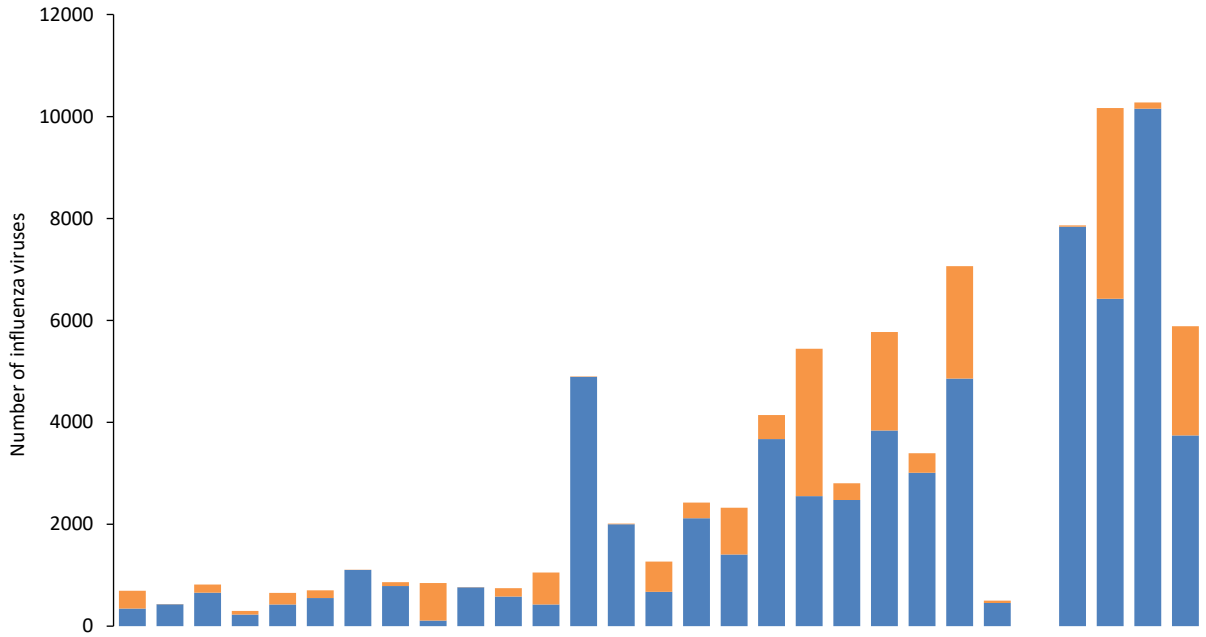


Figure 14 shows the number and percentage of typed influenza viruses from 1997 to 2025. Influenza A is the most frequent predominant influenza type. Of 28 influenza seasons during 1997–2025 (Note: 2021 – no influenza circulation due to COVID-19 elimination strategy), influenza A predominated in 24 seasons whereas influenza B only predominated in three seasons (2005, 2008 and 2015). There was one season (1997) with equal proportion of influenza A and B circulation.

Figure 14. Influenza viruses by type, 1997–2025

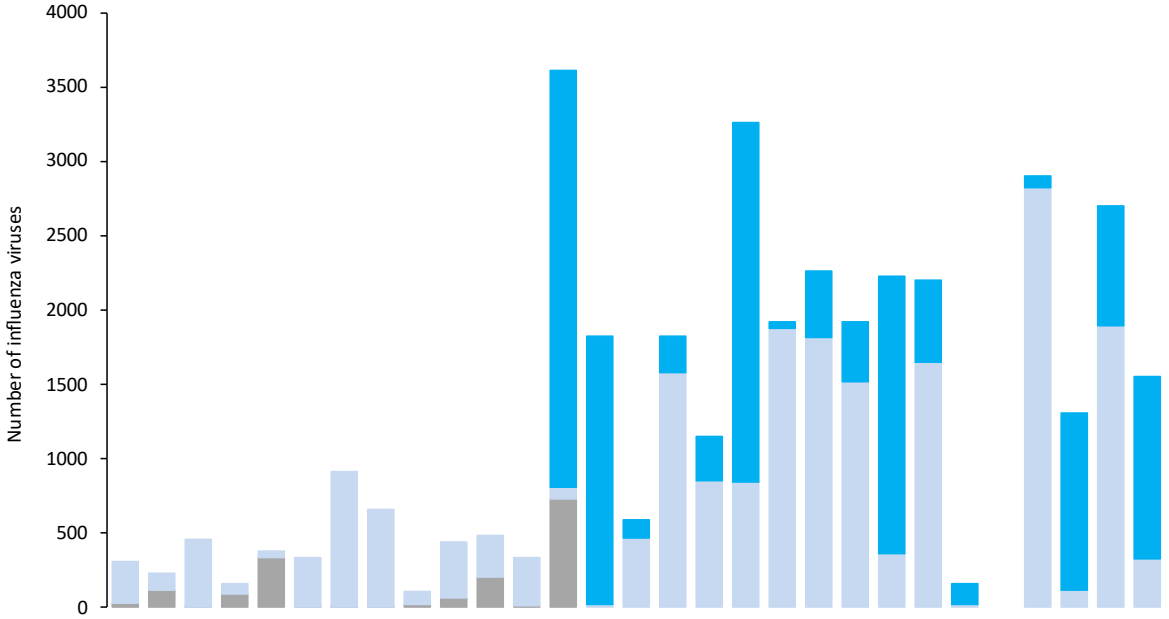


	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Influenza B (%)	50	0	20	24	35	22	0	9	87	1	22	60	0	0	47	13	40	11	53	12	33	11	31	9	0	0	37	1	36
Influenza A (%)	50	100	80	76	65	78	100	91	13	99	78	40	100	100	53	87	60	89	47	88	67	89	69	91	0	100	63	99	64

Figure 15 shows the number and percentage of all sub-typed influenza A viruses from 1997 to 2025 (excluding influenza A not sub-typed). Overall, the patterns of the predominant influenza A subtypes among all sub-typed A viruses during 1997–2025 are described below:

- Influenza A(H3N2) strain predominated for 19 seasons [1997-1999 (3), 2002–2008 (7), 2011–2013 (3), 2015–2017 (3), 2019, 2022, 2024].
- Influenza A(H1N1)pdm09 strain has become the predominant strain for 7 seasons in 2009, 2010, 2014, 2018, 2020, 2023, 2025.
- Seasonal influenza A(H1N1) strain predominated in two seasons (2000 and 2001) with associated relatively low hospitalisations. It has not been detected in New Zealand since 2010.

Figure 15. Influenza A viruses by subtypes 1997–2025



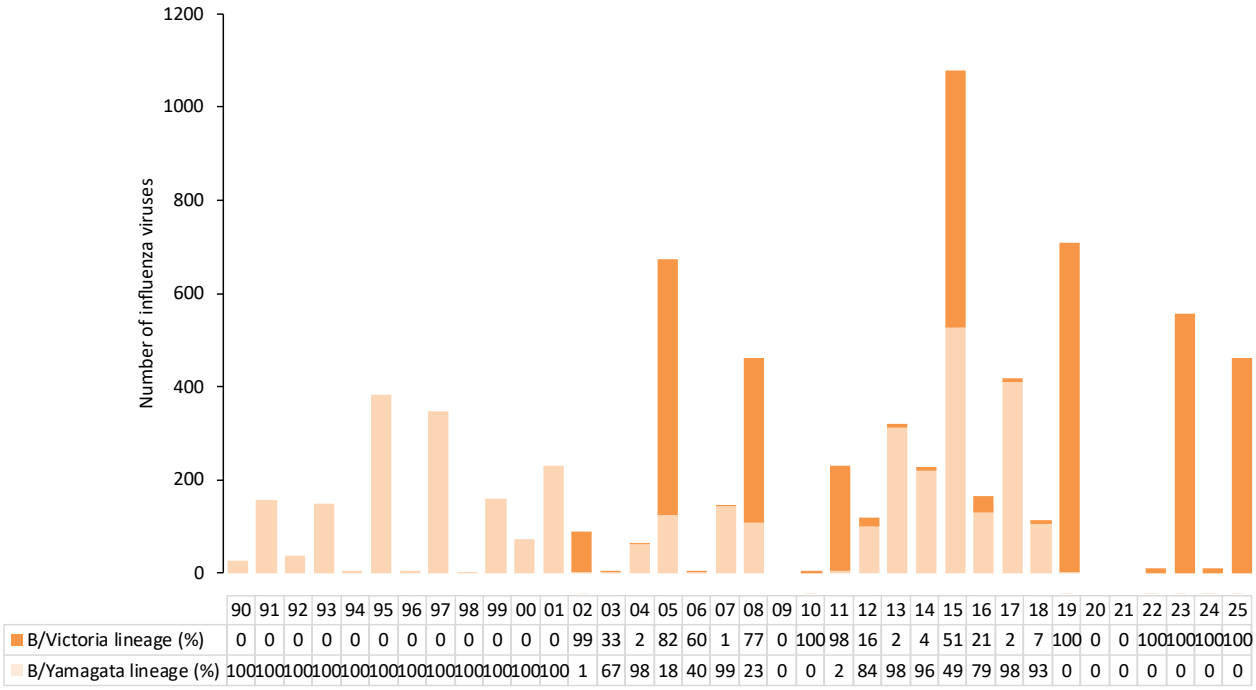
	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
A(H1N1)pdm09 %	0	0	0	0	0	0	0	0	0	0	0	0	78	99	20	14	26	74	2	20	21	84	25	90	0	3	9	28	79
A(H3N2) %	92	52	100	48	13	99	100	100	82	87	58	98	2	1	80	86	74	26	98	80	79	16	75	10	0	97	0	67	21
Seasonal A(H1N1) %	8	48	0	52	87	1	0	0	18	13	42	2	20	0	0	0	0	0	0	0	0	0	0	0	0	0	23	0	0

Figure 16 shows the number and percentage of all B viruses from 1990 to 2025 (excluding influenza B not lineage-typed). Overall, the patterns of the predominant influenza B among all lineage-typed B viruses during 1990–2025 are described below:

- Influenza B/Yamagata lineage: During 1990–2001, Influenza B/Yamagata lineage was the only lineage circulating in New Zealand. Relatively high number of influenza B viruses were recorded in 1995 and 1997. Among 18 influenza seasons during 2002-2019, B/Yamagata lineage viruses predominated over B/Victoria lineage virus for 9 seasons during 2003-2004 (2), 2007 (1), 2012–2014 (3), and 2016–2018 (3). Since 2019, no B/Yamagata lineage virus has been detected in New Zealand.

- B/Victoria lineage: In 2002, B/Victoria lineage viruses were introduced into New Zealand. Since then, this lineage has co-circulated with B/Yamagata lineage viruses. During 2002–2011, B/Victoria lineage viruses predominated over the B/Yamagata lineage viruses in every three years in New Zealand (2002, 2005, 2008 and 2011). In 2005, the disease burden was high in children aged 5–19 years with associated deaths in 3 children. During 2012-2019, B/Victoria lineage viruses predominated over the B/Yamagata lineage viruses in every four years (2015 and 2019).

Figure 16. Influenza B viruses by lineages, 1990–2025



	90	91	92	93	94	95	96	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
B/Victoria lineage (%)	0	0	0	0	0	0	0	0	0	0	0	0	99	33	2	82	60	1	77	0	100	98	16	2	4	51	21	2	7	100	0	0	100	100	100	100
B/Yamagata lineage (%)	100	100	100	100	100	100	100	100	100	100	100	100	1	67	98	18	40	99	23	0	0	2	84	98	96	49	79	98	93	0	0	0	0	0	0	0

4.2 ANTIGENIC AND GENETIC CHARACTERIZATION

4.2.1 Influenza A(H1N1)pdm09

Representative of influenza A(H1N1)pdm09 isolates were antigenically typed at the WHO National Influenza Centre at PHF Science using ferret antisera supplied by the WHO Collaborating Centre (WHOCC). Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 24 August 2025, a total of 49 influenza A(H1N1)pdm09 isolates were antigenically typed with hemagglutination inhibition assay using antisera raised against A/Victoria/4897/2022(H1N1)-like virus. All of them were inhibited well by the antisera against the vaccine strain A/Victoria/4897/2022(H1N1). Genetically, most of influenza A(H1N1) viruses fell into group 6B.1A.5a.2a.1 (CDC designations) (Figure 17).

Since February 2025, A(H1N1)pdm09 viruses circulated globally, predominating in most countries in East and West Africa, the Americas, East and Southeast Asia, and Oceania.

The haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades. Clade 5a.2a HA genes have further diversified into designated subclades C.1, C.1.8, C.1.9, C.1.9.1, C.1.9.2, C.1.9.3, C.1.9.4, while clade 5a.2a.1 HA genes diversified into D, D.1, D.2, D.3, D.3.1, D.4, D.5. In February 2025, 5a.2a viruses from subclade C.1.9.3 predominated in most regions but decreased in proportion throughout the current reporting period. In contrast, 5a.2a.1 viruses from subclade D.3.1 increased in all regions and have become the predominant subclade since June 2025. HA subclade D.3.1 viruses (sharing substitutions T120A, T216A, I372V, I460T, V520A) continue to diversify genetically, including emerging viruses with R113K, A139D and E283K substitutions. Viruses from subclade D.3.1 have now largely displaced 5a.2a viruses and other subclades of 5a.2a.1 viruses in all regions.

The antigenic properties of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) assays with post-infection ferret antisera. HI results for viruses with collection dates since February 2025 showed that ferret antisera raised against cell culture-propagated A/Wisconsin/67/2022-like and egg- propagated A/Victoria/4897/2022-like viruses from the 5a.2a.1 clade recognized viruses in both 5a.2a and 5a.2a.1 clades well. However, post-infection ferret antisera raised against viruses from HA clade 5a.2a showed some reduction in recognition of the now predominating D.3.1 HA subclade viruses. Post-infection ferret antisera raised against viruses from HA subclade D.3.1 (e.g., A/Missouri/11/2025) recognized recently circulating viruses from both 5a.2a and 5a.2a.1 clades well.

Human serology studies used six serum panels from adults (18 to 64 years) and older adults (≥65 years) who had received egg-propagated inactivated, cell culture-propagated inactivated or adjuvanted trivalent or quadrivalent vaccines with SH 2025 or NH 2024-2025 influenza vaccine formulations. SH 2025 egg-based vaccines contained A/Victoria/4897/2022 (H1N1)pdm09-like, A/Croatia/10136RV/2023 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and, in quadrivalent vaccines, B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens. Cell culture-propagated vaccines contained A/Wisconsin/67/2022 (H1N1)pdm09-like, A/District of Columbia/27/2023 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens. NH 2024-2025 egg-based vaccine contained A/Victoria/4897/2022 (H1N1)pdm09-like, A/Thailand/8/2022 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) virus antigens.

Recent A(H1N1)pdm09 viruses with HA genes from clades 5a.2a (subclades C.1.9 and C.1.9.3) and 5a.2a.1 (subclades D.3.1 and D.5) were analysed in HI and virus neutralization (VN) assays using these human serum panels. When compared to the responses to cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like vaccine reference viruses, post-vaccination geometric

mean titres (GMTs) were significantly reduced for some recently circulating viruses from across the genetic diversity.

In summary, A(H1N1)pdm09 viruses circulated globally and predominated in most regions since February 2025. While viruses expressing HA genes from 5a.2a and 5a.2a.1 clades previously co-circulated, 5a.2a.1 viruses from subclade D.3.1 (e.g., A/Missouri/11/2025) have largely displaced 5a.2a and other subclades of 5a.2a.1 viruses over the reporting period and now predominate in all regions. Post-infection ferret antisera raised against the SH 2025 and NH 2025-26 A(H1N1)pdm09 vaccine viruses (cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022) from the 5a.2a.1 clade recognized most 5a.2a and 5a.2a.1 viruses well. However post-infection ferret antisera raised against viruses from HA subclade D.3.1 (e.g., A/Missouri/11/2025) better recognized recently circulating viruses from both 5a.2a and 5a.2a.1 clades compared to post-infection ferret antisera raised against recent viruses from HA subclades C.1.9 and C.1.9.3. Additionally, when compared to the responses to cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like vaccine reference viruses, human post-vaccination GMTs were significantly reduced for some recently circulating viruses from across the genetic diversity.

Based on all of the available data, the WHO consultation recommended to use an egg-propagated or cell culture-propagated A/Missouri/11/2025 (H1N1)pdm09-like as the vaccine strains for 2026. The AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2025-sh-recommendations_seasonal_final.pdf (who.int) and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

4.2.2 Influenza A(H3N2)

Representative seasonal influenza A(H3N2) isolates were antigenically typed at the WHO National Influenza Centre at PHF Science using HAI typing kit supplied by the WHO Collaborating Centre (WHOCC) in Melbourne. Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 24 August 2025, a total of 2 influenza A(H3N2) isolates were antigenically typed with hemagglutination inhibition assay using antisera raised against A/Croatia/10136RV/2023 (H3N2)-like virus. All H3N2 isolates were inhibited well by the antisera against the vaccine strain A/Croatia/10136RV/2023 (H3N2)-like. Genetically, most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2a.3a.1 (CDC designations) (Figure 18).

Since February 2025, A(H3N2) viruses circulated globally and predominated in several WHO regions, including Europe, Southern and Central Asia, Central America and Caribbean.

Phylogenetic analysis of the HA gene sequences of A(H3N2) viruses collected since February 2025 showed that the vast majority of viruses belonged to clade 2a.3a.1. HA genes diversified within clade 2a.3a.1 into subclades J.1-J.4, and viruses expressing HA N122D and K276E substitutions (J.2) predominated globally during this reporting period. Ongoing evolution in the HA gene of J.2 viruses observed globally necessitated the creation of J.2 subclades (J.2.1-J.2.5) to track the emerging viruses. Viruses expressing HA from subclade J.2.1 (sharing substitutions F79L and P239S) were detected in very low numbers. Viruses expressing HA subclade J.2.2 (sharing an S124N substitution) circulated globally and were detected in higher proportions in parts of Africa and Asia. Small numbers of viruses expressing HA subclade J.2.3 (sharing substitutions N158K, K189R and S378N) circulated globally with higher proportions detected in South America. Viruses expressing HA subclade J.2.4 (sharing T135K (potential loss of an N-glycosylation site) and K189R substitutions) continue to circulate, and a new group of J.2.4 viruses has emerged recently and expanded rapidly in nearly all regions. Globally, small numbers of viruses expressing HA subclade J.2.5 (sharing substitutions D104N, S145N and N158K) circulated, with higher proportions observed in North America.

Post-infection ferret antisera raised against cell culture-propagated A/District of Columbia/27/2023-like and egg-propagated A/Croatia/10136RV/2023-like (clade 2a.3a.1, subclade J.2) viruses, representing the A(H3N2) component for the SH 2025 and the NH 2025-26 influenza vaccines, recognized the majority of viruses well but recognized recent viruses in the J.2.3 (e.g., A/Netherlands/10685/2024), J.2.4 (e.g., A/Sydney/1359/2024) and J.2.5 (e.g., A/Kentucky/29/2024) HA subclades poorly. While ferret antisera raised against reference viruses from J.2.3 and J.2.5 HA subclades showed cross-recognition with each other likely due to a shared HA substitution (N158K), ferret antisera raised against reference viruses from J.2.4 showed poor recognition of viruses from all other J.2 subclades apart from those with a shared HA substitution (T135K). Post-infection ferret antisera raised against cell culture-propagated A/Sydney/1359/2024-like and egg-propagated A/Singapore/GP20238/2024-like viruses from subclade J.2.4 recognized other J.2.4 viruses well including those with notable additional HA substitutions S144N (a potential addition of an N-glycosylation site), N158D, I160K and Q173R, which have recently emerged.

Human serology studies were conducted using the SH 2025 serum panels as described above by HI and VN assays with recent circulating A(H3N2) viruses with HA genes from 2a.3a.1 subclades J.2, J.2.1, J.2.2, J.2.3, J.2.4 and J.2.5. When compared to titres against cell-propagated A/District of Columbia/27/2023-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against many of the recent viruses in J.2.2, J.2.3, J.2.4 and J.2.5 subclades were significantly reduced.

In summary, A(H3N2) viruses circulated globally and predominated in several regions since February 2025. The vast majority of A(H3N2) viruses collected had HA genes derived from 2a.3a.1 subclade J.2 and have continued to diversify. Post-infection ferret antisera raised against SH 2025 and NH 2025-26 influenza season vaccine viruses (cell culture-propagated A/District of Columbia/27/2023 and egg-propagated A/Croatia/10136RV/2023) recognized many J.2 viruses well but showed poor recognition of viruses from emerging subclades J.2.3, J.2.4 and J.2.5. Post-infection ferret antisera raised against reference viruses from emerging subclades J.2.3, J.2.4 and J.2.5 generally showed good recognition of viruses from their respective subclades or those with similar HA substitutions. Post-infection ferret antisera raised against J.2.4 viruses (represented by A/Sydney/1359/2024 and A/Singapore/GP20238/2024) showed improved recognition of J.2.4 viruses, including the genetically divergent viruses in this subclade which have recently emerged, compared to post-infection antisera raised against SH 2025 and NH 2025-26 A(H3N2) vaccine viruses. When compared to titres against cell-propagated A/District of Columbia/27/2023-like vaccine reference viruses, human post-vaccination HI GMTs or VN GMTs against many of the recent viruses in J.2.2, J.2.3, J.2.4 and J.2.5 subclades were significantly reduced.

Based on all available data, the WHO Consultative Group recommended to use an egg-propagated A/Singapore/GP20238/2024 (H3N2)-like strain or cell culture-propagated A/Sydney/1359/2024 (H3N2)-like strain as the vaccine strains for 2026. AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2025-sh-recommendations_seasonal_final.pdf (who.int) and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

4.2.3 Influenza B

Representative seasonal influenza B isolates were antigenically typed at the WHO National Influenza Centre at PHF Science using HAI typing kit supplied by the WHO Collaborating Centre (WHOCC). Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 24 August 2025, a total of 150 influenza B/Victoria-lineage isolates were antigenically typed with hemagglutination inhibition assay using antisera raised against B/Austria/1359417/2021-like virus. All B/Victoria-lineage isolates except one were inhibited well by the antisera against the vaccine

strain B/Austria/1359417/2021. Genetically, influenza B/Victoria lineage viruses fell into group V1.3a.2 (Figure 19).

Globally, influenza B viruses were lower than those of influenza A viruses with predominance only in Central Asia, Eastern and South West Europe, Middle African in earlier reporting period and Northern Africa and Northern Europe in later reporting period. All influenza B viruses where lineage was confirmed belonged to the B/Victoria/2/87 lineage. There have been no confirmed detections of circulating B/Yamagata/16/88 lineage viruses after March 2020.

All HA genes of B/Victoria lineage viruses characterized during this period belonged to clade 3a.2 with HA substitutions A127T, P144L and K203R. Viruses with clade 3a.2 HA genes have diversified further, with the vast majority sharing the substitution D197E, along with further amino acid substitutions, forming several subclades, the most predominant being designated as C.5.1, C.5.6 and C.5.7. Other subclades were detected at lower proportions, such as C.5.6.1, C.3.1 and C.3.2, with the latter two sharing substitution D197N, which adds a potential N-glycosylation site.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2), representing the vaccine viruses for the SH 2025 and NH 2025-26 influenza seasons, recognized the vast majority of viruses including those with additional HA substitutions within the C.5.1, C.5.6, C.5.6.1 and C.5.7 subclades well. Viruses within HA subclades C.3.1 and C.3.2 were recognized poorly.

In human serology studies using the serum panels described above, post-vaccination HI GMTs against recent B/Victoria lineage viruses with HA genes from clade 3a.2 subclades C.5.1, C.5.6, C.5.6.1 and C.5.7 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses. Titres against viruses with HA genes from subclade C.3.1 were significantly reduced in most assays.

In summary, influenza B viruses circulated at lower levels than influenza A viruses globally, predominating in only a few regions since February 2025. All circulating influenza B viruses characterized belonged to B/Victoria lineage. All recent viruses expressed HA genes belonging to clade 3a.2. The majority of circulating viruses were recognized well by post-infection ferret antisera raised against SH 2025 and NH 2025-2026 B/Victoria lineage vaccine viruses (cell culture- and egg-propagated B/Austria/1359417/2021) except for a small number of viruses expressing HA from subclades C.3.1 and C.3.2 which were recognized poorly. Human serology assays showed that post-vaccination GMTs against nearly all representative B/Victoria lineage viruses expressing 3a.2 HA genes were not significantly reduced compared to titres against cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses, apart from viruses from subclade C.3.1 which showed significantly reduced titres in most assays.

Based on all available data, the WHO Consultative Group recommended to continue to use cell culture- and egg-propagated B/Austria/1359417/2021-like strain for 2026. AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2025-sh-recommendations_seasonal_final.pdf (who.int) and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

Figure 17. Phylogenetic relationships among influenza A(H1N1)pdm09 virus haemagglutinin gene

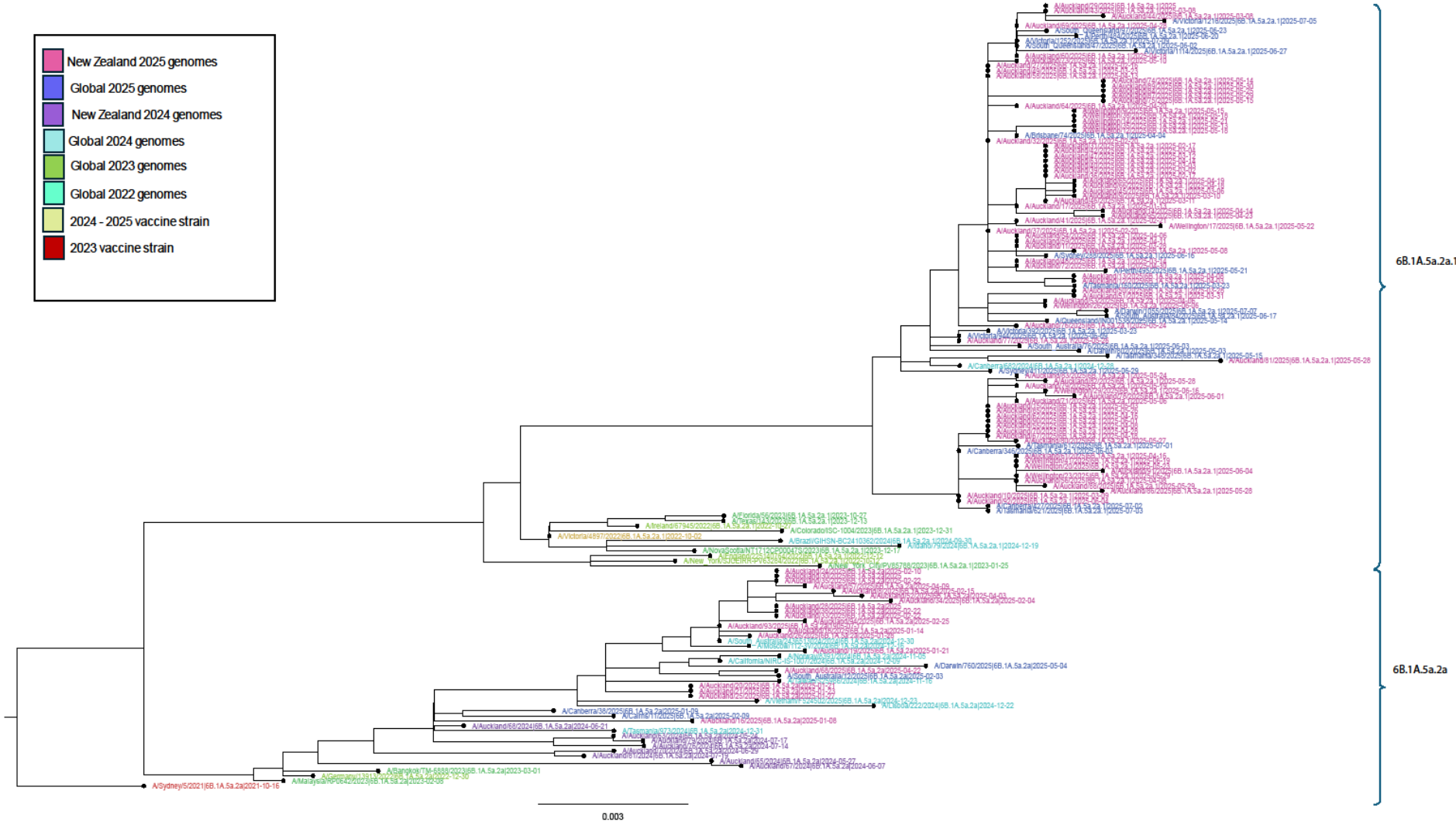


Figure 18. Phylogenetic relationships among influenza A(H3N2) virus haemagglutinin gene

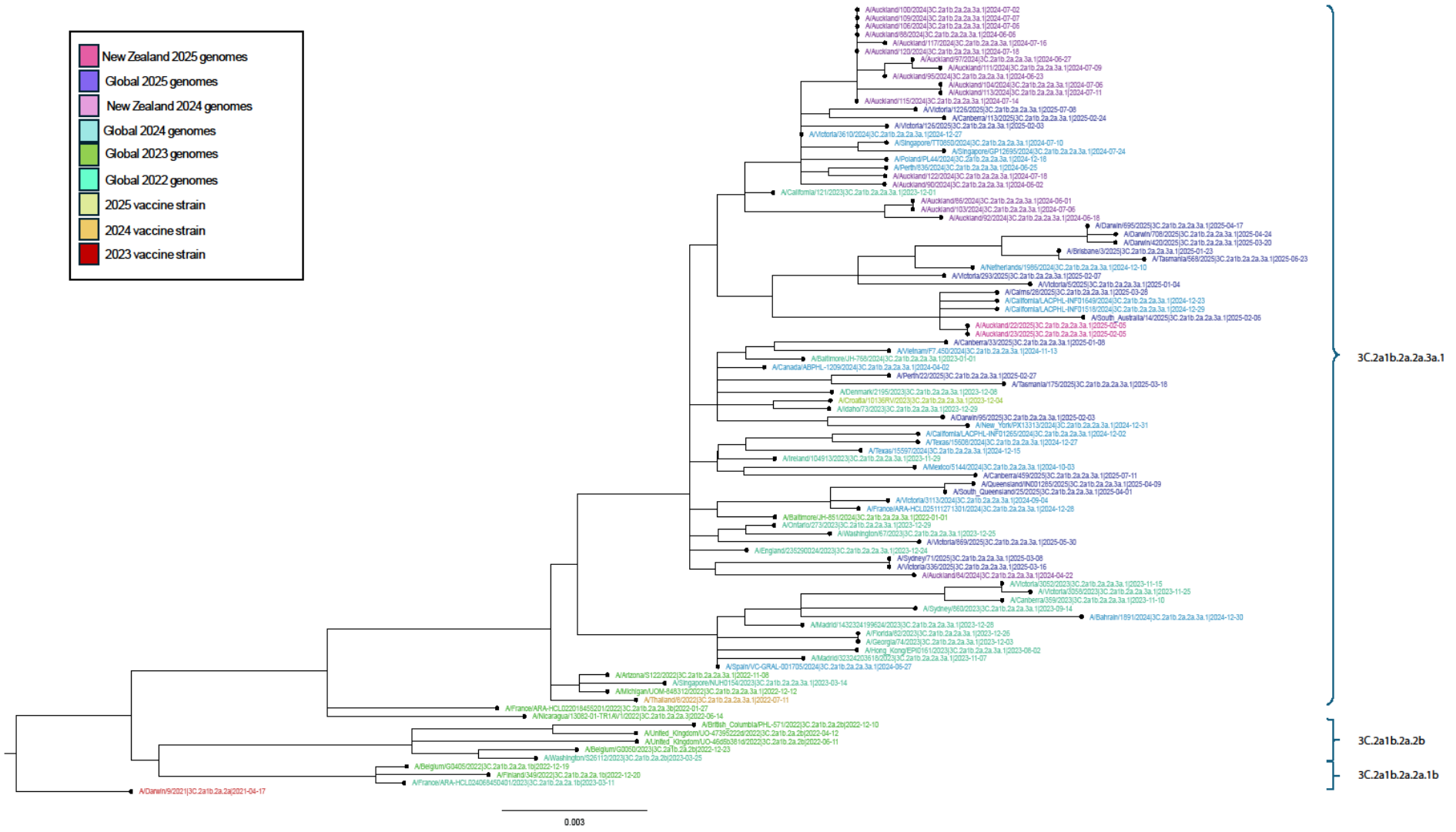
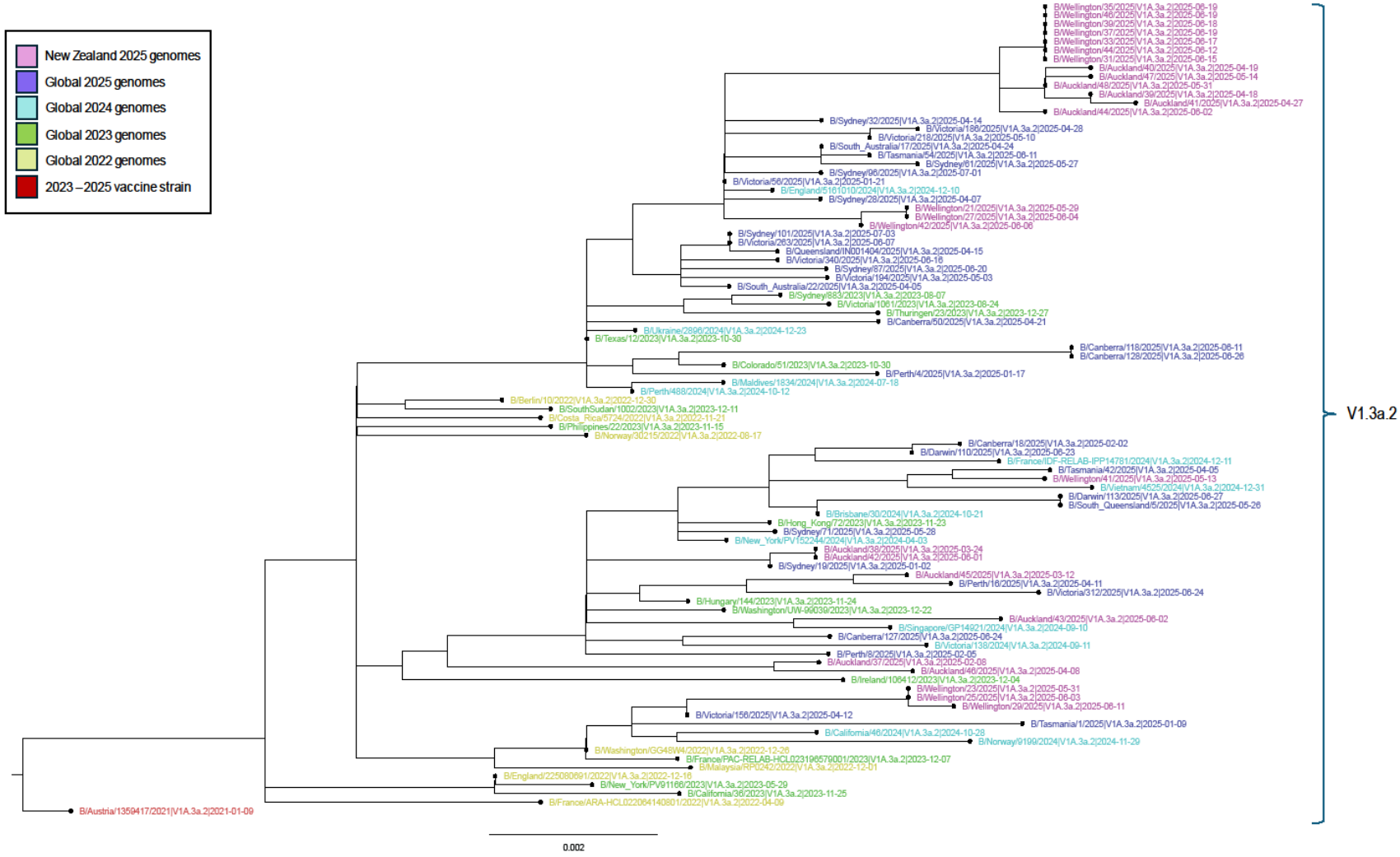


Figure 19. Phylogenetic relationships among influenza B/Victoria lineage virus haemagglutinin gene



4.3 ANTIVIRAL RESISTANCE

The WHO National Influenza Centre at PHF employed a phenotypic method (fluorometric neuraminidase inhibition assay) for the surveillance of anti-viral drug resistance in influenza viruses. In addition, NIC at PHF employed a molecular method (PCR and sequencing) to monitor the H275Y mutation (histidine-to-tyrosine mutation at the codon of 275 in N1 numbering) which is known to confer resistance to oseltamivir.

In 2025, fluorometric neuraminidase inhibition assay was used to test 172 influenza viruses against oseltamivir and zanamivir. The preliminary results showed that all were sensitive to both oseltamivir and zanamivir (Tables 7 & 8).

Table 7. Antiviral susceptibility to oseltamivir for influenza viruses, 2019–2025^

Influenza	NA inhibition to Oseltamivir*	Fold change in IC50 of test viruses (No. of viruses)**						
		2019	2020	2021	2022	2023	2024	2025
A(H1N1)pdm09	Normal	0-3 (20)	5	1	0-3 (16)	0-6 (360)	0-3 (112)	0-3 (45)
	Reduced	-	-	-	-	-	-	
	Highly reduced	-	-	-	-	-	-	
A(H3N2)	Normal	0-4 (75)		3	0-4 (442)	0-2 (54)	0-2 (107)	
	Reduced	-	-	-	-	-	-	
	Highly reduced	-	-	-	-	-	-	
Influenza B	Normal	0-5 (226)		2	0-1 (2)	0-2 (280)	0-2 (9)	0-2 (127)
	Reduced	28-29 (1)	-	-	-	10-10 (1)	-	
	Highly reduced	-	-	-	-	-	-	

Table 8. Antiviral susceptibility to zanamivir for influenza viruses, 2019–2025^

Influenza	NA inhibition to Zanamivir*	Fold change in IC50 of test viruses (No. of viruses)**						
		2019	2020	2021	2022	2023	2024	2025
A(H1N1)pdm09	Normal	0-5 (22)	5	1	0-2 (15)	0-3 (361)	0-6 (112)	0-2 (45)
	Reduced	15-16 (1)	-	-	-	-	-	
	Highly reduced	-	-	-	-	-	-	
A(H3N2)	Normal	0-6 (75)		3	0-3 (442)	0-2 (54)	0-3 (107)	
	Reduced	-	-	-	-	-	-	
	Highly reduced	-	-	-	-	-	-	
Influenza B	Normal	0-2 (228)		2	0-2 (2)	0-3 (279)	0-1 (9)	0-3 (127)
	Reduced	10-11 (1)	-	-	-	12-13 (1)	-	
	Highly reduced	-	-	-	-	-	-	

Note: For Tables above:
Neuraminidase inhibition was defined as:
Normal inhibition = IC50 values which are within or close to the median IC50 of the type/subtype matched viruses as detailed in the table above.
Reduced inhibition = IC50 values which are 10 to 100 fold above the median value of viruses with normal inhibition (5 to 50 fold for influenza B viruses)
Highly reduced inhibition = IC50 values which are greater than 100 fold above the median value of viruses with normal inhibition (above 50 fold for influenza B viruses)

5. INFLUENZA VACCINE EFFECTIVENESS

In New Zealand seasonal quadrivalent influenza vaccine is offered annually free of charge to all adults aged 65 years and over, pregnant women and all those over six months of age with chronic medical conditions that are likely to increase the severity of the infection. Since 2013, free influenza vaccines have been offered to children (6-months to 4-years) who have been hospitalised or have a history of significant respiratory illness. Influenza vaccines are also available on the private market for all others over six months of age. The influenza season usually occurs between May and September.

Using the case test-negative design to estimate propensity-adjusted vaccine effectiveness (VE). VE was estimated from the odds ratio (OR) comparing vaccination among patients with laboratory-confirmed influenza versus patients who test negative by RT-PCR for influenza, where V E = (1 − ORadj) × 100%. Odds ratios were estimated using logistic regression models where influenza test status was the dependent (i.e. outcome) variable and vaccination status was the main effect variable of interest. Logistic regression allows adjustment for other variables that may influence the estimate, such as age category, and calendar time. VE is interpreted as the relative reduction in odds of medically-attended influenza (either outpatient or hospital) or non-medically-attended influenza (such as cohort participants) among vaccinated vs. unvaccinated individuals. VE of 0% represents no protection and VE of 100% represents complete protection. The method for calculating VE allows the point estimate to be less than 0. A negative estimate suggests a lack of protection. Estimates are reported with a 95% confidence interval. Confidence intervals will generally be wider when the sample size is lower. In order for an estimate to have narrow confidence intervals, a substantially larger sample may be needed. We have excluded any estimates where the confidence interval spanned more than 150.

We estimated the effectiveness of seasonal inactivated influenza vaccine in preventing laboratory-confirmed influenza among patients hospitalised with severe acute respiratory infections (SARI), among GP-consultation seeking patients with influenza-like illness, and among WellKiwis participants with an acute respiratory illness (ARI) during the influenza season. The influenza season was defined as starting when there were two consecutive weeks with two or more cases; The data is contributed to I-GIVE project for the WHO vaccine strain selection meeting in September for southern hemisphere countries.

Most ARI, ILI and SARI patients with laboratory-confirmed influenza are included except those with incomplete data for vaccination status, infants under 6 months of age, children under 9 years who were only given one dose of vaccine, those vaccinated less than 14 days before admission or presentation. For patients with multiple episodes, the first influenza virus-positive episode was used for the analysis or the first illness episode if there was no influenza virus-positive episode.

The proportion vaccinated did not change throughout the season. For influenza-confirmed SARI cases among acutely admitted hospital patients, the estimated adjusted vaccine effectiveness (VE) was 69.5% (95% CI: 58.2, 78.0) (Table 9). For influenza-confirmed ILI cases among GP consultation patients, the estimated adjusted vaccine effectiveness (VE) was 72.8% (95% CI: 59.3, 82.4). For influenza-confirmed ARI among cohort participants, the estimated adjusted vaccine effectiveness (VE) was 56.8% (95% CI: 41.6, 68.1).

Table 9. Estimated influenza vaccine effectiveness against medically and non-medically attended influenza infections, 2025

Outcome Measure	Virus/Age Group		Influenza Positive		Influenza Negative		Crude	Adjusted*
			Vaccinated Yes	Vaccinated No	Vaccinated Yes	Vaccinated No	VE% (95%CI)	VE% (95%CI)
Hospital SARI	Influenza	All ages	66	396	321	743	61.4 (48.0, 71.6)	69.5 (58.2, 78.0)
		0-17 years	2	220	81	488	94.5 (79.2, 99.4)	94.5 (82.5, 99.1)
		18-64 years	20	121	87	166	68.4 (44.7, 82.6)	68.7 (47.2, 82.2)
		65+ years	44	55	153	89	53.4 (23.1, 71.9)	51.8 (22.3, 70.2)
	A(H1N1) [1]	All ages	12	100	235	525	73.2 (49.8, 86.8)	78.7 (60.7, 89.4)
		0-17 years	0	52	56	318	N/A	N/A
		18-64 years	1	31	69	146	93.1 (57.0, 99.8)	93.4 (67.9, 99.6)
		65+ years	11	17	110	61	63.9 (12.3, 85.7)	60.2 (8.3, 83.3)
	B/Victoria lineage	All ages	10	156	378	986	83.3 (67.9, 92.2)	79.1 (61.0, 90.0)
		0-17 years	1	103	82	607	92.8 (57.7, 99.8)	92.8 (67.1, 99.6)
		18-64 years	5	43	103	244	72.4 (27.6, 91.7)	73.1 (35.8, 90.9)
		65+ years	4	10	193	135	71.9 (0.1, 93.7)	72.8 (16.0, 92.7)
GP virology	Influenza	All ages	30	321	250	609	77.2 (65.7, 85.3)	72.8 (59.3, 82.4)
		0-17 years	6	119	30	198	66.6 (15.3, 89.0)	66.0 (21.1, 87.5)
		18-64 years	13	191	146	368	82.8 (68.6, 91.3)	81.3 (67.3, 90.2)
		65+ years	11	11	74	43	N/A	N/A
	A(H1N1)	All ages	17	132	263	794	61.1 (33.8, 78.4)	67.7 (44.9, 82.1)
		0-17 years	2	36	34	281	N/A	N/A
		18-64 years	6	89	153	468	79.3 (51.9, 92.8)	79.3 (55.3, 92.1)
		65+ years	9	7	76	45	N/A	N/A
	B/Victoria lineage	All ages	9	183	275	741	86.7 (73.8, 94.1)	79.8 (61.7, 90.6)
		0-17 years	3	83	33	237	73.0 (10.3, 94.8)	71.1 (16.0, 93.2)
		18-64 years	5	100	157	454	85.5 (64.1, 95.5)	83.2 (61.8, 94.2)
		65+ years	1	3	85	50	N/A	N/A
WellKiwis cohort	Influenza	All ages	85	212	597	607	65.7 (60.7, 70.1)	56.8 (41.6, 68.1)
		0-17 years	24	162	189	402	68.5 (50.0, 80.2)	69.0 (50.4, 80.6)
		18-64 years	56	49	372	199	38.9 (6.9, 59.8)	43.5 (12.5, 63.5)
		65+ years	5	1	36	6	N/A	N/A
	A(H1N1)	All ages	53	103	629	716	41.4 (17.0, 58.6)	41.1 (13.3, 60.1)
		0-17 years	10	79	203	485	69.8 (40.4, 84.6)	68.7 (37.4, 84.4)
		18-64 years	38	23	390	225	N/A	N/A
		65+ years	5	1	36	6	N/A	N/A
	B/Victoria lineage	All ages	32	118	650	701	70.8 (56.2, 80.5)	69.9 (53.5, 80.5)
		0-17 years	14	90	199	474	62.9 (33.4, 79.4)	68.5 (42.8, 82.6)
		18-64 years	18	28	410	220	65.5 (36.2, 81.3)	73.3 (48.4, 86.1)
		65+ years	0	0	41	7	N/A	N/A

*Adjusted for age and week in season
[1]Only among Middlemore patients (Auckland patients uncommonly had testing results for influenza virus subtypes)
N/A: not applicable as numbers to too low to reach any significance; CI: Confidence interval; ILI: Influenza-like illness; ARI: acute respiratory illness; SARI: severe acute respiratory infections. Highlighted cells indicate low numbers

6. ACKNOWLEDGEMENTS

This report is compiled by Sue Huang, Tim Wood, Andrew Anglemyer, Tegan Slater, Lauren Jelley, Jing Wang, Liza Lopez, Maritza Marull at the New Zealand Institute for Public Health and Forensic Science (PHF) in New Zealand.

Hospital-based SARI surveillance, GP ILI surveillance and ICD code based hospital surveillance is funded by the Ministry of Health, New Zealand.

SHIVERS-II, III and IV study is funded by US-NIAID through St Jude Children's Research Hospital.

The WHO National Influenza Centre, Health Intelligence Team and SHIVERS study team, PHF.

PHF's Clinical Virology Laboratory and Sequencing Laboratory.

Virus Laboratories in ADHB and CMDHB, CCDHB, BOPDHB and CDHB.

Research nurses at ADHB and CMDHB and Regional Public Health.

Participants in the Influenza surveillance and research programme SHIVERS study.

SHIVERS Clinical Advisory Group and Key collaborating organizations (HVDHB, CCDHB, University of Otago and Auckland), Wellington Maternity Health Professional.s

Practice nurses and GPs in sentinel GP ARI surveillance programme.

WHO Collaborating Centre, Melbourne.

WHO Collaborating Centre, Atlanta.

WHO Collaborating Centre, St Jude Children's Research Hospital, Memphis.

PHF Science

NEW ZEALAND INSTITUTE FOR PUBLIC HEALTH AND FORENSIC SCIENCE LIMITED

- **Kenepuru Science Centre**
  34 Kenepuru Drive, Kenepuru, Porirua 5022
  PO Box 50348, Porirua 5240
  New Zealand
  T: +64 4 914 0700
- **Mt Albert Science Centre**
  120 Mt Albert Road, Sandringham, Auckland 1025
  Private Bag 92021, Auckland 1142
  New Zealand
  T: +64 9 815 3670
- **Wallaceville Science Centre**
  66 Ward Street, Wallaceville, Upper Hutt 5018
  PO Box 40158, Upper Hutt 5140
  New Zealand
  T: +64 4 529 0600
- **Christchurch Science Centre**
  27 Creyke Road, Ilam, Christchurch 8041
  PO Box 29181, Christchurch 8540
  New Zealand
  T: +64 3 351 6019

www.phfscience.nz