Science for Communities
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RECOMMENDATION FOR SEASONAL INFLUENZA VACCINE COMPOSITION FOR NEW ZEALAND FOR 2025

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TABLE OF CONTENTS

1. RECOMMENDATION

The Australian Influenza Vaccine Committee (AIVC) met with a New Zealand representative in Canberra on 9 October 2024 to consult on the influenza vaccine composition for 2025 for New Zealand, Australia and South Africa (Table 1).

Egg-based influenza vaccines:

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Croatia/10136RV/2023 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage) - like virus;

Cell-based or recombinant-based quadrivalent influenza vaccines:

- an A/Wisconsin/67/2022 (H1N1)pdm09-like virus;
- an A/District of Columbia/27/2023 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus;

The recommendation for the B/Yamagata lineage component of quadrivalent influenza vaccines remains unchanged from previous recommendations:

- a B/Phuket/3073/2013 (B/Yamagata 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 recommendations, it remains the opinion of the WHO influenza vaccine composition advisory committee that inclusion of a B/Yamagata lineage antigen in quadrivalent influenza vaccines is no longer warranted, and every effort should be made to exclude this component as soon as possible. The AIVC noted this position and supports the WHO committee's views.

Table 0. Influenza vaccine recommendations for New Zealand, 1994–2024

Decision		Use	A H3N2	A H1N1	B (Trivalent)	B (Quadrivalent)
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(	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**	1992–93		A/Beijing/353/89	A/Singapore/6/86	B/Yamagata/16/88 or B/Panama/45/90	

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

2. SUMMARY

In 2024, 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 low as measured by the ratio of influenza-associated SARI ICU admission over influenza-associated SARI hospitalization. Virus transmissibility which reflects the ease of movements of the influenza virus between individuals and communities was high as measured by influenza-associated acute respiratory illness among the SHIVERS community cohort participants.

The hospital-based severe acute respiratory illness was moderate in 2024. 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 low, like 2023 but lower than 2022. Influenza-associated ARI was higher than 2023 but lower than 2022. 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 Pacific peoples and Māori ethnic groups 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 10276 influenza viruses were detected and reported through this system. Of them, influenza A represented 98.8% (10153) and influenza B 1.2% (123) of all influenza viruses. Among 2706 subtyped and lineage-typed influenza viruses, 1894 (70.0%) were A(H3N2), 802 (29.6%) were A(H1N1)pdm09, 10 (0.4%) were influenza B/Victoria lineage viruses.

WHO National Influenza Centre (NIC) at ESR conducted antigenic/genetic typing: 1) 120 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) 67 (61%) influenza A(H3N2) viruses were antigenically closely related to the vaccine strain A/Thailand/8/2022 (H3N2)-like virus. 42 (39%) were antigenically drifted away from the vaccine strain. Genetically most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2a.3a.1. 3) 9 influenza B/Victoria-lineage viruses were antigenically closely related to the vaccine strain B/Austria/1359417/2021-like virus. Genetically, no influenza B virus was available for sequencing.

3. EPIDEMIOLOGY - NEW ZEALAND INFLUENZA SEASON IN 2024

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 (SARI surveillance, Ministry of Health data on publicly funded hospital discharges, laboratory-based surveillance for outpatients and hospital in-patients). The surveillance system also includes community-based surveillance (community-based longitudinal cohort surveillance and sentinel GP based virological surveillance).

3.1 HOSPITAL-BASED SURVEILLANCE

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

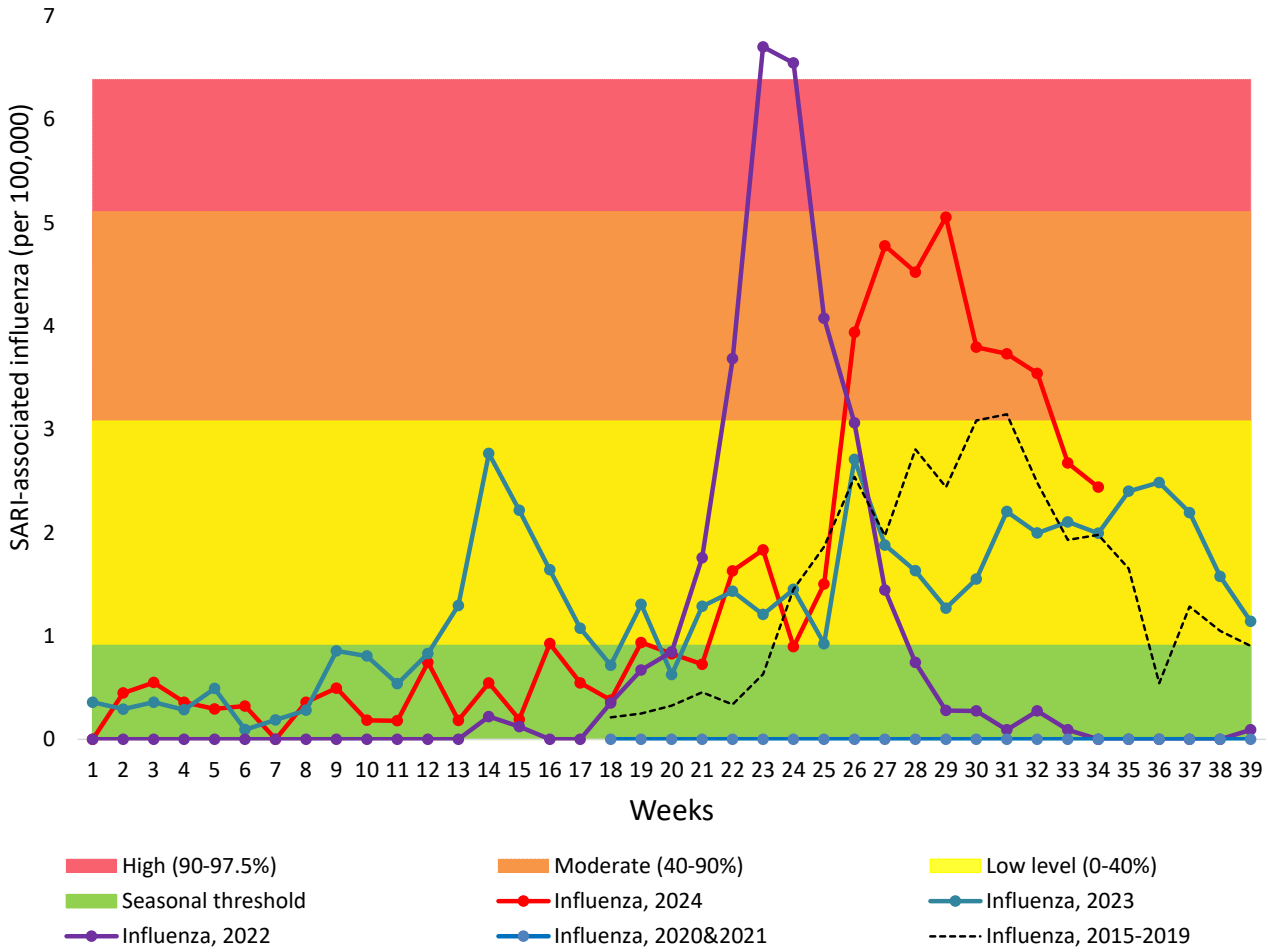
Inpatients with suspected respiratory infections admitted overnight to any of the four hospitals (Auckland City Hospital and the associated Starship Children's Hospital, Middlemore Hospital and the associated Kidz First Children's Hospital) in the Auckland District Health Board (ADHB) and Counties Manukau 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.

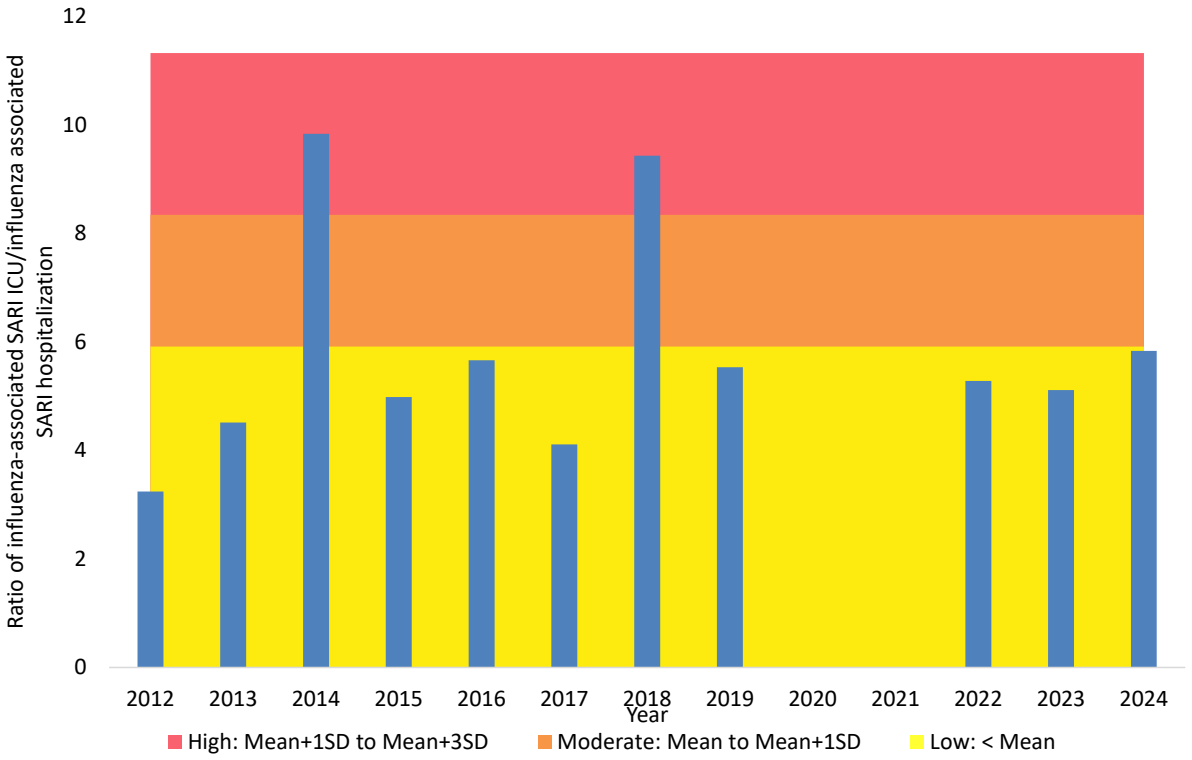
Overall impact on healthcare use is measured by influenza-associated severe acute respiratory illness (SARI) hospitalizations. During the study period from week 1 (commencing 1 January 2024) to week 34 (ending 25 August 2024), influenza-associated SARI hospitalizations were at moderate level in 2024 (Figure 1). Influenza hospitalizations peaked at week 29.

Figure 1. Influenza-associated SARI hospitalizations in 2024 compared to pre-pandemic 2015-2019, and during pandemic 2020-2023



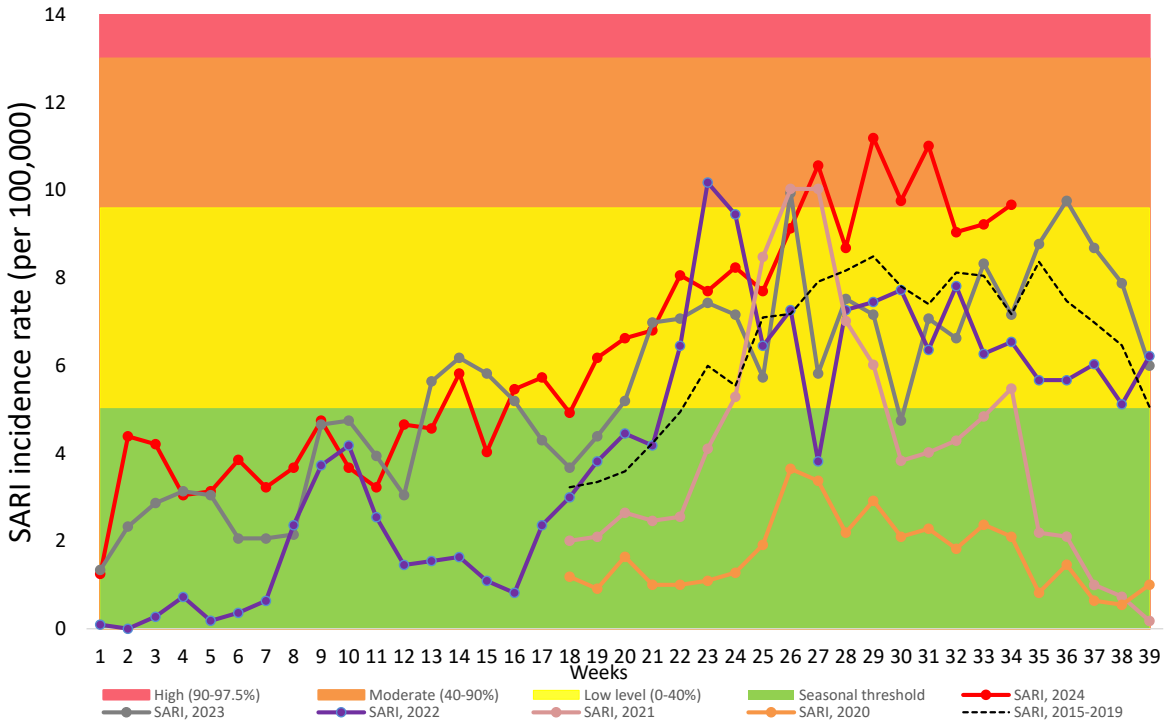
Seriousness of disease (i.e. clinical severity) that indicates the extent to which individuals get sick when infected with the influenza virus as measured by the ratio of influenza-associated SARI ICU admission over influenza-associated SARI hospitalization. Seriousness of disease was low in 2024 (Figure 2).

Figure 2. Seriousness of disease indicator in 2024 compared to 2012–2023



SARI hospitalization was moderate. It was below baseline during weeks 1-13, then increased to low level in week 14, and peaked at week 29 and then declined gradually (Figure 3).

Figure 3. Weekly hospitalisation rates for SARI in 2024 compared to pre-pandemic 2015-2019, during pandemic 2020-2023



From 1 January to 25 August 2024, there were 109185 acute admissions to ADHB and CMDHB hospitals. A total of 5595 patients with suspected respiratory infections were assessed in these hospitals. Of these, 2583 (46%) patients met the SARI case definition and 3012 not met the SARI cases (i.e. non-SARI cases). Among these SARI cases, 2364 were residents of ADHB and CMDHB, giving the SARI incidence rate of 214.2 per 100 000 population (186.8 per 100 000 in 2023) (Table 1). Among the SARI cases who were ADHB and CMDHB residents, 536 (22.7%) had positive influenza virus results. This gives influenza-associated SARI incidence of 48.6 per 100 000 population, 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 cases and related influenza cases, weeks 1-34, 2024

Characteristics	Admissions	Assessed	SARI & influenza cases among all hospital patients			SARI & influenza cases among ADHB & CMDHB residents					
			SARI Cases	SARI proportion per 1000 hospital patients	Influenza positive	SARI cases	SARI incidence (per 100 000)	Influenza Cases (SARI)	Influenza incidence (SARI) (per 100 000)	Influenza (SARI & non SARI)	Influenza incidence (SARI & non SARI) (per 100 000)
Overall	**109185**	**5595**	**2583**	**23.7**	**883**	**2364**	**214.2**	**536**	**48.6**	**837**	**75.8**
Age group (years)											
<1	3355	828	418	124.6	52	356	2652.8	33	245.9	50	372.6
1–4	7503	773	511	68.1	115	451	888.1	85	167.4	105	206.8
5–19	11949	498	319	26.7	70	273	127.5	51	23.8	60	28.0
20–34	20135	286	153	7.6	67	147	51.8	48	16.9	64	22.6
35–49	17534	383	179	10.2	77	168	76.5	50	22.8	73	33.3
50–64	18199	776	322	17.7	162	307	164.4	93	49.8	155	83.0
65–79	18702	1183	404	21.6	217	391	375.1	111	106.5	209	200.5
>80	11808	868	277	23.5	123	271	864.2	65	207.3	121	385.8
Unknown	0	0	0		0	0	0.0	0	0.0	0	0.0
Ethnicity											
Māori	15213	1112	469	30.8	158	436	305.5	98	68.7	153	107.2
Pacific peoples	24400	1621	811	33.2	289	789	408.2	190	98.3	282	145.9
Asian	22990	705	351	15.3	112	318	89.3	79	22.2	106	29.8
European and Other	46227	2012	837	18.1	309	750	182.3	159	38.6	283	68.8
Unknown	341	145	115		15	71		10		13	
DHB of Residence											
ADHB	61912	2409	1052	17.0	348	1052	211.7	229	46.1	348	70.0
CMDHB	47273	3186	1312	27.8	489	1312	216.3	307	50.6	489	80.6
Other			219		46	0					
Sex											
Female	56804	2712	1271	22.4	458	1175	212.3	274	49.5	434	78.4
Male	52339	2876	1271	24.3	425	1186	215.6	262	47.6	403	73.3
Unknown	42	7	3		0	3					

From 1 January to 25 August 2024, 2435 SARI specimens have been tested and 564 (23%) were positive for influenza viruses (Table 2). Of the 207 specimens collected from ICU admitted patients with acute respiratory illness (SARI and non-SARI), 43 (21%) were positive for influenza viruses. Of the 133 specimens collected from fatal cases with acute respiratory illness (SARI and non-SARI), 20 were positive for influenza A viruses. Influenza A(H3N2) was the predominant strain.

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

Table 2. Influenza and non-influenza respiratory viruses among SARI cases, 2024

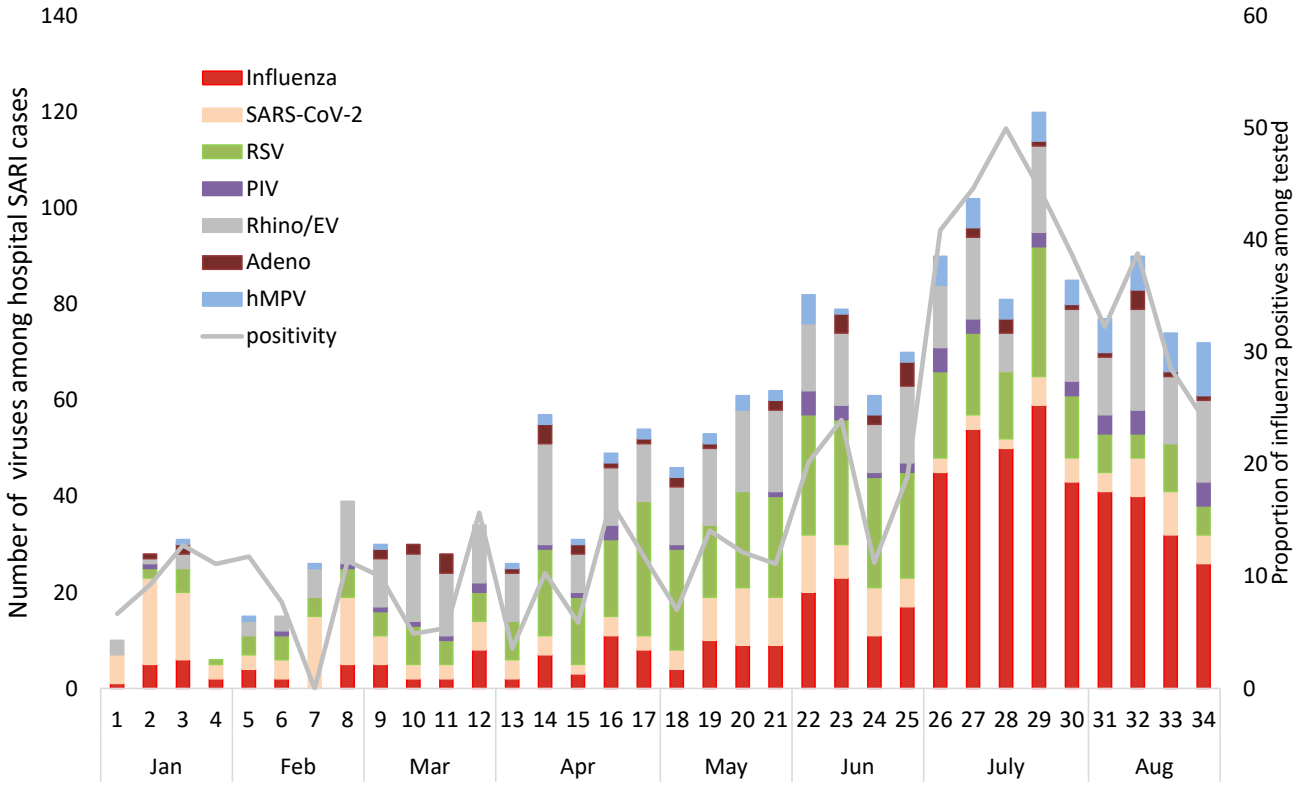
Influenza viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2435	207	133
No. of positive specimens (%)[1]	564 (23.0)	43 (21.0)	20 (15.0)
Influenza A	552	42	20
A (not subtyped)			
A(H1N1)pdm09	93	11	4
A(H1N1)pdm09 by PCR			
A/Victoria/4897/2022 (H1N1)pdm09-like			
A(H3N2)	136	15	3
A(H3N2) by PCR			
A/Thailand/8/2022 (H3N2)-like			
Influenza B	13	1	0
B (lineage not determined)			
B/Yamagata lineage			
B/Yamagata lineage by PCR			
B/Phuket/3073/2013 - like			
B/Victoria lineage			
B/Victoria lineage by PCR			
B/Austria/1359417/2021-like			
Influenza and non-influenza co-detection (% +ve)	36 (6.4)	6 (3.0)	0 (-)

Non-influenza respiratory viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2436	207	133
No. of positive specimens (%)[1]	1068 (43.8)	110 (53.1)	42 (31.6)
Respiratory syncytial virus (RSV)	426	32	8
Parainfluenza (PIV)	54	10	2
Rhinovirus (RV)/Enterovirus	391	57	2
Adenovirus (AdV)	50	7	1
Human metapneumovirus (hMPV)	94	13	0
SARS-Cov-2	227	13	33
Single virus detection (% of positives)	896 (83.9)	90 (81.8)	41 (97.6)
Multiple virus detection (% of positives)	172 (16.1)	20 (18.2)	1 (2.4)

[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 4. Influenza was the dominant virus among all common respiratory viruses in 2024.

Figure 4. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1] in 2024



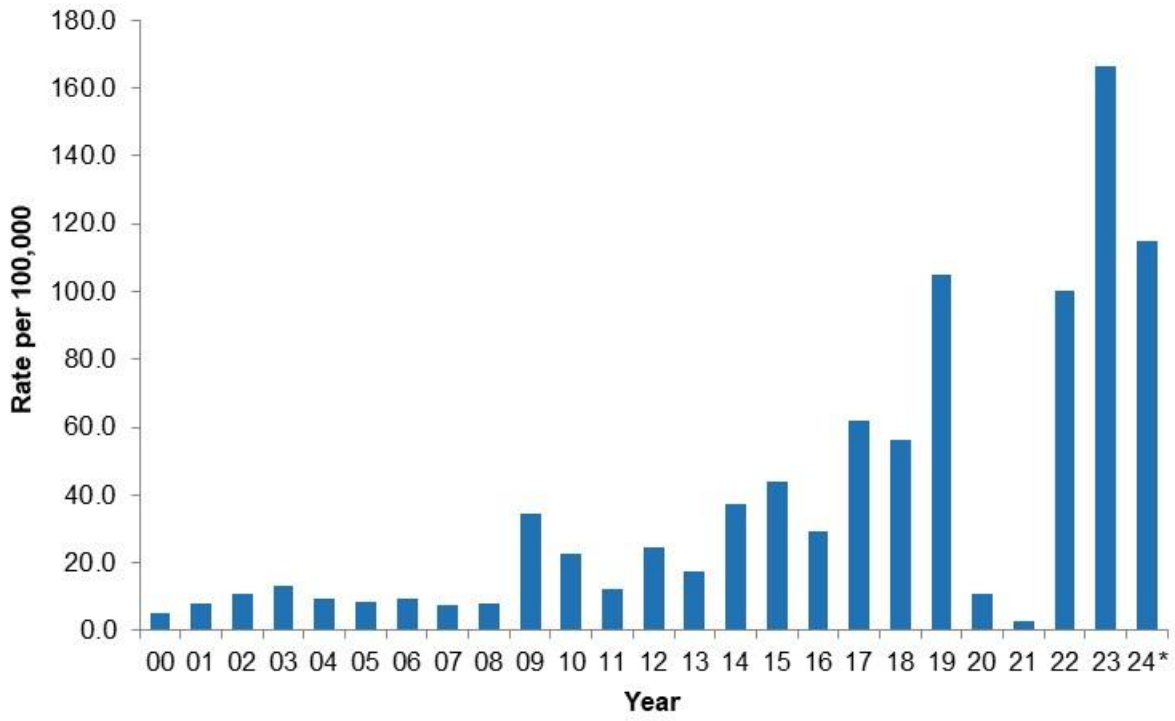
[1]Numbers for recent weeks will be underestimates due to time lag in receiving laboratory test results

3.1.2 Ministry of Health data on publicly funded hospital discharges

Hospitalisation data for influenza (ICD-9-CMA-II code 487) for 2024 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 2000–2024. 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 16 August 2024, there were a total of 5992 hospitalisations (114.7 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 2024.

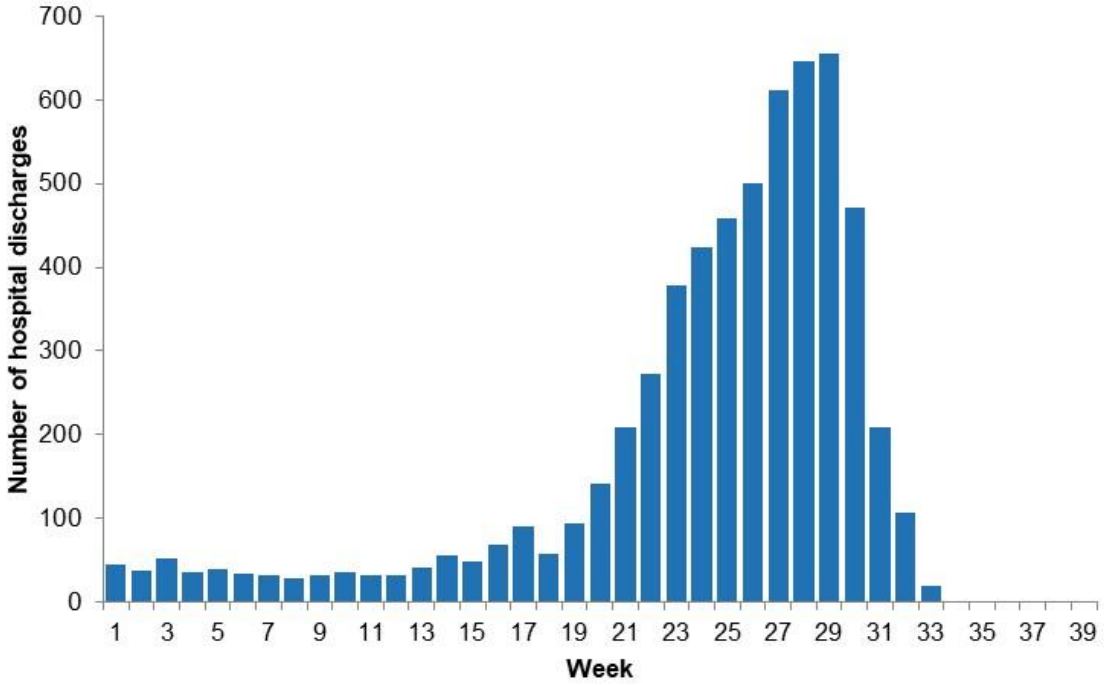
Figure 5. Influenza hospital discharge rates, 2000–2024*



*2024 preliminary data from 1 Jan to 16 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

Figure 6 shows influenza hospitalisations by week discharged. The highest number of hospitalisations (656) occurred in week 29 (week ending 20 July 2024).

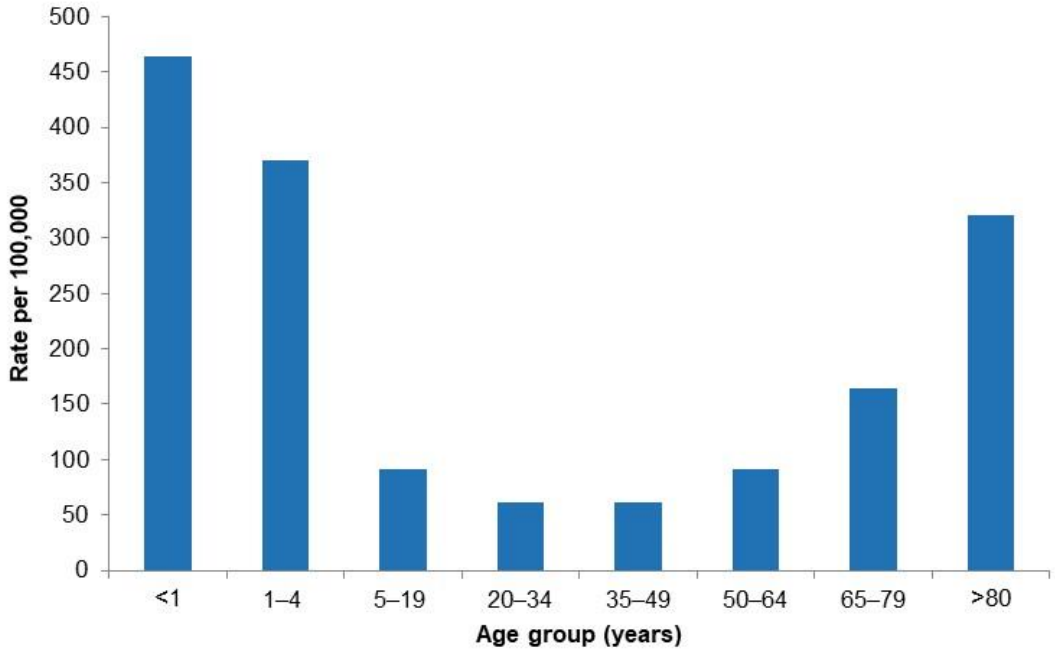
Figure 6. Influenza hospital discharges by week, 2024*



*2024 preliminary data from 1 Jan to 16 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

From 1 January to 16 August, the highest influenza hospitalisation rates were recorded among infants <1 year (463.6 per 100,000) followed by young children aged 1–4 years (370.7 per 100,000) (Figure 7).

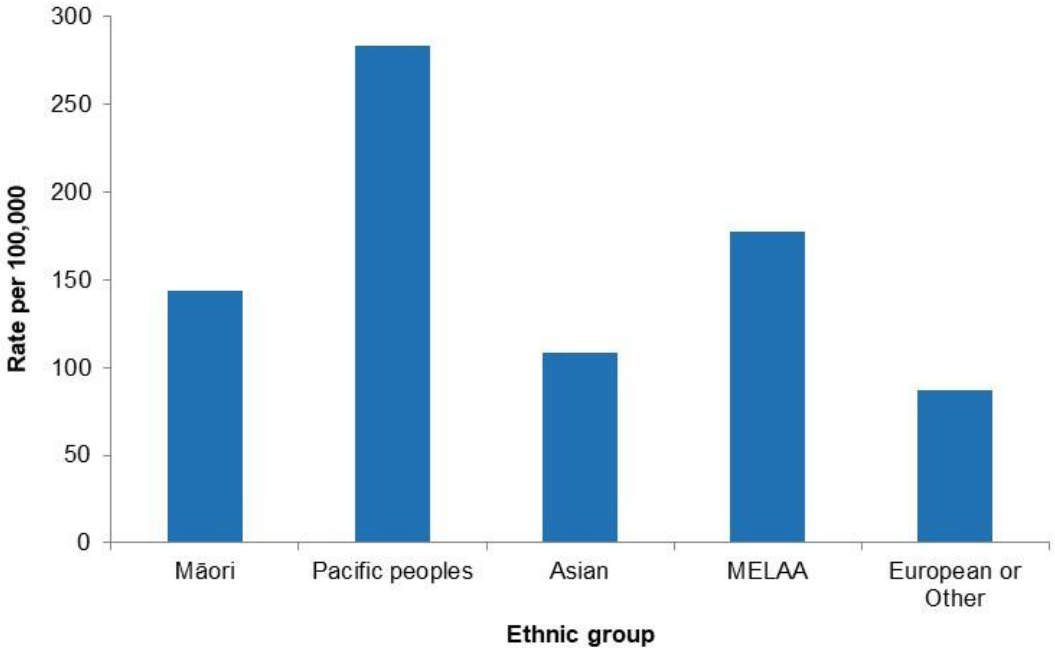
Figure 7. Influenza hospital discharge rates by age group, 2024*



*2024 preliminary data from 1 Jan to 16 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

The ethnic distribution of influenza hospitalisations in 2024 is shown in Figure 8. Pacific peoples had the highest hospitalisation rate (283.4 per 100,000) followed by MELAA (177.5 per 100,000) and Māori 143.5 per 100,000. Asian (108.3 per 100,000) and European or Other (87.2 per 100,000) ethnic groups had the lowest rates of hospitalisations.

Figure 8. Hospital discharge rates by prioritised ethnic group, 2024*



*2024 preliminary data from 1 Jan to 16 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 2024, SHIVERS-II study staff followed these participants (~900) and monitored their ILIs and acute respiratory illness (ARI)s.

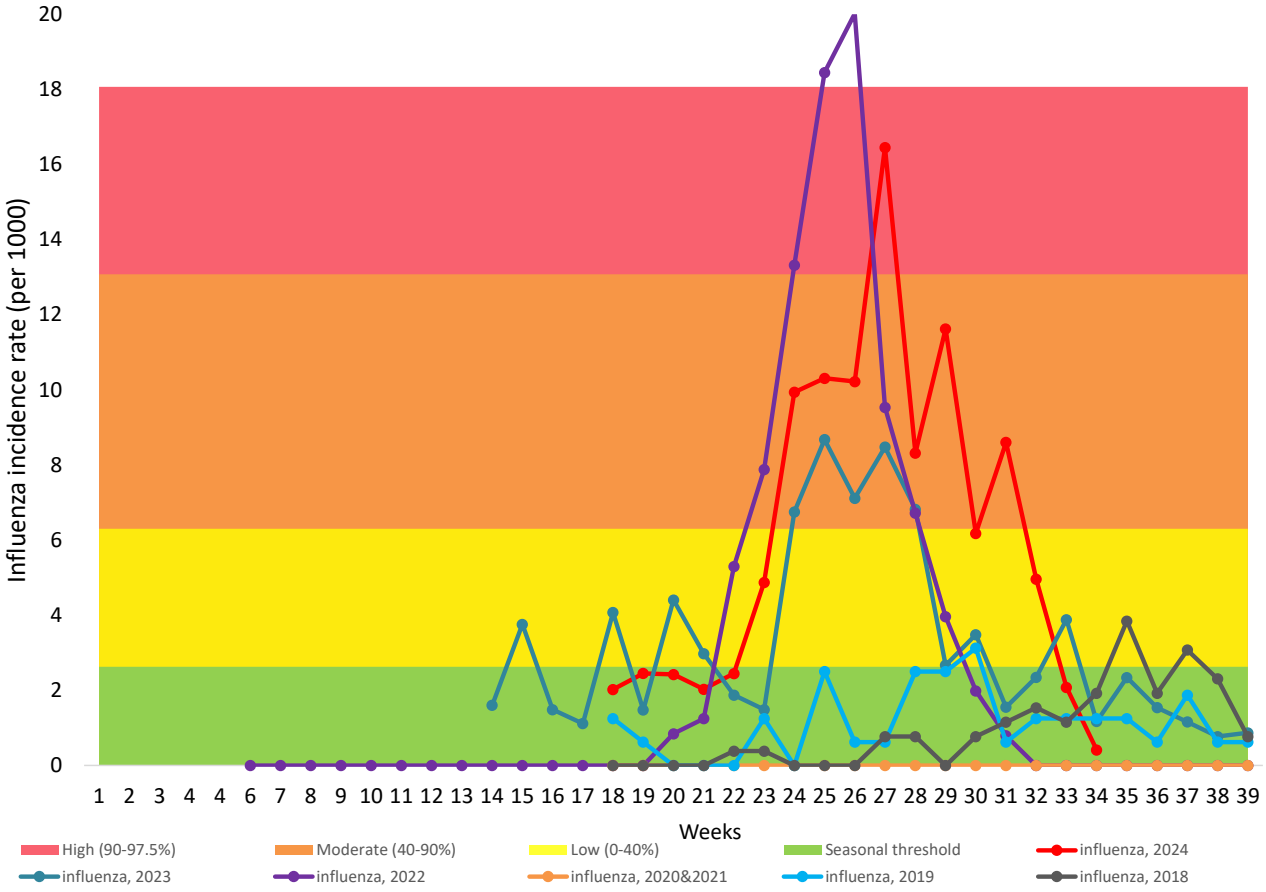
SHIVERS-III (i.e. WellKiwis Infant) is a prospective Wellington infant cohort aiming to recruit 600 infant-mother pairs from Oct 2019-Sept 2022 (200 pairs a year) and follow them until 2026. In 2024, the study staff followed up ~700 infants and monitored their ILIs and ARIs.

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 2024, the study staff followed up ~1800 household members and monitored their ILIs and ARIs.

During 29-April to 25-August 2024, SHIVERS-II, III and IV 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.

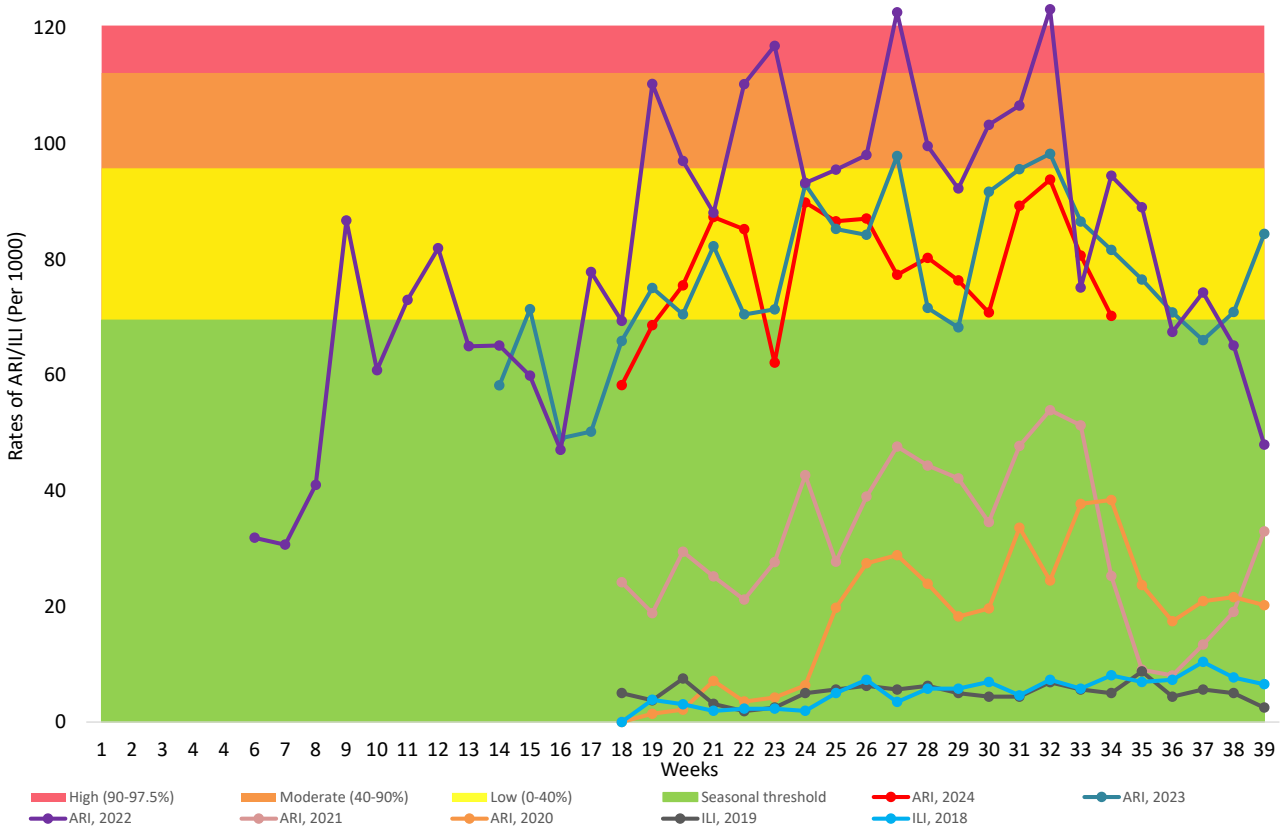
Virus transmissibility which reflects the ease of movements of the influenza virus between individuals and communities and it is measured by influenza-associated ARI. In 2024, the influenza-associated ARI was at a high level, lower than 2022, but higher than other years (Figure 9).

Figure 9. Weekly influenza associated ARI rates in 2024, compared to 2018-2023



The ARI rates in 2024 was at a low level. It is similar to 2023, but lower than 2022 (Figure 10).

Figure 10. Weekly ARI/ILI incidence rates in 2024, compared to 2018-2023



From 29-April to 25-August 2024, a total of 3262 patients with acute respiratory illness (ARI) were reported, giving the ARI incidence rate of 107.3 per 100 population (132.4 per 100 in 2023) (Table 3). Of the ARI cases, 256 had positive influenza virus results. This gave the influenza-associated ARI incidence of 8.4 per 100, higher than 6.4 per 100 in 2023.

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 Pacific peoples and Māori ethnic groups than Asians and Europeans ethnic groups.

Table 3. Demographic characteristics of ARI cases and related influenza cases, during 29-Apr to 25-Aug 2024

Characteristics	ARI cases among WellKiwis		Influenza cases among WellKiwis	
	ARI Cases	ARI incidence (per 100)	Influenza Cases	Influenza incidence (per 100)
Overall	**3262**	**107.3 (103.7, 110.9)**	**256**	**8.4 (7.4, 9.5)**
Age group (years)				
<1	92	306.7 (251.6, 368.2)	4	13.3 (3.6, 33.9)
1–4	1296	168.8 (160.1, 177.7)	99	12.9 (10.5, 15.7)
5–19	426	98.2 (89.3, 107.6)	51	11.8 (8.8, 15.4)
20–34	317	123.3 (110.6, 137.1)	18	7.0 (4.2, 11.1)
35–49	801	104.0 (97.1, 111.2)	59	7.7 (5.8, 9.9)
50–64	249	48.8 (43.0, 55.2)	22	4.3 (2.7, 6.5)
≥65	81	29.8 (23.7, 36.9)	3	1.1 (0.2, 3.2)
Ethnicity				
Māori	333	112.5 (101.1, 124.8)	32	10.8 (7.4, 15.2)
Pacific peoples	143	124.3 (105.4, 145.5)	15	13.0 (7.3, 21.5)
Asian	295	109.3 (97.5, 122.0)	25	9.3 (6.0, 13.7)
European and Other	2491	105.6 (101.6, 109.6)	184	7.8 (6.7, 9.0)
Sex				
Female	1867	108.4 (103.6, 113.2)	150	8.7 (7.4, 10.2)
Male	1388	106.0 (100.6, 111.5)	106	8.1 (6.6, 9.8)
Other	7	87.5 (35.6, 175.4)	0	0.0 (0.0, 45.5)

From 29-Apr to 25-Aug 2024, 2624 respiratory specimens have been tested and 256 (9.8%) were positive for influenza viruses. Of which, A(H3N2) (151) was the predominant strain. A(H1N1) (91) co-circulated throughout this period (Table 4). Additionally, 2607 specimens were tested for non-influenza respiratory viruses.

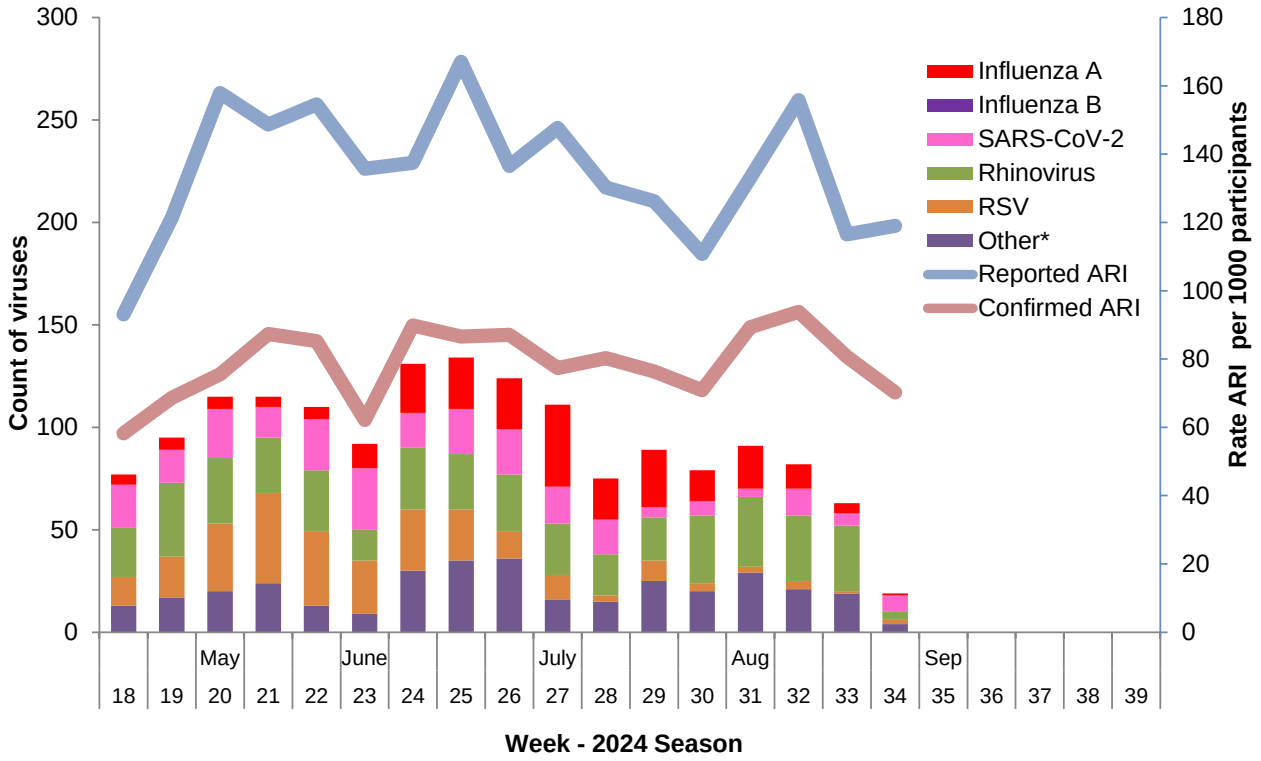
Table 4 Influenza and Non-influenza respiratory viruses among ARI cases, 29-Apr to 25-Aug, 2024

Influenza viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	**1925**	**404**	**295**	**2624**
No. of positive specimens (%)[1]	176 (9.1)	48 (11.9)	32 (10.8)	256 (9.8)
Influenza A	176	48	32	256
A (not subtyped)	11	2	1	14
A(H1N1)pdm09	67	12	12	91
A(H1N1)pdm09 by PCR	67	12	12	91
A/Victoria/4897/2022 (H1N1)pdm09-like	0	0	0	0
A(H3N2)	98	34	19	151
A(H3N2) by PCR	98	34	19	151
A/Thailand/8/2022 (H3N2)-like	0	0	0	0
Influenza B	0	0	0	0
B (lineage not determined)	0	0	0	0
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	0	0	0	0
B/Victoria lineage by PCR	0	0	0	0
B/Austria/1359417/2021-like virus	0	0	0	0
Influenza and non-influenza co-detection (% +ve)	16 (9.1)	4 (8.3)	2 (6.3)	22 (8.6)

Non-influenza respiratory viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	**1909**	**404**	**294**	**2607**
No. of positive specimens (%)[1]	843 (44.2)	227 (56.2)	132 (44.9)	1202 (46.1)
Respiratory syncytial virus (RSV)	193	76	11	280
Parainfluenza 1 (PIV1)	48	7	3	58
Parainfluenza 2 (PIV2)	7	2	0	9
Parainfluenza 3 (PIV3)	5	1	2	8
Rhinovirus (RV)	324	87	39	450
Adenovirus (AdV)	62	27	0	89
Human metapneumovirus (hMPV)	53	25	3	81
Enterovirus	77	20	4	101
SARS-CoV-2	182	14	74	270
Single virus detection (% of positives)	742 (88.0)	197 (86.8)	128 (97.0)	1067 (88.8)
Multiple virus detection (% of positives)	101 (12.0)	30 (13.2)	4 (3.0)	135 (11.2)

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 2024.

Figure 11. Weekly incidence rate of acute respiratory illness and associated viruses in 2024



*Note: other viruses include enterovirus, adenovirus, parainfluenza virus types 1-3 and human metapneumovirus. 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 ARI reported by participants (per 1000), and the orange line the rate of nurse-confirmed ARI meeting the case definition.

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 of some of the ILI patients they see each week. The samples are sent to ESR and tested for influenza, SARS-CoV-2, RSV and other respiratory viruses.

In 2024, 81 sentinel general practices participated in this surveillance. Between 29 April to 25 August 2024, a total of 2178 ILI specimens were tested for influenza viruses (Table 5) and 576 (26.4%) were positive, with 571 influenza A and 5 influenza B viruses detected. 284 A(H3N2) and 264 A(H1N1)pdm09 were detected.

Additionally, a total of 2178 ILI specimens were tested for non-influenza viruses and 565 (25.9%) were positive with non-influenza viruses.

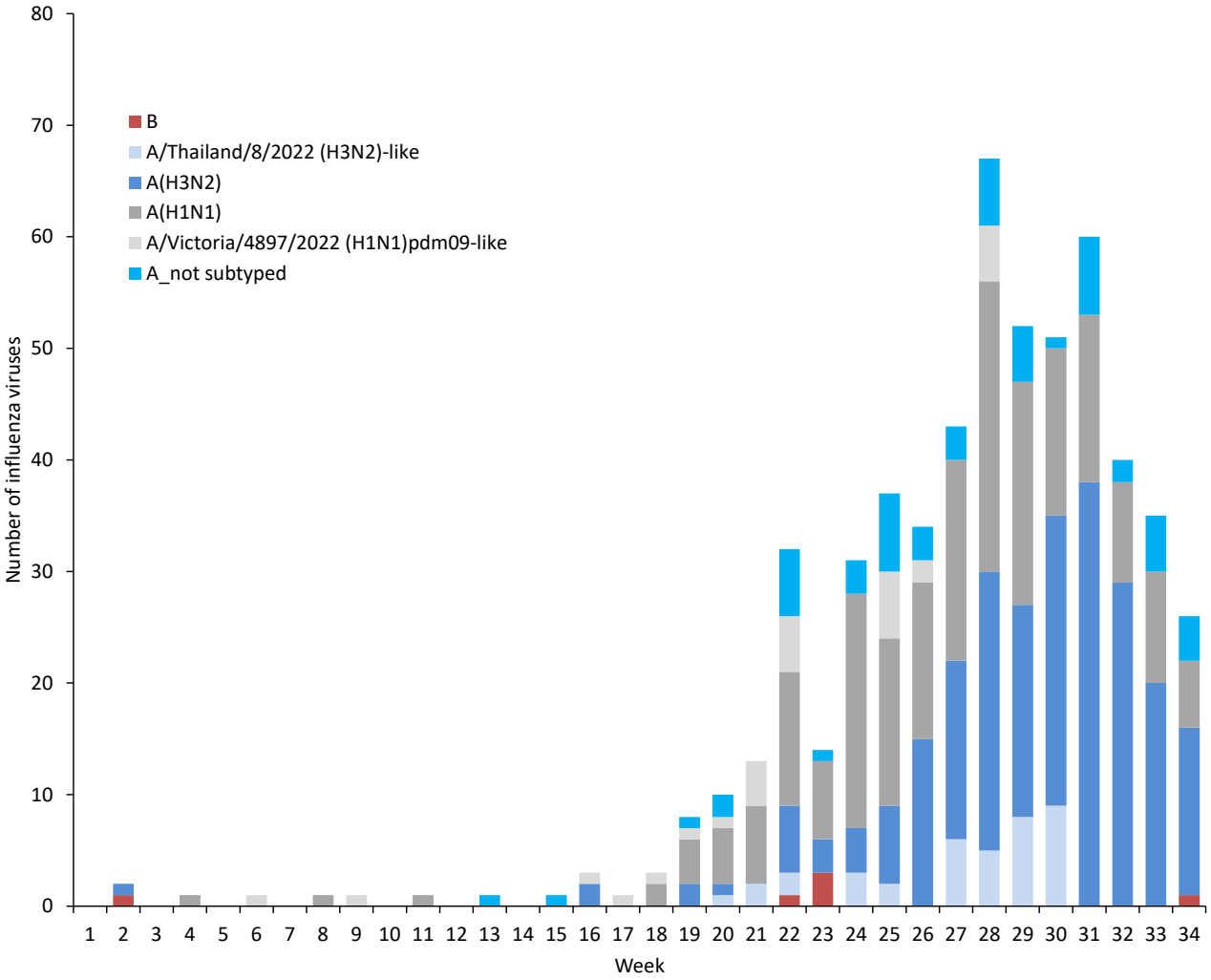
Table 5. Influenza and non-influenza respiratory viruses among ILI cases, 29 April – 25 August 2024

Influenza viruses	**ILI**
	Cases (%)
No. of specimens tested	2178
No. of positive specimens (%)	576 (26.4)
Influenza A	571
A (not subtyped)	23
A(H1N1)pdm09	264
A(H1N1)pdm09 by PCR	264
A/Victoria/4897/2022 (H1N1)pdm09-like	29
A(H3N2)	284
A(H3N2) by PCR	284
A/Thailand/8/2022 (H3N2)-like	38
Influenza B	5
B (lineage not determined)	5
B/Yamagata lineage	
B/Yamagata lineage by PCR	
B/Phuket/3073/2013 - like	
B/Victoria lineage	
B/Victoria lineage by PCR	
B/Austria/1359417/2021-like	2

Non-influenza respiratory viruses	**ILI**
	Cases (%)
No. of specimens tested	2178
No. of positive specimens (%)	565 (25.9)
Respiratory syncytial virus (RSV)	164
Parainfluenza (PIV)	65
Rhinovirus (RV)/Enterovirus	231
Adenovirus (AdV)	32
Human metapneumovirus (hMPV)	46
SARS-Cov-2	27

The temporal distribution of the number and proportion of the influenza viruses and non-influenza respiratory viruses, from 1 January to 25 August 2024, is shown in Figure 12. Influenza A(H3N2) and A(H1N1)pdm09 viruses were the two main predominant strains co-circulating at almost the same level with A(H1N1)pdm09 circulated slightly earlier than A(H3N2) during this period.

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



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 ESR and 6 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 ESR 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 2024

During 1-Jan to 25-August-2024, a total of 10276 influenza viruses were detected and reported through any surveillance system, with influenza A representing 98.8% (10153/10276) and influenza B 1.2% (123/10276) of all influenza viruses (Table 6). Among 2706 subtyped and lineage-typed viruses, 70% (1894/2706) were A(H3N2) viruses, 29.6% (802/2706) were A(H1N1)pdm09 viruses, and 0.4% (10/2706) were B/Victoria lineage viruses.

Table 6. Influenza virus identifications by type and sub-type and lineage-typed, 2024

Viruses	All viruses		Sub-typed and lineage-typed	
	N.	Col%	N.	%
Influenza virus	**10276**	**100.0**	**2706**	**100.0**
Influenza A	**10153**	**98.8**	**2696**	**99.6**
Influenza A (not sub-typed)	7457	72.6		
Influenza A(H1N1)pdm09	802	7.8	802	29.6
A(H1N1)pdm09 by PCR	690	6.7		
A/Victoria/4897/2022 (H1N1)pdm09-like	112	1.1		
Influenza A(H3N2)	1894	18.4	1894	70.0
A(H3N2) by PCR	1788	17.4		
A/Thailand/8/2022 (H3N2)-like	106	1.0		
Influenza B	**123**	**1.2**		
Influenza B (not lineage-typed)	113	1.1		
B/Victoria lineage	10	0.1	10	0.4
B/Victoria lineage by PCR	1			
B/Austria/1359417/2021-like	9			
B/Yamagata lineage	0		0	
B/Yamagata lineage by PCR	0			
B/Phuket/3073/2013-like	0			

Figure 13 shows the influenza virus identifications by type and sub-type and lineage for each week throughout 2024. A(H3N2) and A(H1N1)pdm09 were two main strains cocirculating throughout the season.

Figure 13. Total influenza A and B viruses by week specimen taken, 2024

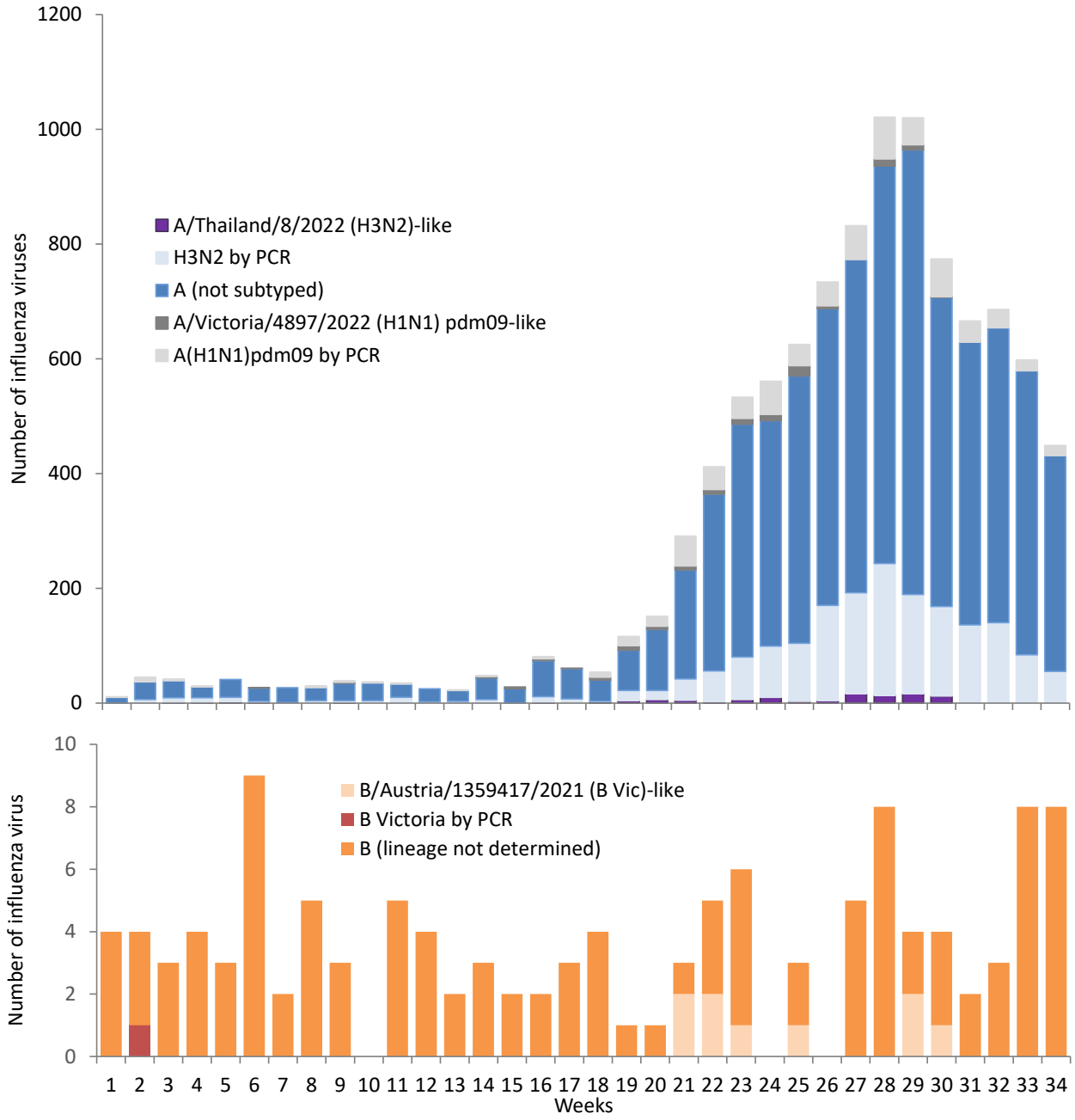
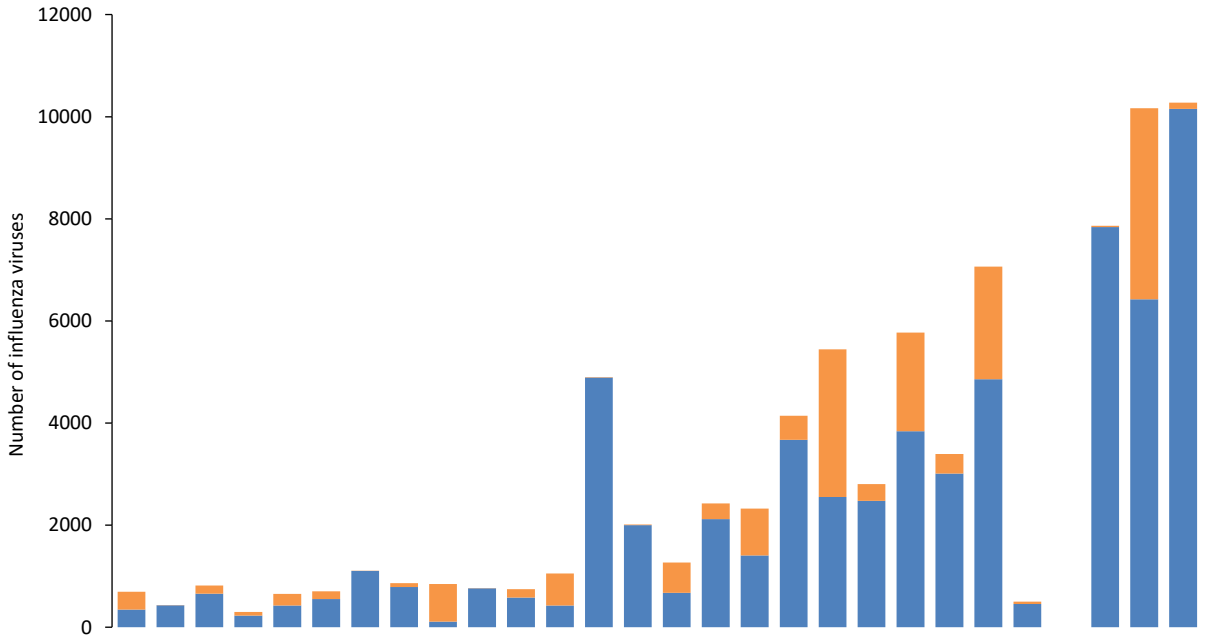


Figure 14 shows the number and percentage of typed influenza viruses from 1997 to 2024. Influenza A is the most frequent predominant influenza type. Of 27 influenza seasons during 1997–2024 (Note: 2021 – no influenza circulation due to COVID-19 elimination strategy), influenza A predominated in 23 seasons 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, 1997–2024

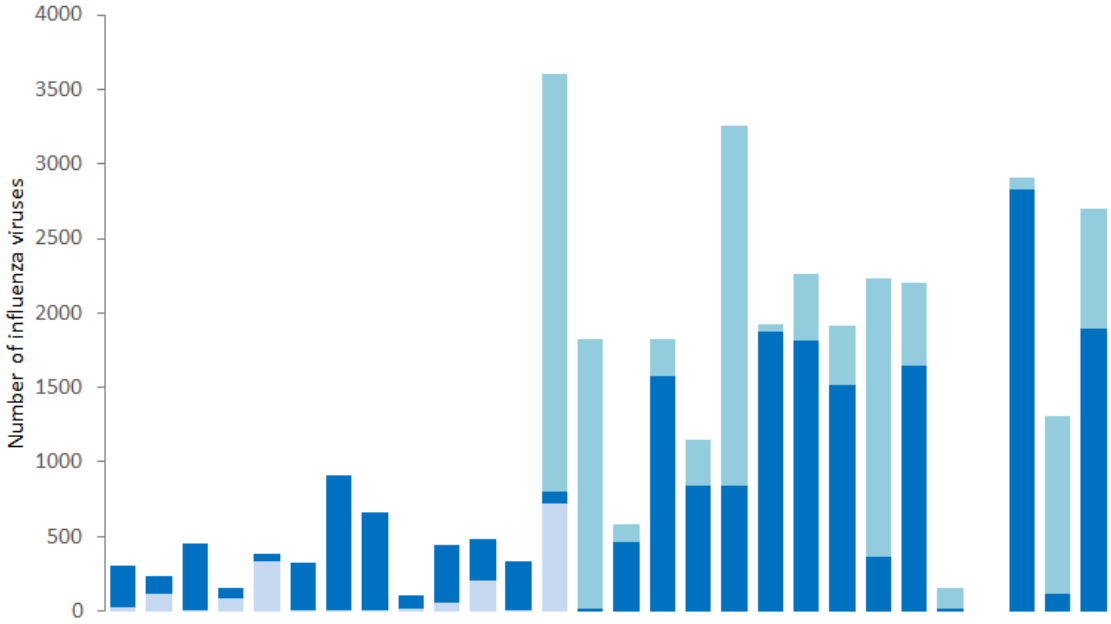


	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
Influenza B (%)	50	0	20	24	35	22	0	9	87	1	22	60	0	0	47	13	40	11	53	12	33	11	31	9	0	0	37	1
Influenza A (%)	50	100	80	76	65	78	100	91	13	99	78	40	100	100	53	87	60	89	47	88	67	89	69	91	0	100	63	99

Figure 15 shows the number and percentage of all sub-typed influenza A viruses from 1997 to 2024 (excluding influenza A not sub-typed). Overall, the patterns of the predominant influenza A subtypes among all sub-typed A viruses during 1997–2023 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 six seasons in 2009, 2010, 2014, 2018, 2020 and 2023.
- 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 1997–2024



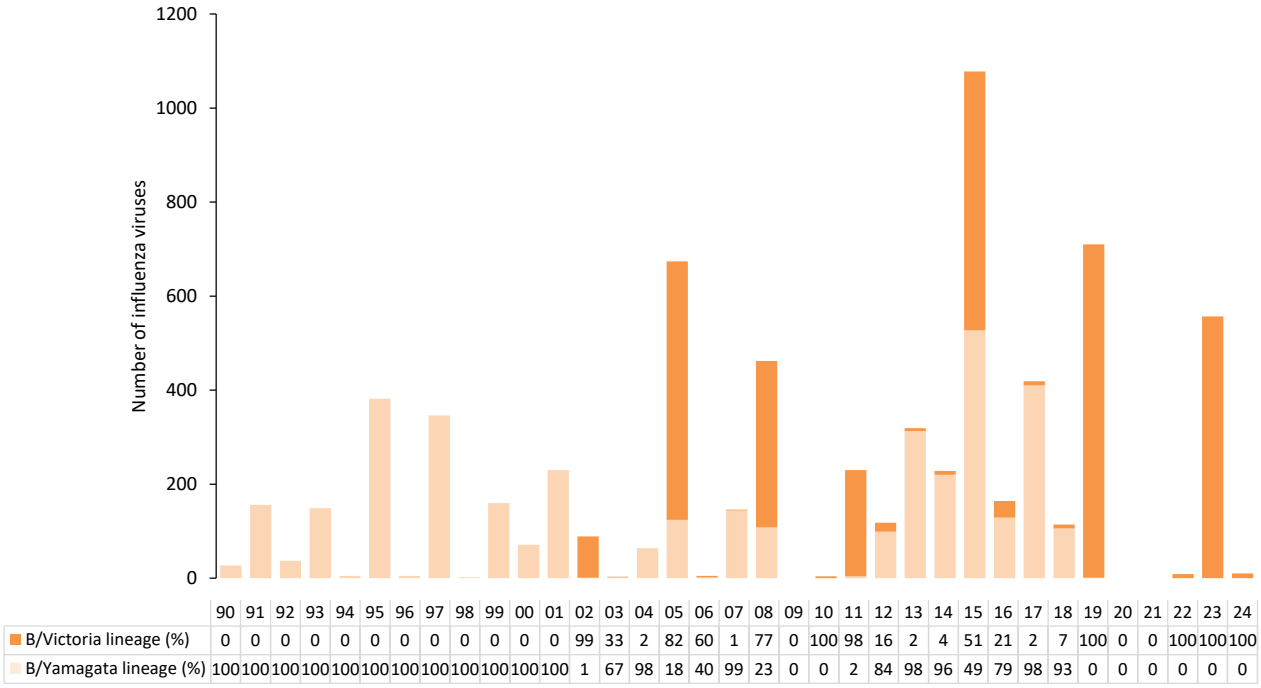
	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A(H1N1)pdm09 %	0	0	0	0	0	0	0	0	0	0	0	0	78	99	20	14	26	74	2	20	21	84	25	90	0	3	91	28
A(H3N2) %	92	52	100	48	13	99	100	100	82	87	58	98	2	1	80	86	74	26	98	80	79	16	75	10	0	97	9	67
Seasonal A(H1N1) %	8	48	0	52	87	1	0	0	18	13	42	2	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 16 shows the number and percentage of all B viruses from 1990 to 2024 (excluding influenza B not lineage-typed). Overall, the patterns of the predominant influenza B among all lineage-typed B viruses during 1990–2024 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, 1990–2024



	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
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
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

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 ESR using ferret antisera supplied by the WHO Collaborating Centre (WHOCC). Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 25 August 2024, a total of 120 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 well inhibited 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 (CDC designations) (Figure 17).

2532 A(H1N1)pdm09 viruses with collection dates between February to September 2024 were characterized at the Melbourne WHOCC from 17 countries. A(H1N1)pdm09 viruses circulated globally and predominated in Southern Africa and Eastern and Southern Asia.

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.1.7, C.1.7.2, C.1.8, C.1.9 and the 5a.2a.1 clade into C.1.1, D, D.1, D.2, D.3, D.4. Viruses from both clades continued to circulate with the C.1.9 subclade predominating in most regions including New Zealand and Australia, except in North America and some countries in Central and South America where the D subclades predominated.

The antigenic characteristics 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 2024 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.

Human serology studies used five serum panels from adults (18 to 64 years) and older adults (≥65 years) who had received egg-based quadrivalent inactivated (standard or adjuvanted) or cell culture-propagated quadrivalent inactivated vaccines with SH 2024 influenza vaccine formulations. Egg-based vaccines 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. Cell culture-propagated vaccines contained A/Wisconsin/67/2022 (H1N1)pdm09-like, A/Massachusetts/18/2022 (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 and 5a.2a.1 were analysed in HI 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 not significantly reduced for most recently circulating viruses.

In summary, the vast majority of the A(H1N1)pdm09 viruses collected since February 2024 that were genetically characterized belonged to the 5a.2a and 5a.2a.1 clades and have further diversified. Post-infection ferret antisera raised against the SH 2024 and NH 2024-25 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 5a.2a and 5a.2a.1 viruses well. Post-vaccination GMTs were not significantly reduced for recently circulating A(H1N1)pdm09 viruses when compared to the responses to cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like vaccine reference viruses.

Based on all of the available data, the WHO consultation recommended to use an egg-propagated A/Victoria/4897/2022 or cell culture-propagated A/Wisconsin/67/2022 (H1N1)pdm09-like strain as the vaccine strains for 2025. The AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2024-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 ESR 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 25 August 2024, a total of 109 influenza A(H3N2) isolates were antigenically typed with hemagglutination inhibition assay using antisera raised against A/Thailand/8/2022 (H3N2)-like virus. 67 (61%) H3N2 isolates were well inhibited by the ferret antisera against the vaccine strain A/Thailand/8/2022 (H3N2)-like, but 42 (39%) were inhibited poorly. Genetically, most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2a.3a.1 (CDC designations) (Figure 18).

2666 A(H3N2) viruses with collection dates between February to September 2024 were characterized at the Melbourne WHOCC from 14 countries. A(H3N2) viruses circulated globally and predominated in the Americas (apart from North America), Northen and Western Africa and Oceania Melanesia and Polynesia.

Phylogenetic analysis of the HA gene of A(H3N2) viruses showed that most viruses circulating in this period belonged to clade 2a.3a.1, with only small numbers of 2a.3a viruses detected. Further diversification within clade 2a.3a.1 HA genes into subclades (J.1-J.4) has occurred with viruses expressing HA N122D and K276E substitutions (J.2) predominating globally, including New Zealand and Australia. Viruses with I25V and V347M HA substitutions (J.1) co-circulated at lower levels in many countries except in a few countries in Asia and Africa where it predominated. Some countries in west Africa also had circulation of viruses in HA subclades 2a.3a (G.1.3.1) and 2a.3a.1 (J.4).

Generally, post-infection ferret antisera raised against cell culture-propagated A/Massachusetts/18/2022- like viruses and egg-propagated A/Thailand/8/2022-like viruses (clade 2a.3a.1), representing the vaccine viruses for the SH 2024 and NH 2024-25 influenza seasons, recognized many recent clade 2a.3a.1 viruses well, but reduced reactivity was seen for some viruses within the J.2 subclade with either S145N, N158K or K189R HA substitutions or combinations of these substitutions. J.2 viruses with S145N were more frequently detected while those with N158K or K189R were rarely detected. Reduced reactivity was also seen with viruses in the J.4 subclade with K189R substitutions. Ferret antisera raised against J.2 subclade viruses with the S145N substitutions (e.g., cell-propagated A/District of Columbia/27/2023 and egg- propagated A/Croatia/10136RV/2023 reference viruses) recognized most circulating viruses well.

Human serology studies were conducted using the serum panels as described above by HI and virus neutralization (VN) assays with recent circulating A(H3N2) viruses with HA genes from 2a.3a.1 (subclades J, J.1, J.2 and J.4) and 2a.3a (G.1.3.1). When compared to titres against cell-propagated A/Massachusetts/18/2022-like vaccine reference viruses, post-vaccination HI GMTs or VN GMTs against many recent J.1 and J.2 viruses were significantly reduced in most serum panels.

In summary, the majority of A(H3N2) viruses collected since February 2024 had HA genes derived from 2a.3a.1 subclade J.2 and have continued to diversify. Post-infection ferret antisera raised against recent J.2 viruses (including those with HA S145N substitution represented by A/District of Columbia/27/2023 and A/Croatia/10136RV/2023) showed improved recognition of

recently circulating viruses compared to SH 2024 and NH 2024-25 A(H3N2) vaccine viruses (cell culture-propagated A/Massachusetts/18/2022 and egg-propagated A/Thailand/8/2022). Human serology assays showed that post-vaccination GMTs against A(H3N2) viruses with HA genes representing J.1 and J.2 subclades were significantly reduced in most serum panels compared to titres against cell culture-propagated A/Massachusetts/18/2022-like vaccine reference viruses.

Based on all available data, the WHO Consultative Group recommended to use an egg-propagated A/Croatia/10136RV/2023 (H3N2)-like strain or cell culture-propagated A/District of Columbia/27/2023 (H3N2)-like strain as the vaccine strains for 2025. AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2024-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 ESR 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 25 August 2024, a total of 9 influenza B/Victoria-lineage isolates were antigenically typed with hemagglutination inhibition assay using ferret antisera raised against B/Austria/1359417/2021-like virus. All B/Victoria-lineage isolates were inhibited by the antisera against the vaccine strain B/Austria/1359417/2021. Genetically, no influenza B viruses available for genotyping.

258 influenza B viruses with collection dates between February to September 2024 were characterized at the Melbourne WHOCC from 12 countries. Globally, influenza B viruses were detected in all WHO regions and all of those characterized 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.

Phylogenetic analysis of the HA gene of B/Victoria lineage viruses during this period showed that they all 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.

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 2024 and NH 2024-25 influenza seasons, recognized most viruses including those with additional HA substitutions within the C.5.1, C.5.6 and C.5.7 subclades.

Human serology studies were conducted usingthe serum panels described above, post-vaccination HI GMTs against recent B/Victoria lineage viruses across the genetic diversity of clade 3a.2 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021-like vaccine reference viruses. Serology studies were not performed for the B/Yamagata lineage virus, except for a USA population immunity study performed by CDC which showed good levels of seropositivity against B/Phuket/3073/2013, which is the vaccine virus in current quadrivalent vaccines.

In summary, all circulating influenza B viruses characterized since February 2024 were of the B/Victoria/2/87 lineage. All recent viruses expressed HA genes belonging to clade 3a.2. Circulating viruses were recognized well by post-infection ferret antisera raised against SH 2024 and NH 2024-25 B/Victoria lineage vaccine viruses (cell culture- and egg-propagated B/Austria/1359417/2021). 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.

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 2025. AIVC accepted this recommendation.

(*Abridged from WHO website: sep-2024-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

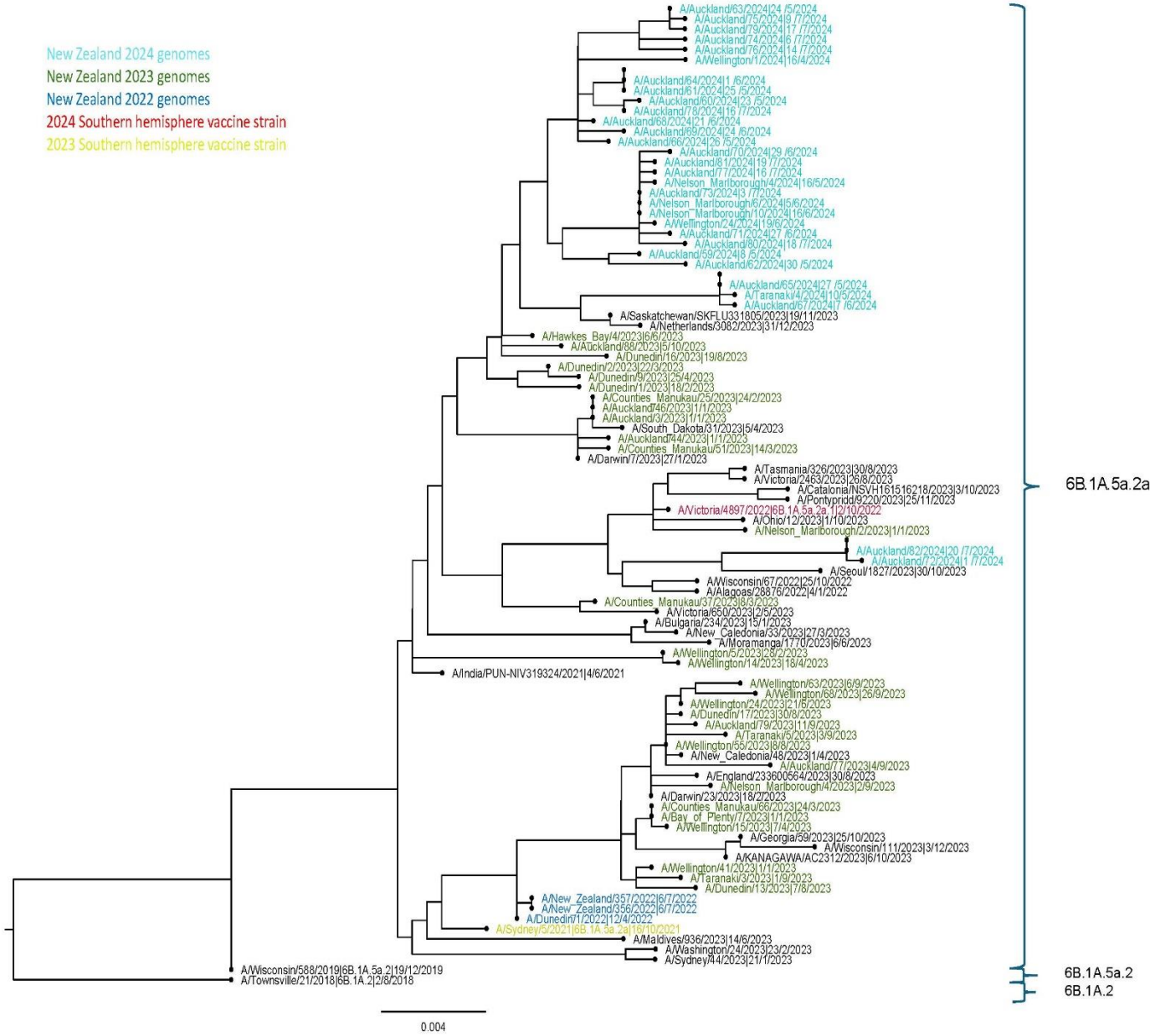
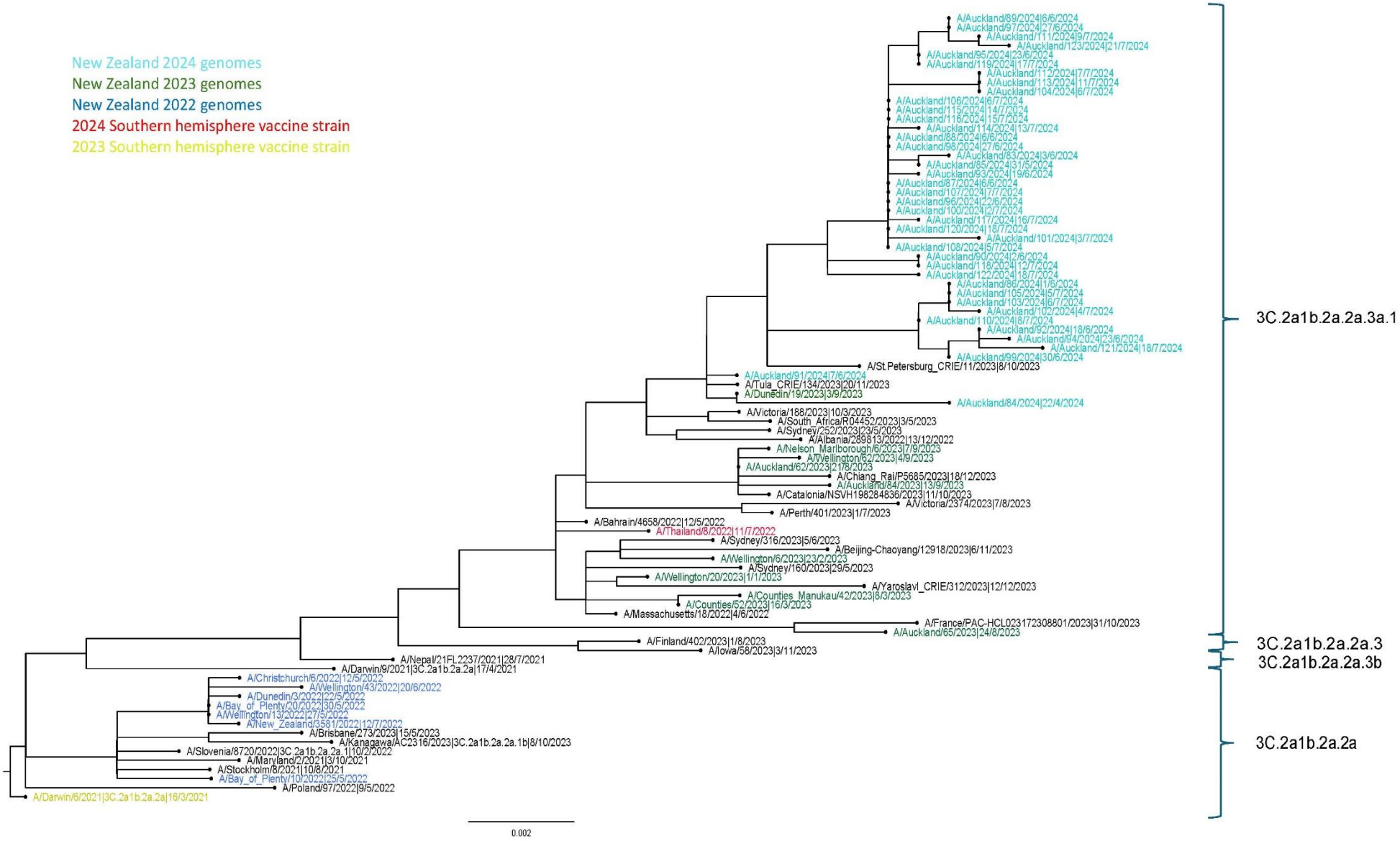


Figure 18. Phylogenetic relationships among influenza A(H3N2) virus haemagglutinin gene



4.3 ANTIVIRAL RESISTANCE

The WHO National Influenza Centre at ESR employed a phenotypic method (fluorometric neuraminidase inhibition assay) for the surveillance of anti-viral drug resistance in influenza viruses. In addition, NIC at ESR 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 2024, fluorometric neuraminidase inhibition assay was used to test 228 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, 2019–2024^

Influenza	NA inhibition to Oseltamivir	No. of Influenza Viruses					
		2019	2020	2021	2022	2023	2024
A(H1N1)pdm09	Normal	20	5	1	16	360	112
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	75	-	3	442	54	107
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	226	-	2	2	280	9
	Reduced	1	-	-	-	1	-
	Highly reduced	-	-	-	-	-	-

Table 8. Antiviral susceptibility to zanamivir for influenza viruses, 2019–2024^

Influenza	NA inhibition to Zanamivir	No. of Influenza Viruses					
		2019	2020	2021	2022	2023	2024
A(H1N1)pdm09	Normal	22	5	1	15	361	112
	Reduced	1	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	75	-	3	442	54	107
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	228	-	2	2	279	9
	Reduced	1	-	-	-	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 VE, we estimated the effectiveness of seasonal inactivated influenza vaccine in preventing laboratory-confirmed influenza among patients hospitalised with severe acute respiratory infections (SARI), 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 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 ARI cases (Table 9), the estimated crude vaccine effectiveness (VE) was 61% (95% CI: 48.6, 70.4). For influenza-confirmed SARI cases, the estimated crude vaccine effectiveness (VE) was 17.4% (95% CI: 0.6, 31.3).

Table 9. Estimated influenza vaccine effectiveness against influenza-associated ARI in community participants and influenza-associated SARI in hospitalized patients, by participant age group and by influenza virus type and subtype in New Zealand, 2024 influenza season

Age and Virus	Influenza Positive		Influenza Negative		Crude VE (%)
	Vaccinated-Yes	Vaccinated-No	Vaccinated-Yes	Vaccinated-No	VE% (95%CI)
WellKiwis cohort					
All ages	92	216	684	627	61.0 (48.6, 70.4)
0-17 years	29	142	214	401	61.7 (40.3, 76.1)
18-64 years	60	74	423	215	58.8 (38.8, 72.3)
65+ years	3	0	46	5	NA
H1	27	63	722	733	56.5 (29.7, 73.7)
0-17 years	6	38	228	480	66.8 (19.1, 88.7)
18-64 years	20	25	445	242	56.5 (16.5, 77.6)
65+ years	1	0	48	5	NA
H3	38	106	711	690	65.2 (48.3, 77.0)
0-17 years	14	79	220	439	64.6 (35.3, 81.9)
18-64 years	22	27	443	240	55.9 (17.5, 76.6)
65+ years	2	0	47	5	NA
SARI					
All ages	200	574	812	1925	17.4 (0.6, 31.3)
0-18 years	4	200	118	1008	82.9 (54.3, 95.5)
19-64 years	44	225	157	464	42.2 (15.4, 61.1)
65+ years	152	149	536	451	14.2 (-12.1, 34.3)
H1	31	94	860	2082	20.2 (-22.0, 49.0)
0-18 years	0	45	120	1080	100.0 (23.0, 100.0)
19-64 years	8	33	175	515	28.7 (-61.4, 72.1)
65+ years	23	16	564	485	NA
H3	48	151	843	2025	23.6 (-7.5, 46.5)
0-18 years	2	66	118	1059	72.8 (-4.7, 96.8)
19-64 years	18	51	165	497	NA
65+ years	28	34	559	467	31.2 (-18.8, 60.4)

N/A: not applicable as numbers too low to reach any significance; CI: Confidence interval; SARI: severe acute respiratory infections; ARI: acute respiratory illness.

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