Science for Communities
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RECOMMENDATION FOR SEASONAL INFLUENZA VACCINE COMPOSITION FOR NEW ZEALAND FOR 2024

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1. RECOMMENDATION

The Australian Influenza Vaccine Committee (AIVC) met with a New Zealand representative in Canberra on 5 October 2022 to consult on the influenza vaccine composition for 2023 for New Zealand, Australia and South Africa (Table 1).

Egg-based quadrivalent influenza vaccines:

- an A/Victoria/4897/2022 (H1N1)pdm09-like virus;
- an A/Thailand/8/2022 (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/Massachusetts/18/2022 (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 recommendation for quadrivalent influenza vaccines for 2024 southern hemisphere season includes the B/Yamagata lineage virus although in the absence of confirmed detection of this virus circulating, WHO Influenza vaccine composition advisory committee recommended that continued inclusion of this antigen is no longer warranted. Further, the WHO committee, highlighted that every effort should be made to exclude this component from vaccines 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*	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/8060/201 7	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/97152 93/2013	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/3/2006	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 2023, influenza activity in New Zealand is described at a low-to-moderate level. Overall impact on healthcare use in hospitals was low 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 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 2023. Influenza–associated SARI hospitalization in 2023 was low to moderate. 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) and influenza-associated ARI were both lower than 2022, and higher than 2020-2021. The influenza-associated ARI disease burden was higher in children aged 1–19 years compared to other age groups. Influenza–associated ARI were higher in Pacific peoples and Asians than Māori 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 10165 influenza viruses were detected and reported through this system. Of them, influenza A represented 63.2% (6423) and influenza B 36.8% (3742) of all influenza viruses. Among 1861 of subtyped and lineage-typed influenza viruses, 1190 (63.9%) were A(H1N1)pdm09 and 557 (29.9%) were influenza B/Victoria lineage viruses.

WHO National Influenza Centre (NIC) at ESR conducted antigenic/genetic typing: 1) 151 influenza A(H1N1)pdm09 viruses were antigenically closely related to the vaccine strain A/Sydney/5/2021 (H1N1)pdm09. Genetically most of influenza A(H1N1)pdm09 viruses fell into group 5a.2a; 2) 11 influenza A(H3N2) viruses were antigenically closely related to the vaccine strain A/Darwin/6/2021 (H3N2). Genetically most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2. 3) 118 influenza B/Victoria-lineage viruses were antigenically closely related to the vaccine strain B/Austria/1359417/2021. Genetically most of influenza B/Victoria lineage viruses fell into group V1A.3a2.

3. EPIDEMIOLOGY - NEW ZEALAND INFLUENZA SEASON IN 2023

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 influenza-like illness surveillance).

3.1 HOSPITAL-BASED SURVEILLANCE

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

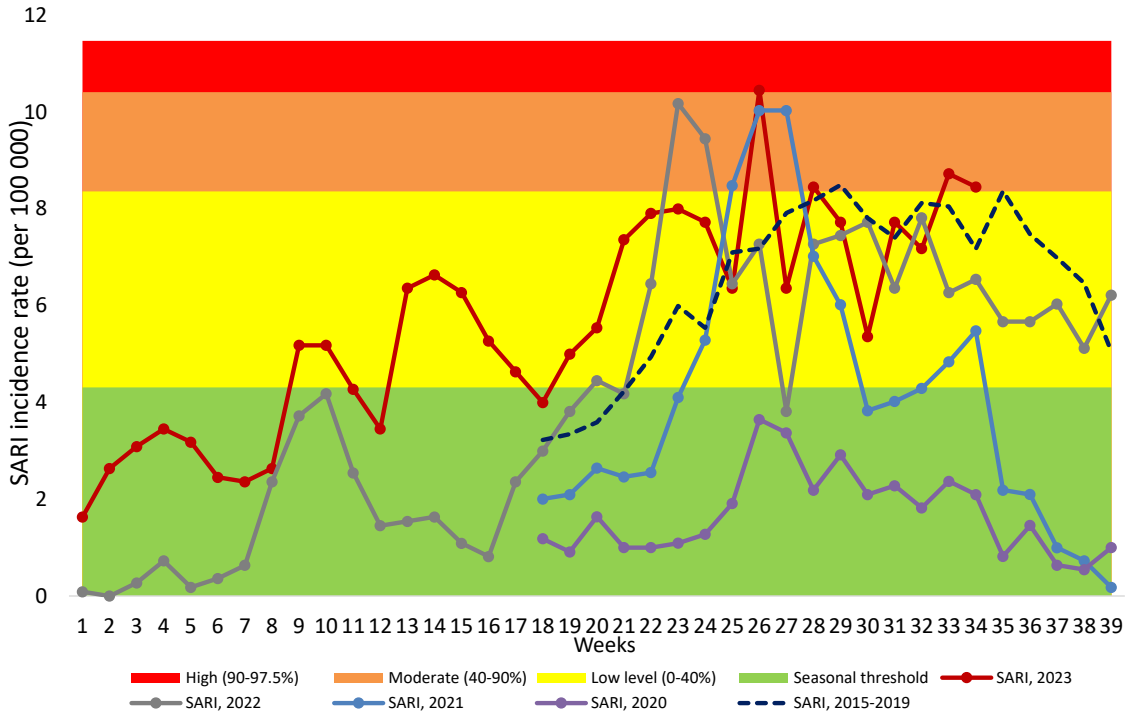
Inpatients with suspected respiratory infections admitted overnight to any of the four hospitals (Auckland City Hospital and the associated Starship Children's Hospital, Middlemore Hospital and the associated Kidz First Children's Hospital) in the Auckland District Health Board (ADHB) and Counties Manukau 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 2013 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.

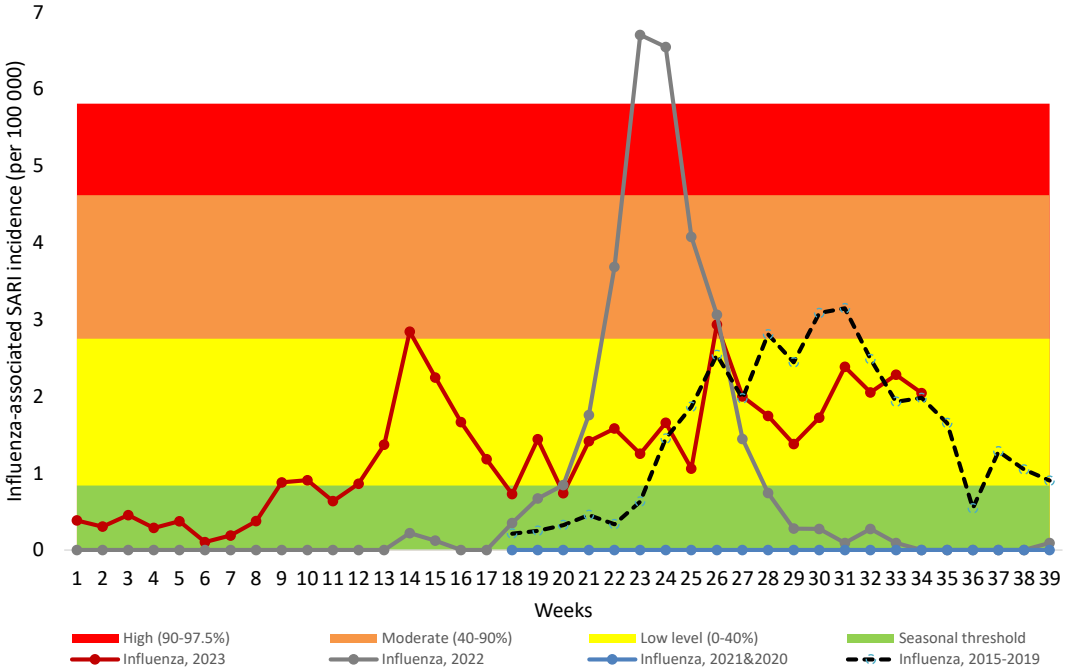
From week 1 (commencing 1 January 2023) through week 34 (ending 27 August 2023), severe acute respiratory illness (SARI) hospitalization rates were below baseline during weeks 1-8, then increased earlier than usual and peaked at week 26 and then declined gradually (Figure 1).

Figure 1. Weekly hospitalisation rates for SARI in 2023 compared to pre-pandemic 2015-2019, during pandemic 2020-2022



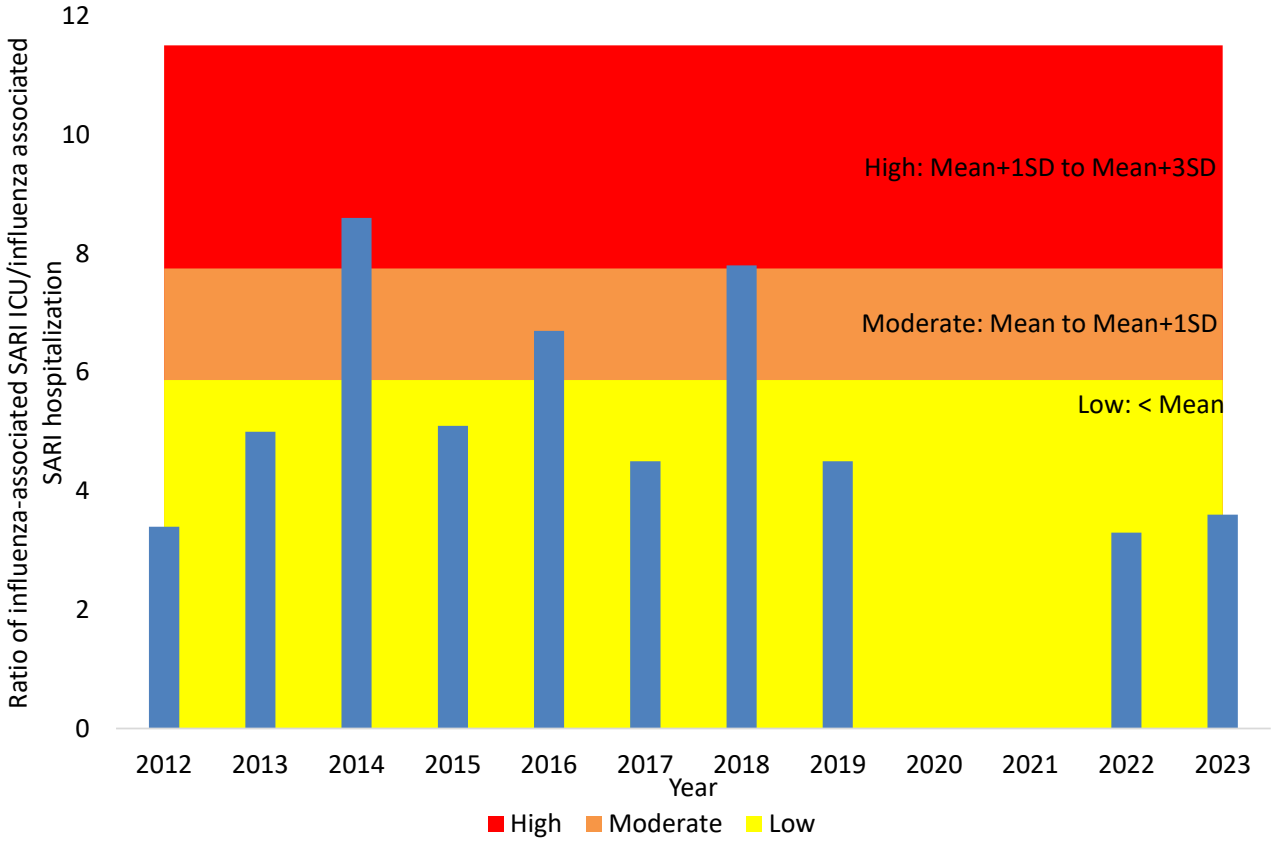
Overall impact on healthcare use is measured by influenza-associated SARI hospitalizations. SARI-associated influenza hospitalizations were at low to moderate level in 2023 (Figure 2).

Figure 2. Influenza-associated SARI hospitalizations in 2023 compared to pre-pandemic 2015-2019, and during pandemic 2020-2022



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 2023 (Figure 3).

Figure 3. Seriousness of disease indicator in 2023 compared to 2012–2022



From 1 January to 27 August 2023, a total of 2207 hospitalized patients with severe acute respiratory illness (SARI) met the SARI case definition. Among these, 2061 were residents of ADHB and CMDHB, giving the SARI incidence rate of 186.8 per 100 000 population (103.6 per 100 000 in 2022 and 78.6 per 100,000 in 2021) (Table 1). Among the SARI cases who were ADHB and CMDHB residents, 467 (22.7%) had positive influenza virus results. This gives a SARI related influenza incidence of 42.3 per 100 000 population, higher than 27.4 per 100 000 in 2022 (Note: it was 0 in 2021 and 37.4 per 100,000 in 2019).

Table 1. Demographic characteristics of SARI cases and related influenza cases, since 1 January 2023

Characteristics	SARI & influenza cases among all hospital patients		SARI & influenza cases among ADHB & CMDHB residents					
	SARI Cases	Influenza positive	SARI cases	SARI incidence (per 100 000)	Influenza Cases (SARI)	Influenza incidence (SARI) (per 100 000)	Influenza Cases (SARI & non SARI)	Influenza incidence (SARI & non SARI) (per 100 000)
Overall	**2207**	**809**	**2061**	**186.8**	**467**	**42.3**	**764**	**69.2**
Age group (years)								
<1	345	71	317	2362.1	43	320.4	68	506.7
1–4	454	132	405	797.6	89	175.3	123	242.2
5–19	188	109	159	74.3	71	33.2	97	45.3
20–34	122	67	117	41.3	36	12.7	65	22.9
35–49	182	100	175	79.7	62	28.2	97	44.2
50–64	312	138	300	160.7	77	41.2	133	71.2
65–79	361	126	352	337.6	62	59.5	119	114.1
>80	243	66	236	752.6	27	86.1	62	197.7
Unknown	0	0	0	0.0	0	0.0	0	0.0
Ethnicity								
Māori	402	152	372	260.7	95	66.6	145	101.6
Pacific peoples	826	341	804	415.9	212	109.7	338	174.9
Asian	247	75	229	64.3	36	10.1	72	20.2
European and Other	650	210	588	142.9	105	25.5	181	44.0
Unknown	82	31	68		19		28	
DHB of Residence								
ADHB	802	275	802	161.4	167	32.6	275	55.3
CMDHB	1259	489	1259	207.6	300	49.5	489	80.6
Other	146	45	0					
Sex								
Female	1058	434	996	180.0	245	44.3	408	73.7
Male	1140	373	1064	193.4	221	40.2	355	64.5
Unknown	1	1	1		1		1	

From 1 January to 27 August 2023, 2118 SARI specimens have been tested and 487 (23%) were positive for influenza viruses (Table 2). Of the 117 specimens collected from ICU admitted patients with acute respiratory illness (SARI and non-SARI), 25 (21.4%) were positive for influenza viruses. Of the 72 specimens collected from fatal cases with acute respiratory illness (SARI and non-SARI), 4 were positive for influenza A viruses. Influenza A(H1N1)pdm09 was the predominant strain among typed and subtyped viruses.

Additionally, 2220 SARI specimens were tested for non-influenza respiratory viruses (Table 2).

Table 2. Influenza and non-influenza respiratory viruses among SARI cases, 2023

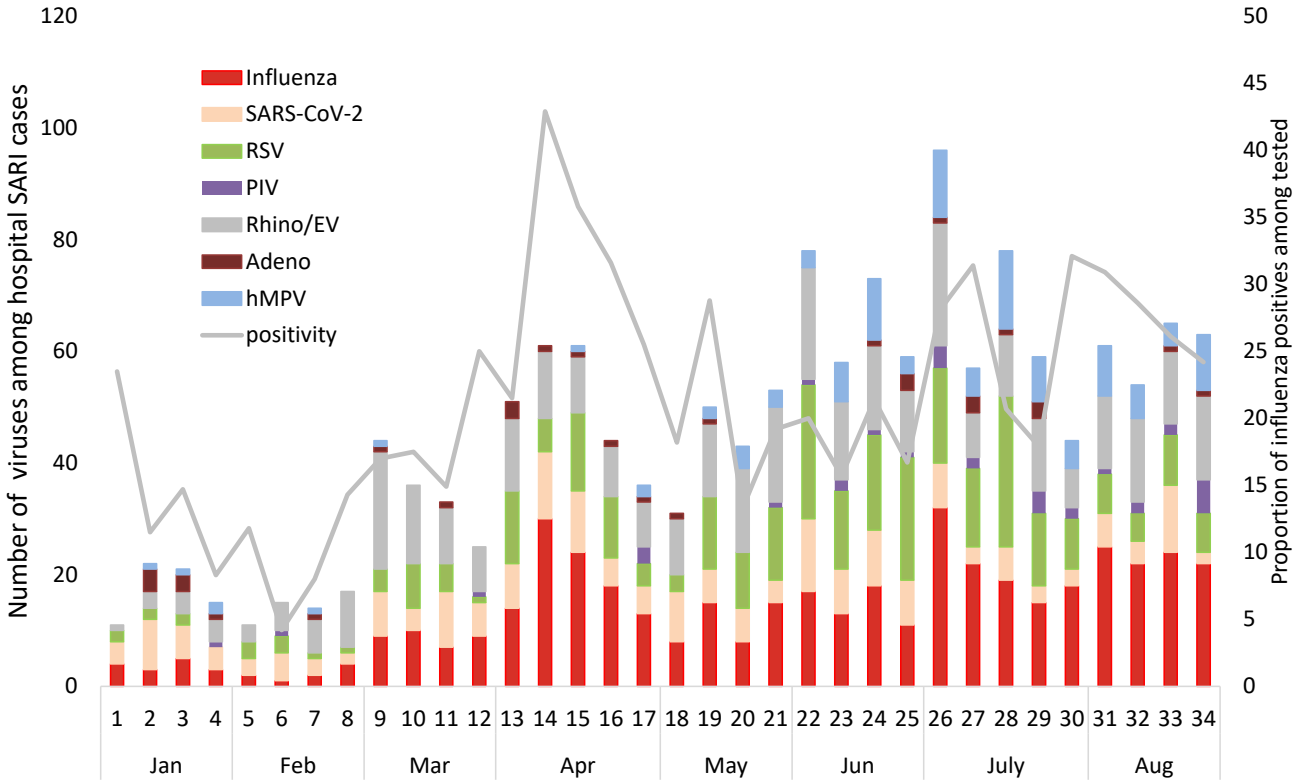
Influenza viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2118	117	72
No. of positive specimens (%)[1]	487 (23.0)	25 (21.4)	4 (5.6)
Influenza A	343	12	4
A (not subtyped)	168	1	1
A(H1N1)pdm09	165	10	2
A(H1N1)pdm09 by PCR			0
A/Victoria/2570/2019 (H1N1)pdm09 - like			0
A(H3N2)	10	1	1
A(H3N2) by PCR			0
A/Darwin/9/2021 (H3N2)-like			0
Influenza B	147	13	0
B (lineage not determined)			0
B/Yamagata lineage			0
B/Yamagata lineage by PCR			0
B/Phuket/3073/2013 - like			0
B/Victoria lineage			0
B/Victoria lineage by PCR			0
B/Austria/1359417/2021-like			0
Influenza and non-influenza co-detection (% +ve)	61 (12.5)	4 (16.0)	0 (-)

Non-influenza respiratory viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	2220	117	72
No. of positive specimens (%)[1]	963 (43.4)	62 (53.0)	20 (27.8)
Respiratory syncytial virus (RSV)	308	14	2
Parainfluenza (PIV)	37	2	0
Rhinovirus (RV)/Enterovirus	389	44	1
Adenovirus (AdV)	35	1	0
Human metapneumovirus (hMPV)	124	8	0
SARS-Cov-2	222	4	18
Single virus detection (% of positives)	820 (85.2)	48 (77.4)	19 (95.0)
Multiple virus detection (% of positives)	143 (14.8)	14 (22.6)	1 (5.0)

[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 4. Influenza was the dominant virus in 2023.

Figure 4. Temporal distribution of the number and proportion of non-influenza viruses from SARI specimens, by type and week[1] in 2023



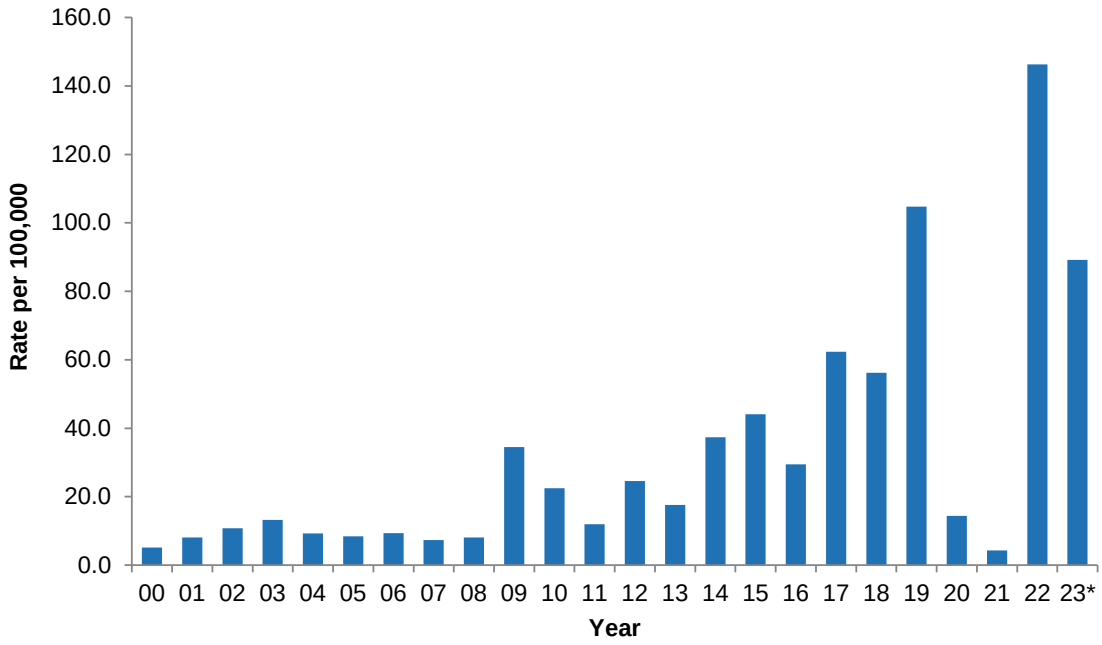
[1]Figures for recent weeks will be underestimates due to time lag in receiving laboratory test results

3.1.2 Ministry of Health data on publicly funded hospital discharges

Hospitalisation data for influenza (ICD-9-CMA-II code 487) for 2023 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 2000–2023. 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 20 August 2023, there were a total of 4569 hospitalisations (89.2 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 2023.

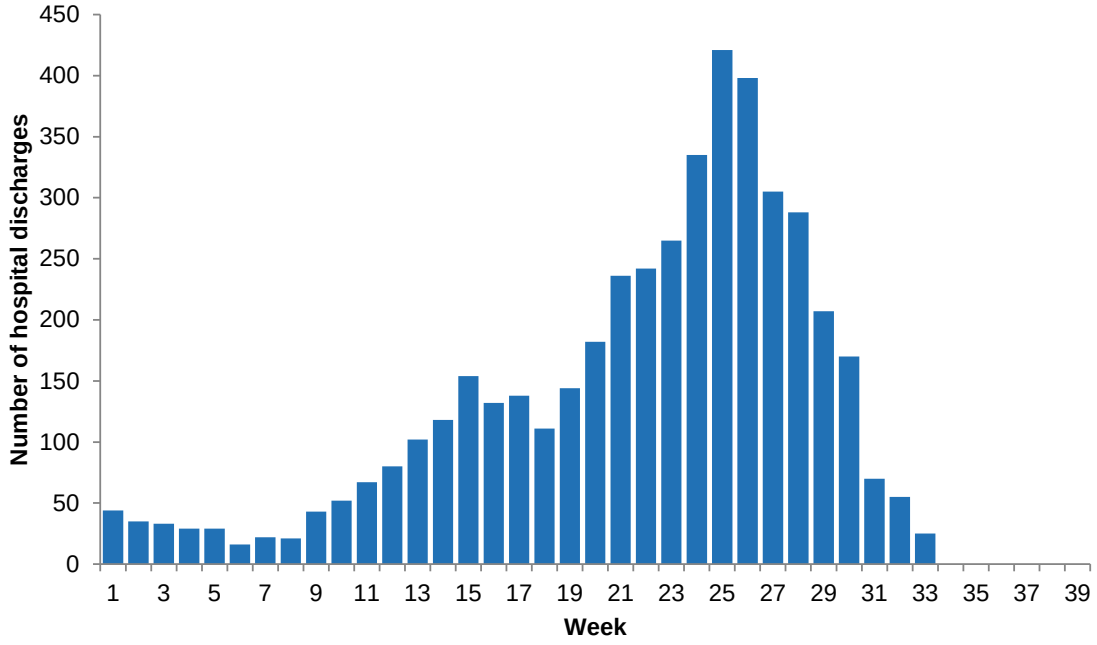
Figure 5. Influenza hospital discharge rates, 2000–2023*



*2023 preliminary data from 1 Jan to 20 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

Figure 6 shows influenza hospitalisations by week discharged. The highest number of hospitalisations (421) occurred in week 25 (week ending 24 June 2023).

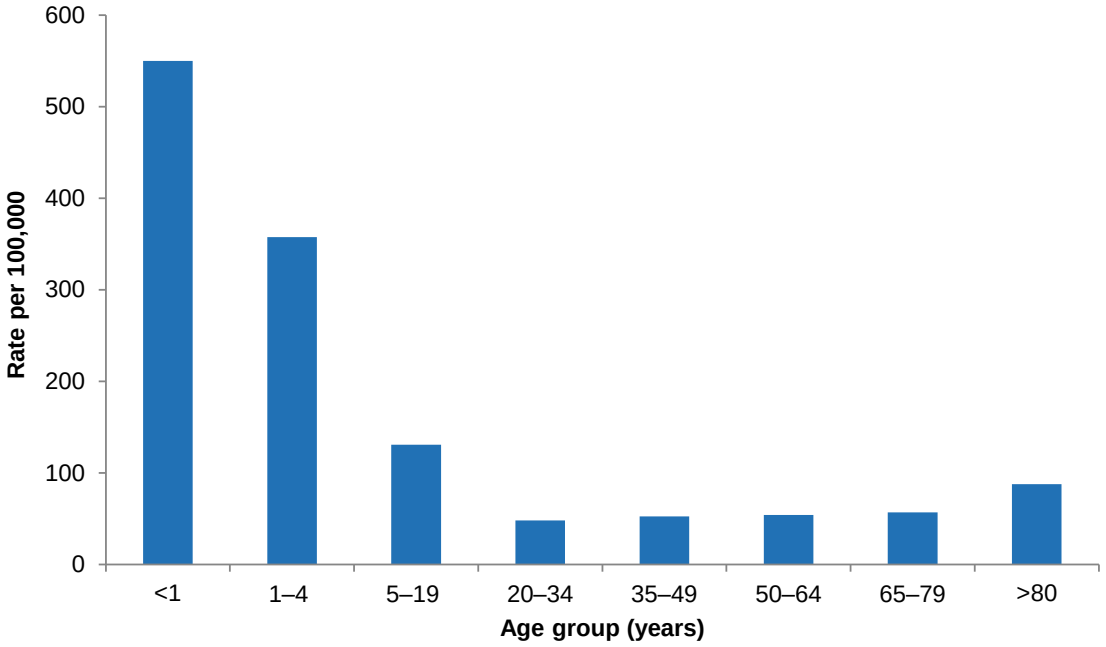
Figure 6. Influenza hospital discharges by week, 2023*



*2023 preliminary data from 1 Jan to 20 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

From 1 January to 20 August, the highest influenza hospitalisation rates were recorded among infants <1 year (550.1 per 100,000) followed by young children aged 1–4 years (357.7 per 100,000) (Figure 7).

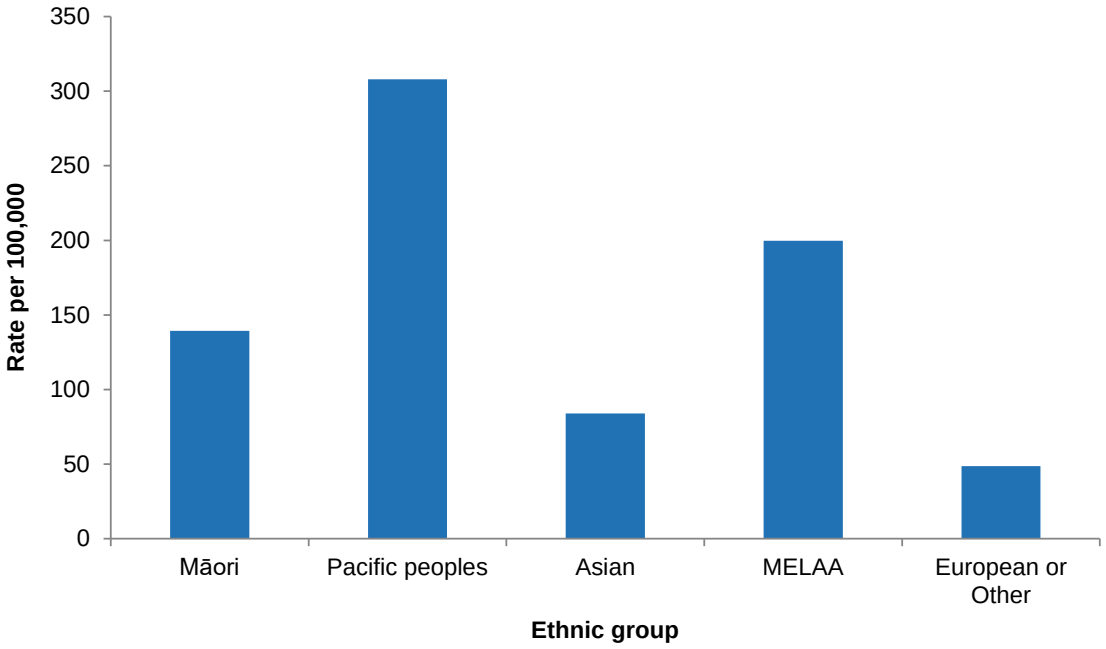
Figure 7. Influenza hospital discharge rates by age group, 2023*



*2023 preliminary data from 1 Jan to 20 Aug only; Source: Ministry of Health, NMDS (Hospital Events)

The ethnic distribution of influenza hospitalisations in 2023 is shown in Figure 8. Pacific peoples had the highest hospitalisation rate (307.9 per 100,000) followed by MELAA (199.7 per 100,000) and Māori 139.3 per 100,000. Asian (84.0 per 100,000) and European or Other (48.7 per 100,000) ethnic groups had the lowest rates of hospitalisations.

Figure 8. Hospital discharge rates by prioritised ethnic group, 2023*



*2023 preliminary data from 1 Jan to 20 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 2023, SHIVERS-II study staff followed these participants (~900) and monitored their ILIs and acute respiratory illness (ARI)s.

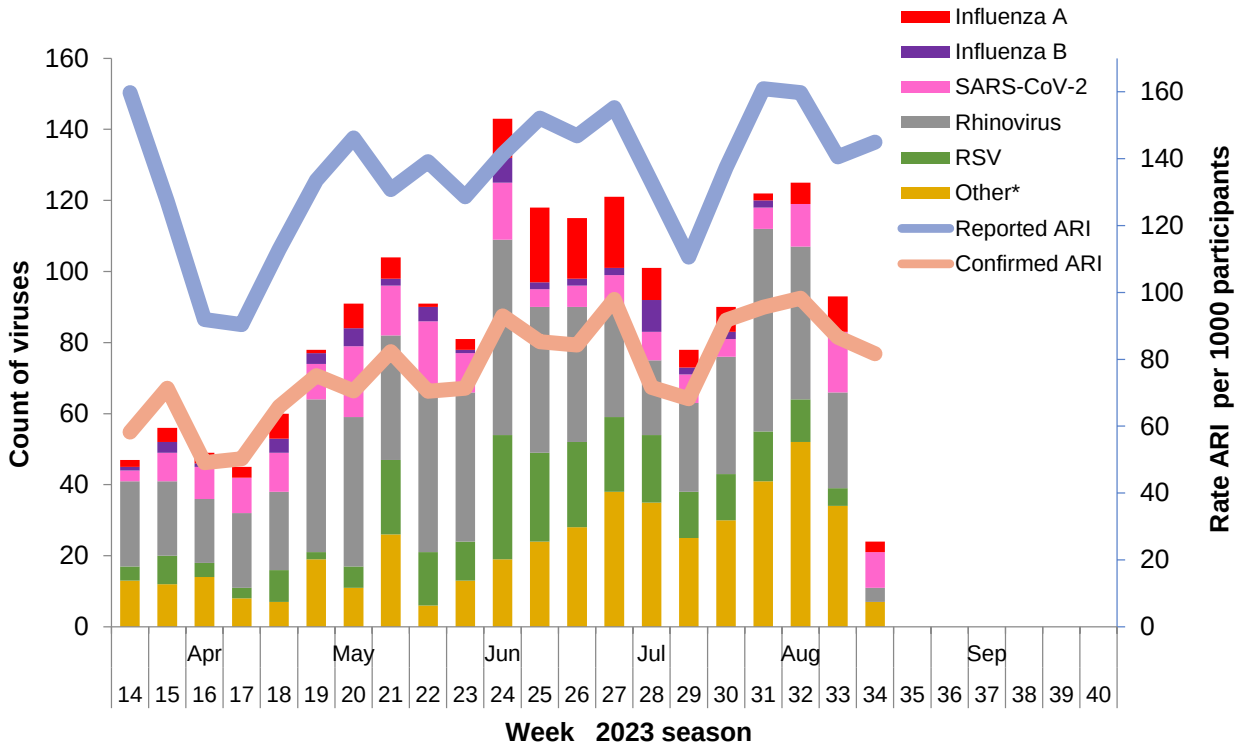
SHIVERS-III (i.e. WellKiwis Infant) is a prospective Wellington infant cohort aiming to recruit 600 infant-mother pairs from Oct 2019-Sept 2022 (200 pairs a year) and follow them until 2026. In 2023, the study staff followed up ~700 infants and monitored their ILIs and ARIs.

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 2023, the study staff followed up ~1800 household members and monitored their ILIs and ARIs.

During 3-April to 27-August 2023, 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.

Figure 9 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 2023.

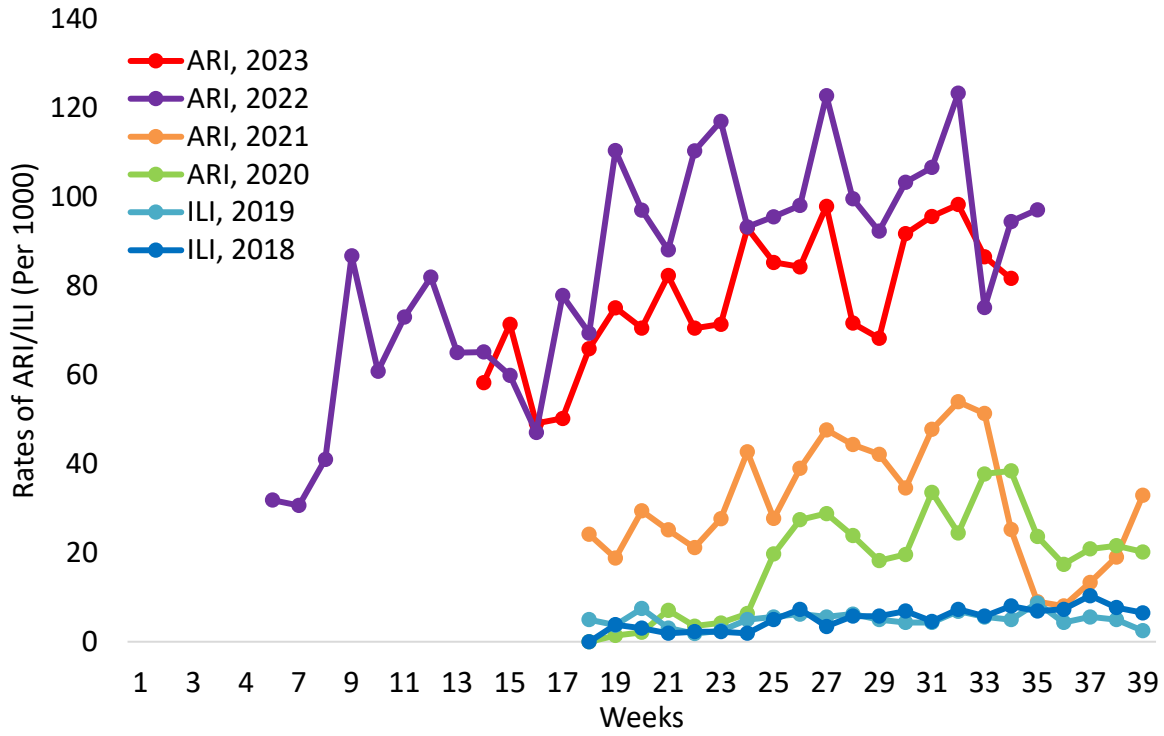
Figure 9. Weekly incidence rate of acute respiratory illness and associated viruses in 2023



*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 ILI rates - the blue line is the weekly rate of ILI reported by participants (per 1000), and the orange line the rate of nurse-confirmed ILI meeting the case definition. National Level 4 lockdown occurred 17-31 August 2021.

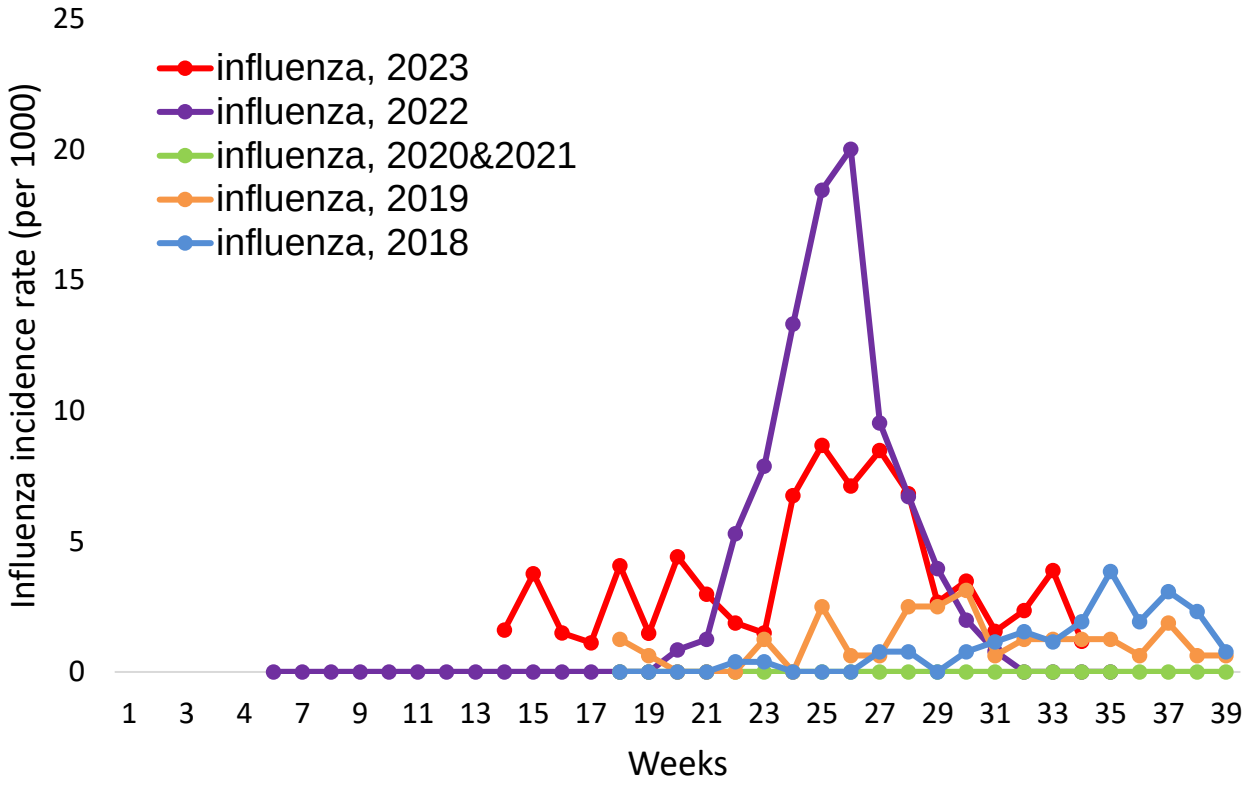
The ARI rates in 2023 was lower than 2022, but much higher than the previous years of 2021 and 2020 (Figure 10).

Figure 10. Weekly ARI/ILI incidence rates in 2023, compared to 2018-2022



Virus transmissibility which reflects the ease of movements of the influenza virus between individuals and communities. The influenza-associated ARI was lower than 2022, higher than pre-pandemic years in 2019 and 2018 (Figure 11).

Figure 11. Weekly influenza associated ARI rates in 2023, compared to 2018-2022



From 3-April to 27-August 2023, a total of 4170 patients with acute respiratory illness (ARI) were reported, giving the ARI incidence rate of 132.4 per 100 population (138.8 per 100 in 2022) (Table 3). Of the ARI cases, 201 had positive influenza virus results. This gave the influenza-associated ARI incidence of 6.4 per 100, lower than 7.5 per 100 in 2022.

Table 3. Demographic characteristics of ARI cases and related influenza cases, during 3-Apr to 27-Aug 2023

Characteristics	ARI cases among WellKiwis participants		Influenza cases among WellKiwis participants	
	ARI Cases	ARI incidence (per 100)	Influenza Cases	Influenza incidence (per 100)
Overall	**4170**	**132.4 (128.5, 136.3)**	**201**	**6.4 (5.5, 7.3)**
Age group (years)				
<1	643	229.6 (213.1, 247.0)	22	7.9 (4.9, 11.9)
1–4	1310	220.2 (209.0, 231.7)	61	10.3 (7.8, 13.2)
5–19	487	114.3 (104.6, 124.6)	55	12.9 (9.7, 16.8)
20–34	506	153.8 (141.1, 167.2)	10	3.0 (1.5, 5.6)
35–49	901	123.3 (115.6, 131.3)	37	5.1 (3.6, 7.0)
50–64	226	42.5 (37.2, 48.3)	13	2.4 (1.3, 4.2)
≥65	97	37.7 (30.7, 46.0)	3	1.2 (0.2, 3.4)
Unknown	0	-	0	-
Ethnicity				
Māori	447	133.8 (122.1, 146.4)	14	4.2 (2.3, 7.0)
Pacific peoples	176	146.7 (126.4, 169.1)	10	8.3 (4.0, 15.3)
Asian	343	129.9 (116.9, 143.9)	29	11.0 (7.4, 15.8)
European and Other	3204	131.7 (127.4, 136.2)	148	6.1 (5.1, 7.1)
Unknown	0	-	0	-
Sex				
Female	2393	133.8 (128.7, 139.1)	116	6.5 (5.4, 7.8)
Male	1769	130.4 (124.5, 136.4)	85	6.3 (5.0, 7.7)
Unknown	8	-	0	-

[1]Proportion of cases tested which were positive for influenza viruses

From 3-Apr to 27-Aug 2023, 3169 respiratory specimens have been tested and 201 (6.3%) were positive for influenza viruses. Of which, 133 A(H1N1) were detected and was the predominant strain. Influenza B (B/Victoria lineage) co-circulated throughout this period (Table 4). Additionally, 3187 specimens were tested for non-influenza respiratory viruses (Table 4).

Table 4 Influenza and Non-influenza respiratory viruses among ILI cases, 3-Apr to 27-Aug

Influenza viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	2246	662	261	3169
No. of positive specimens (%)[1]	148	32	20	201
Influenza A	105	26	17	148
A (not subtyped)	8	2	1	11
A(H1N1)pdm09	95	24	14	133
A(H1N1)pdm09 by PCR	95	24	14	133
A/Sydney/5/2021 (H1N1)pdm09 - like	0	0	0	0
A(H3N2)	2	0	2	4
A(H3N2) by PCR	2	0	2	4
A/Darwin/6/2021 (H3N2)-like	0	0	0	0
Influenza B	43	6	3	53
B (lineage not determined)	1	0	0	2
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	42	6	3	51
B/Victoria lineage by PCR	42	6	3	51
B/Austria/1359417/2021-like virus	0	0	0	0
Influenza and non-influenza co-detection (% +ve)	1	0	0	1

Non-influenza respiratory viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	2264	664	259	3187
No. of positive specimens (%)[1]	888	420	114	1422
Respiratory syncytial virus (RSV)	163	88	13	264
Parainfluenza 1 (PIV1)	19	10	1	30
Parainfluenza 2 (PIV2)	10	2	0	12
Parainfluenza 3 (PIV3)	16	12	0	28
Rhinovirus (RV)	423	214	52	689
Adenovirus (AdV)	95	89	2	186
Human metapneumovirus (hMPV)	70	24	9	103
Enterovirus	48	52	1	101
SARS-CoV-2	153	25	40	218
Single virus detection (% of positives)	785	330	111	1226
Multiple virus detection (% of positives)	103	90	3	196

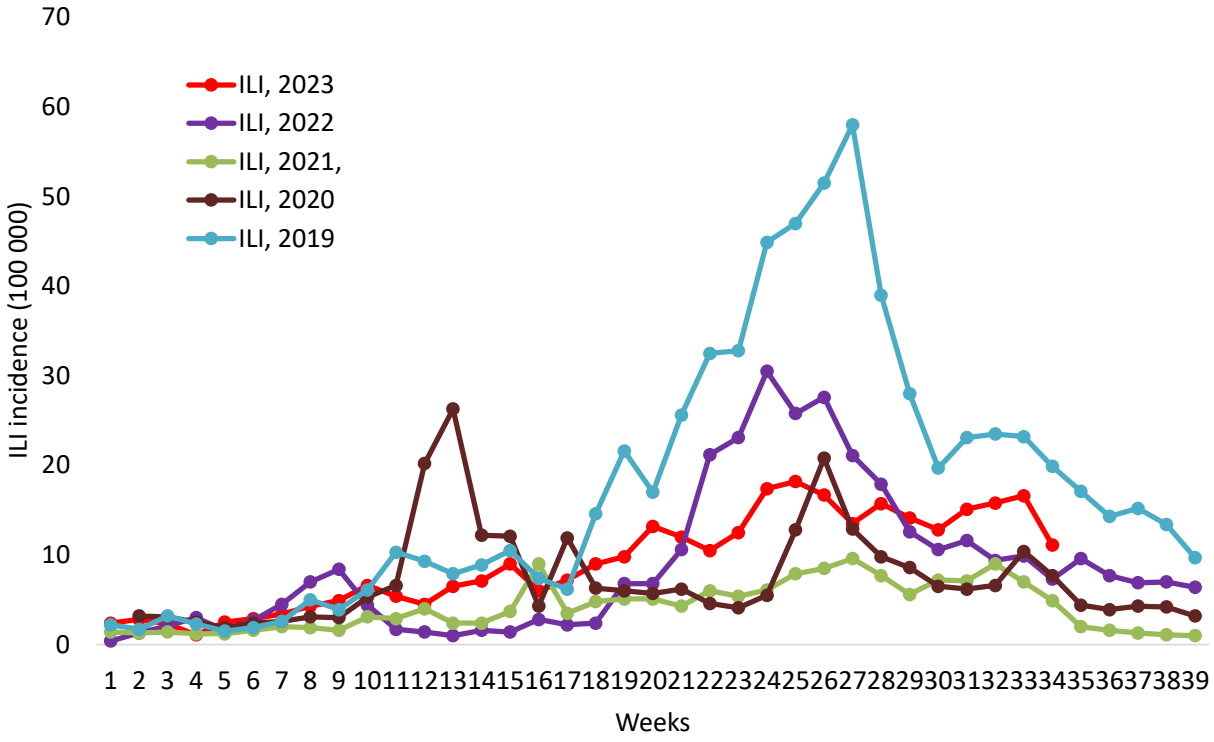
3.2.2 HealthStat sentinel general practice influenza-like illness surveillance

HealthStat is a computer-based routine surveillance system of a nationally representative random sample of approximately 100 general practices that code for influenza-like-illness (ILI). The case definition used for ILI by HealthStat is: “acute URTI, with abrupt onset of 2+ symptoms from chills, fever, headache and myalgia”. This surveillance system monitors the number of people who have primary care (GP) consultations. HealthStat is based on the automated downloads from GP practice management computer systems. This service is provided to ESR by CBG Health Research Ltd. HealthStat GP-based surveillance does not contain a component of the virological surveillance.

Analysis is frequency based with alarms raised by identifying statistical deviations (aberations) from previous counts. The analysis of the ILI count is based on the cumulative summation (CUSUM) algorithm implemented in Early Aberration Reporting System (EARS) application developed by the Centres for Disease Control and Prevention (CDC), Atlanta, United States. EARS has three sensitivity thresholds (high, medium and low). If the daily call count exceeds a threshold a flag is signalled.

Figure 12 below shows the weekly rate of ILI per 100 000 registered population, 2019-2023. The ILI rates in 2023 was lower than 2022. The ILI rate in 2019 (pre-pandemic period) was higher than the rates during 2020-2023 (COVID-19 pandemic periods). It is possible that the pandemic may have interrupted the normal flow and process for sentinel GP-based ILI surveillance which resulted in lower consultations and reporting.

Figure 12. HealthStat ILI consultation rates by week, 2019-2023



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 2023

During 1-Jan to 27-August-2023, a total of 10165 influenza viruses were detected and reported through any surveillance system, with influenza A representing 63.2% (6423/10165) and influenza B 36.8% (3742/10165) of all influenza viruses (Table 5). Among 1861 subtyped and lineage-typed viruses, 63.9% (1190/1861) were A(H1N1)pdm09 viruses, 6.1% (114/1861) were A(H3N2) viruses, and 29.9% (557/1861) were B/Victoria lineage viruses.

Table 5. Influenza virus identifications by type and sub-type and lineage-typed, 2023

Viruses	All viruses		Sub-typed and lineage-typed	
	N.	Col%	N.	%
Influenza virus	**10165**	**100.0**	**1861**	**100.0**
Influenza A	**6423**	**63.2**	**1304**	**100.0**
Influenza A (not sub-typed)	5119	50.4		
Influenza A(H1N1)pdm09	1190	11.7	1190	63.9
A(H1N1)pdm09 by PCR	1116	11.0		
A/Victoria/2570/2019 (H1N1)pdm09-like	74	0.7		
Influenza A(H3N2)	114	1.1	114	6.1
A(H3N2) by PCR	114	1.1		
A/Darwin/6/2021 (H3N2)-like	0	0.0		
Influenza B	**3742**	**36.8**	**557**	29.9
Influenza B (not lineage-typed)	3185	31.3		
B/Victoria lineage	557	5.5	557	
B/Victoria lineage by PCR	517	5.1		
B/Austria/1359417/2021-like	40	0.4		
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 for each week throughout 2023. A(H1N1)pdm09 and influenza B/Victoria were two main strains cocirculating throughout the season.

Figure 13. Total influenza viruses by type and week specimen taken, 2023

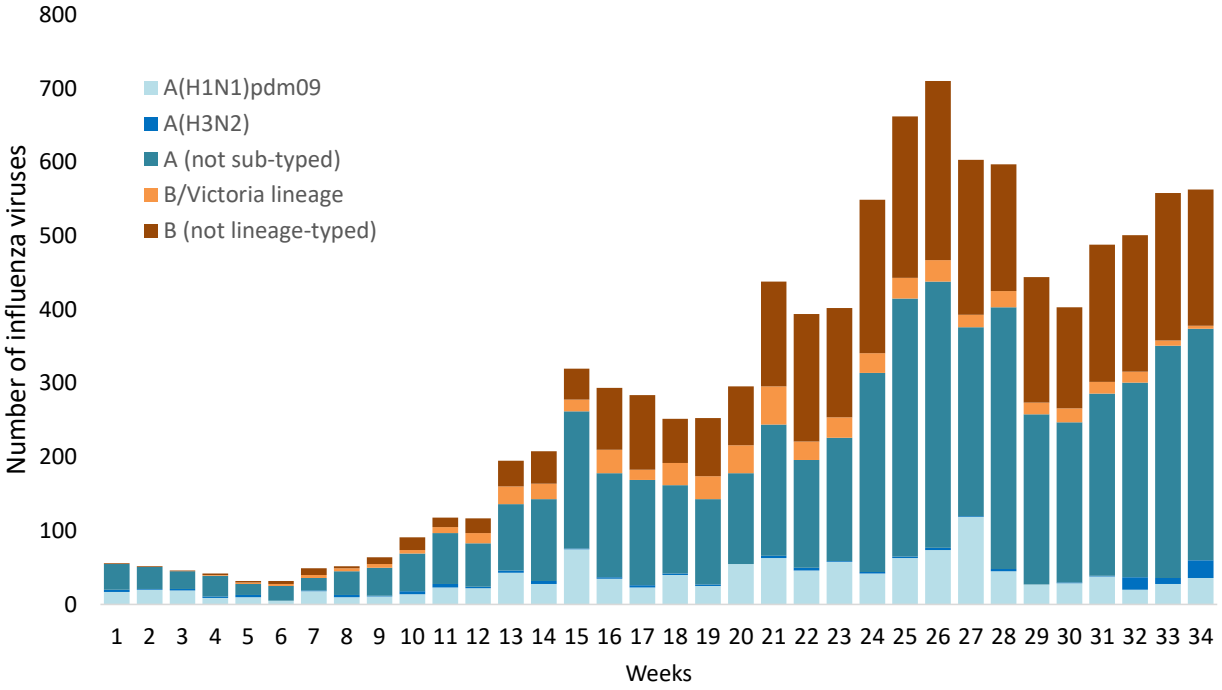


Figure 14 shows the general pattern of influenza virus identifications. Influenza A and B viruses co-circulated throughout the season.

Figure 14. Total influenza A and B viruses by week specimen taken, 2022

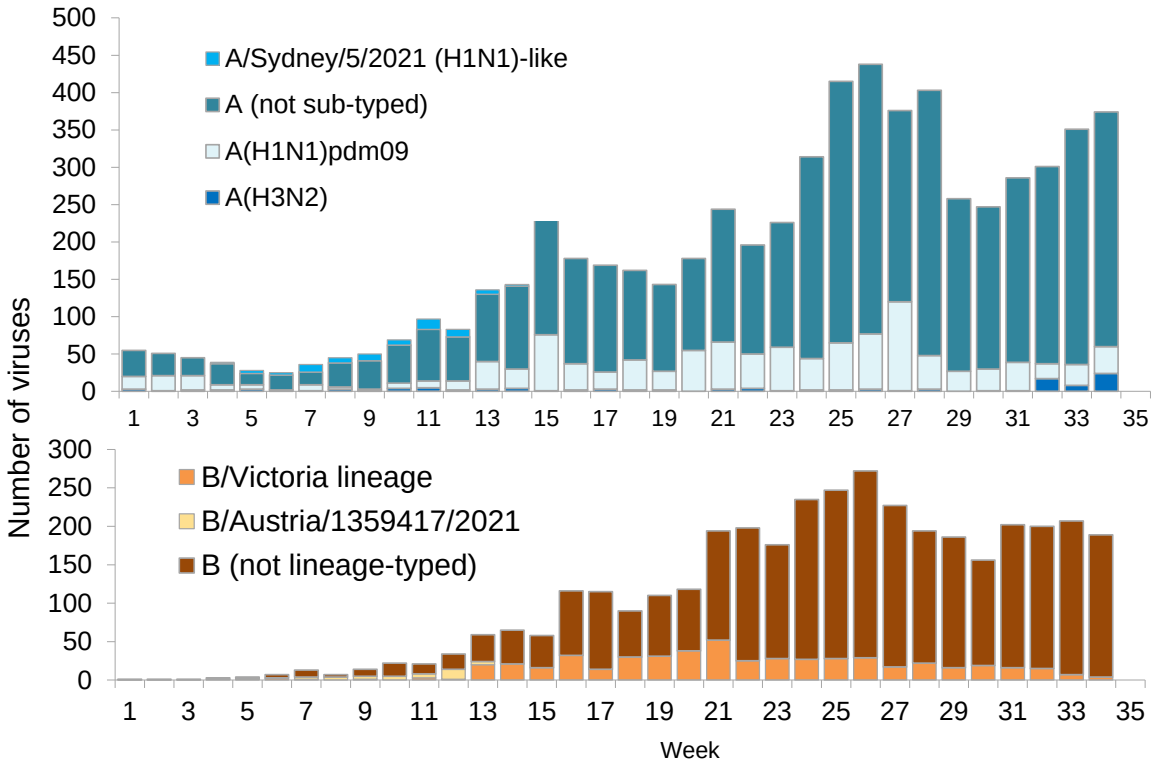
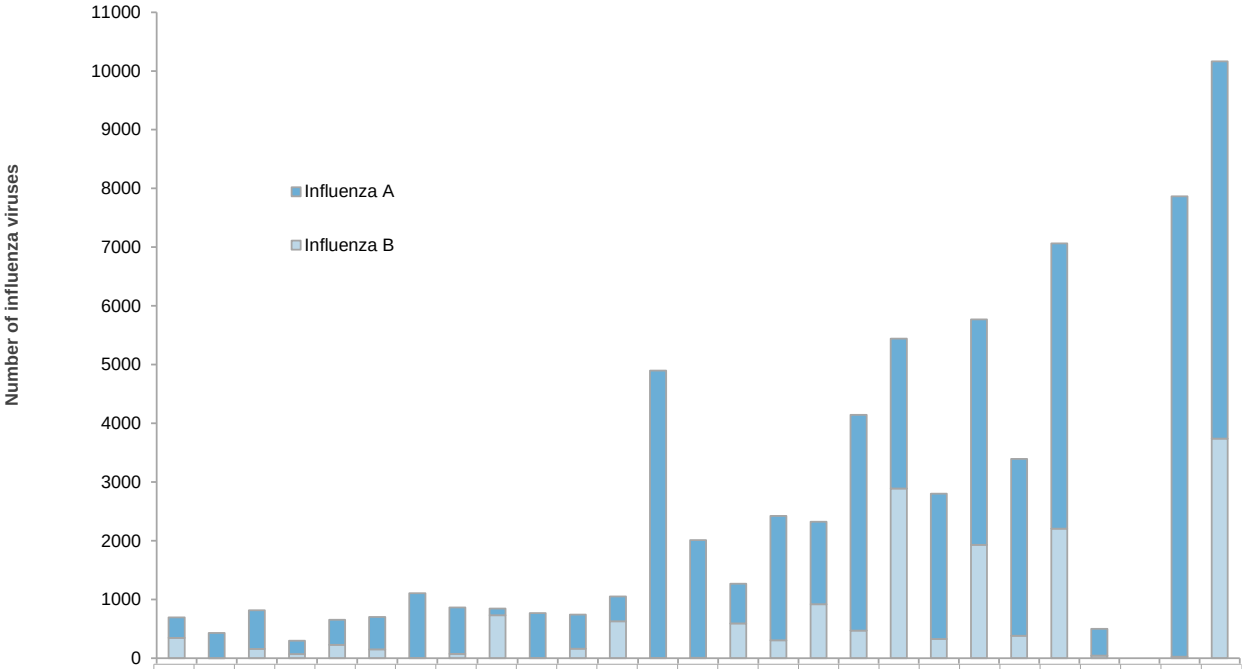


Figure 15 shows the number and percentage of typed influenza viruses from 1997 to 2023. Influenza A is the most frequent predominant influenza type. Of 27 influenza seasons during 1997–2023, influenza A predominated in 24 seasons whereas influenza B only predominated in three seasons (2005, 2008 and 2015). There was one season (1997) with equal proportion of influenza A and B circulation.

Figure 15. Influenza viruses by type, 1997–2023

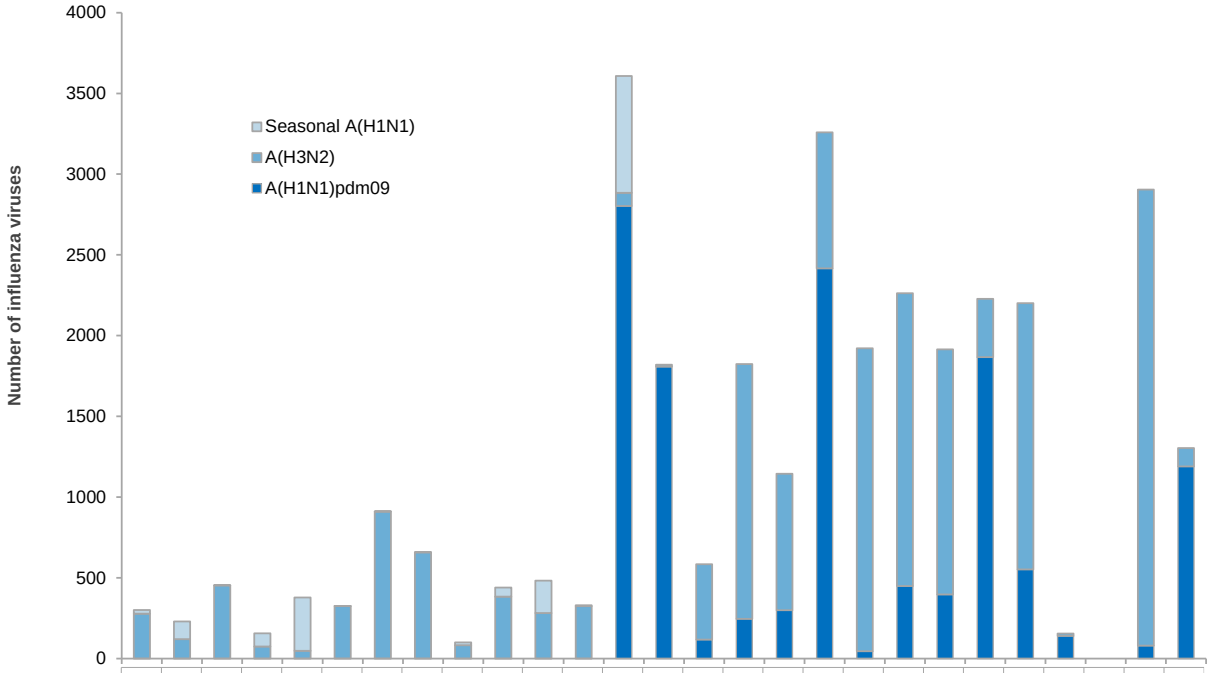


	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Influenza A (%)	50	100	80	76	65	78	100	91	13	99	78	40	100	100	53	87	60	89	47	88	67	89	69	91	0	100	63
Influenza B (%)	50	0	20	24	35	22	0	9	87	1	22	60	0	0	47	13	40	11	53	12	33	11	31	9	0	0	37

Figure 16 shows the number and percentage of all sub-typed influenza A viruses from 1997 to 2023 (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 16 seasons (1997–1999, 2002–2008, 2011–2013, 2015–2017, 2019 and 2022).
- 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 (228 in 2000 and 379 in 2001). It has not been detected in New Zealand since 2010.

Figure 16. Influenza A viruses by subtypes 1997–2023



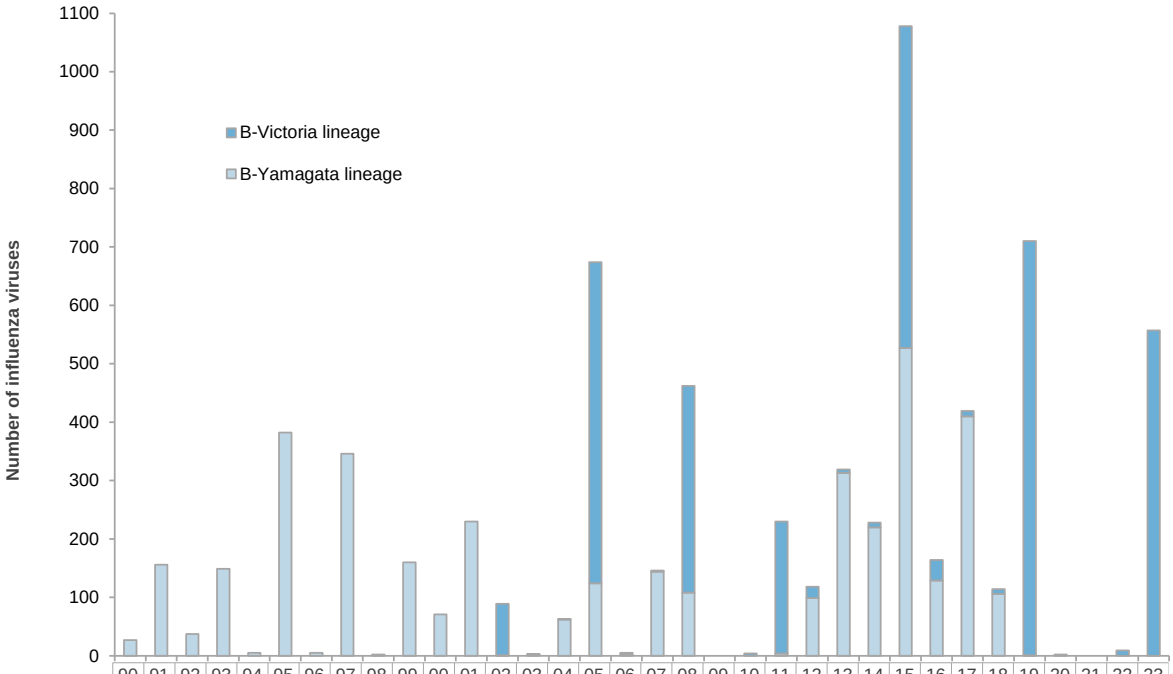
	97	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Seasonal A(H1N1)	8	48	0	52	87	1	0	0	18	13	42	2	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0
A(H3N2)	92	52	100	48	13	99	100	100	82	87	58	98	2	1	80	86	74	26	98	80	79	16	75	10	0	97	8.7
A(H1N1)pdm09	0	0	0	0	0	0	0	0	0	0	0	0	78	99	20	14	26	74	2	20	21	84	25	90	0	3	91.3

Figure 17 shows the number and percentage of all B viruses from 1990 to 2023 (excluding influenza B not lineage-typed). Overall, the patterns of the predominant influenza B among all lineage-typed B viruses during 1990–2023 are described below:

- 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. During 2002-2019, B/Yamagata lineage viruses was the predominant lineage over B/Victoria lineage virus during 2012–2014, and 2016–2018. Since 2019, no B/Yamagata lineage virus has been detected in New Zealand.

- 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 2012-2023, B/Victoria lineage viruses predominated over the B/Yamagata lineage viruses in every four years (2015, 2019 and 2023).

Figure 17. Influenza B viruses by lineages, 1990–2023



	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
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
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	100	0	0	0

4.2 ANTIGENIC TYPING

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 rabbit antisera supplied by the WHO Collaborating Centre (WHOCC) at CDC-Atlanta. Some of these isolates were also sent to WHOCC-Melbourne. During 1 January to 6 September 2023, a total of 74 influenza A(H1N1)pdm09 isolates were antigenically typed using antisera against A/Indiana/02/2020(H1N1)-like virus and 151 typed using A/Sydney/5/2021 (H1N1)-like virus. All of them were antigenically closely related the vaccine strain A/Sydney/5/2021 (H1N1). Genetically, most of influenza A(H1N1)pdm09 viruses fell into group 5a.2a (CDC designations) (Figure 18).

3573 A(H1N1)pdm09 viruses with collection dates between February to September 2023 were characterized at the Melbourne WHOCC from 16 countries. A(H1N1)pdm09 viruses circulated globally and predominated in most geographic regions. The vast majority of haemagglutinin (HA) genes of viruses that were genetically characterized belonged to the 6B.1A.5a.2 clade, with only 1% of HA genes characterized belonging to the 6B.1A.5a.1 clade.

All viruses expressing clade 5a.2 HA genes collected since 1 February 2023 have further diversified into designated subclades: the 5a.2a, with additional HA1 amino acid substitutions K54Q, A186T, Q189E, E224A, R259K and K308R; and the 5a.2a.1 subclade containing viruses expressing HA genes with additional HA1 substitutions P137S, K142R, D260E and T277A (e.g., A/Wisconsin/67/2022). Many of the 5a.2a.1 viruses also have the HA1 substitution T216A. Viruses within subclades 5a.2a and 5a.2a.1 co-circulated, with regional differences in proportions and continued genetic diversification within both subclades. Subclade 5a.2a viruses predominated in Asia, Africa, Europe and Oceania, while subclade 5a.2a.1 viruses predominated in North America and parts of Central and South America.

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 1 February 2023 showed that ferret antisera raised against the Southern Hemisphere (SH) 2023 vaccine viruses (cell culture-propagated A/Sydney/5/2021-like and egg-propagated A/Sydney/5/2021-like 5a.2a viruses) recognized the very small number of 5a.1 viruses poorly; however, viruses in sub-clades 5a.2a and 5a.2a.1 were well recognized by these antisera. Ferret antisera raised against cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022 from the 5a.2a.1 subclade recognized viruses in both 5a.2a and 5a.2a.1 subclades well.

Human serology studies were conducted with human serum panels from the SH 2022 season, using HI and virus neutralization (VN) assays. Compared to the responses of the cell culture-propagated and/or- egg-propagated A(H1N1)pdm09 vaccine viruses, post-vaccination geometric mean titres (GMTs) were not significantly reduced for the majority of 5a.2a viruses. However, post vaccination GMTs were significantly reduced in some serum panels against recent A(H1N1)pdm09 viruses belonging to subclade 5a.2a.1. The reductions were more pronounced when compared to egg-propagated A/Sydney/5/2021 reference virus.

In summary, the vast majority of the A(H1N1)pdm09 viruses collected since 1 February had HA genes belonging to clade 5a.2 (i.e., 6B.1A.5a.2). Subclade 5a.2a viruses were mainly detected in Africa, Asia, Europe and Oceania, while subclade 5a.2a.1 viruses were mainly detected in North America, Central America and South America. Post-infection ferret antisera raised against the SH 2023 A(H1N1)pdm09 vaccine components (cell culture- and egg-propagated A/Sydney/5/2021 (5a.2a)) recognized 5a.2a and 5a.2a.1 viruses well, but recognized 5a.1 viruses poorly. However,

some human serology panels showed reduced post-vaccination GMTs against a number of recently circulating 5a.2a and 5a.2a.1 viruses when compared to titres against cell culture-propagated or egg-propagated A/Sydney/5/2021 (H1N1)pdm09-like vaccine 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 2024. The AIVC accepted this recommendation.

(*Abridged from WHO website:* 202309_recommendation.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 6 September 2023, a total of 11 influenza A(H3N2) isolates were antigenically typed using antisera against A/Darwin/6/2021 (H3N2)-like virus. All H3N2 isolates were antigenically related to the vaccine strain A/Darwin/6/2021 (H3N2). Genetically, most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2 (CDC designations) (Figure 19).

459 A(H3N2) viruses with collection dates between February to September 2022 were characterized at the Melbourne WHOCC from 12 countries. While A(H3N2) viruses circulated globally since 1 February 2023, they were the predominant A virus in only a few geographic regions. Phylogenetic analysis of the HA gene of A(H3N2) viruses showed that the vast majority of viruses circulating in this period belonged to clade 2 (complete classification 3C.2a1b.2a.**2**). Owing to substantial evolution and co-circulation of multiple clade 2 HA groups, subclade designations were developed to better define and track the HA evolution. The various HA subclades were found in different regions globally and viruses with HA genes from multiple subclades co-circulated in several geographic regions in varying proportions.

Antigenic characterisation of A(H3N2) viruses was performed by HI and virus neutralization (VN) assays. Generally, post-infection ferret antisera raised against the SH 2023 vaccine viruses (cell culture-propagated A/Darwin/6/2021-like viruses and egg-propagated A/Darwin/9/2021-like 2a viruses) recognized viruses expressing 2a (including subclades) HA genes well. However, some viruses expressing 2a.3a.1 or 2b HA genes reacted less well with these antisera. Additionally, ferret antisera raised against recent 2b viruses did not recognize some viruses in 2a subclades well. Ferret antisera raised against 2a.3a.1-like viruses (e.g., cell-propagated A/Massachusetts/18/2022 and egg-propagated A/Thailand/8/2022) recognized most circulating viruses well.

Human serology studies were conducted with human serum panels from the SH 2022 season, using HI and virus neutralization (VN) assays. When compared to titres against cell-propagated A/Darwin/6/2021-like vaccine reference viruses, post- vaccination HI and virus neutralization (VN) GMTs against some recent A(H3N2) viruses from the 2a.1b, 2a.3a.1 and 2b genetic subgroups were significantly reduced in some serum panels. The reductions were more pronounced when compared to egg-propagated A/Darwin/9/2021 reference virus.

In summary, the vast majority of A(H3N2) viruses collected since 1 February 2023 have HA genes derived from clade 2 (i.e., 3C.2a1b.2a.2) and have diversified into several new subclades. Some recently circulating viruses showed reduced recognition by post-infection ferret antisera raised against NH 2022-2023 and SH 2023 vaccine viruses, cell culture-propagated A/Darwin/6/2021 and egg-propagated A/Darwin/9/2021 (2a). Human serology assays showed that post-vaccination GMTs against A(H3N2) viruses with HA genes representing 2a.3a.1, 2a.1b and 2b genetic subgroups were significantly reduced in some serum panels compared to titres against cell-propagated

A/Darwin/6/2021-like vaccine reference viruses.

Based on all available data, the WHO Consultative Group recommended to use an egg-propagated A/Thailand/8/2022 or cell culture-propagated A/Massachusetts/18/2022 (H3N2)-like strain as the vaccine strains for 2024. AIVC accepted this recommendation.

(*Abridged from WHO website:* 202309_recommendation.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 6 September 2023, a total of 41 influenza B/Victoria-lineage isolates were antigenically typed using antisera against B/Washington/02/2019-like virus and 118 were antigenically typed using antisera against B/Austria/1359417/2021-like virus. All B/Victoria-lineage isolates were antigenically related to the vaccine strain B/Austria/1359417/2021. Genetically, most of influenza B viruses fell into group V1A.3a.2 (CDC designations) (Figure 20).

4334 influenza B viruses with collection dates between February to September 2022 were characterized at the Melbourne WHOCC from 15 countries. Globally, influenza B viruses represented approximately one-third of the viruses detected since 1 February 2023, 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.

The HA genes of B/Victoria lineage viruses characterized during this period belonged to clade 1A.3 which share the encoded amino acid substitutions G133R and K136E, and a triple amino acid deletion (positions 162-164) in HA1. A small number of viruses expressing 1A.3 HA genes with additional substitutions T73I and N233K (resulting in the loss of a glycosylation site) in HA1 were detected in North and Central America. The vast majority of clade 1A.3 HA genes encode further substitutions N150K, G184E, N197D (resulting in the loss of a glycosylation site) and R279K in HA1 and are designated as 1A.3a. The 1A.3a HA diversified into two main subclades, one with additional HA1 substitutions V220M and P241Q (designated as 3a.1) and the other with HA1 substitutions A127T, P144L and K203R (designated as 3a.2). Viruses with 3a.1 HA genes have continued to decline and very few were detected in this period. The 3a.2 HA genes have predominated globally with most recent circulation in Africa and Oceania. The 3a.2 HA genes have diversified further, with the majority sharing the substitution D197E in HA1.

Antigenic characterisation of A(H3N2) viruses was performed by HI and virus neutralization (VN) assays. Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021- like viruses (3a.2) recognized representative viruses from various clusters of 3a.2 HA genes well. The small number of viruses in clade 1A.3 were recognized well by ferret antisera raised against B/Washington/02/2019-like viruses (1A.3) and were poorly recognized by ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2).

Human serology studies were conducted using most recent serum panels against the SH 2023 vaccine viruses, post-vaccination HI GMTs against recent B/Victoria lineage viruses of clade 3a.2 were not significantly reduced when compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021 vaccine viruses. Significant reductions were detected with most serum panels for viruses with HAs of the 1A.3 clade. Due to the lack of recent viruses, serology studies were not performed for the B/Yamagata lineage.

In summary, all circulating influenza B viruses characterized since 1 February 2023 were of the

B/Victoria/2/87 lineage. Most recent viruses expressed HA genes belonging to subclade 3a.2 (i.e., 1A.3a.2). A few viruses belonging to clade 1A.3 were detected in North and Central America. Nearly all circulating viruses were recognized well by post-infection ferret antisera raised against cell culture- and egg- propagated B/Austria/1359417/2021-like viruses (3a.2). Human serology assays showed that post- vaccination GMTs against representative B/Victoria lineage viruses expressing 3a.2 HA genes were not significantly reduced compared to titres against egg- or cell culture-propagated B/Austria/1359417/2021 vaccine virus.

Based on all available data, the WHO Consultative Group recommended to continue to use the same vaccine strain for 2024. AIVC accepted this recommendation.

(*Abridged from WHO website:* 202309_recommendation.pdf (who.int) *and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

Figure 18. Phylogenetic relationships among influenza A(H1N1)pdm09 virus haemagglutinin gene

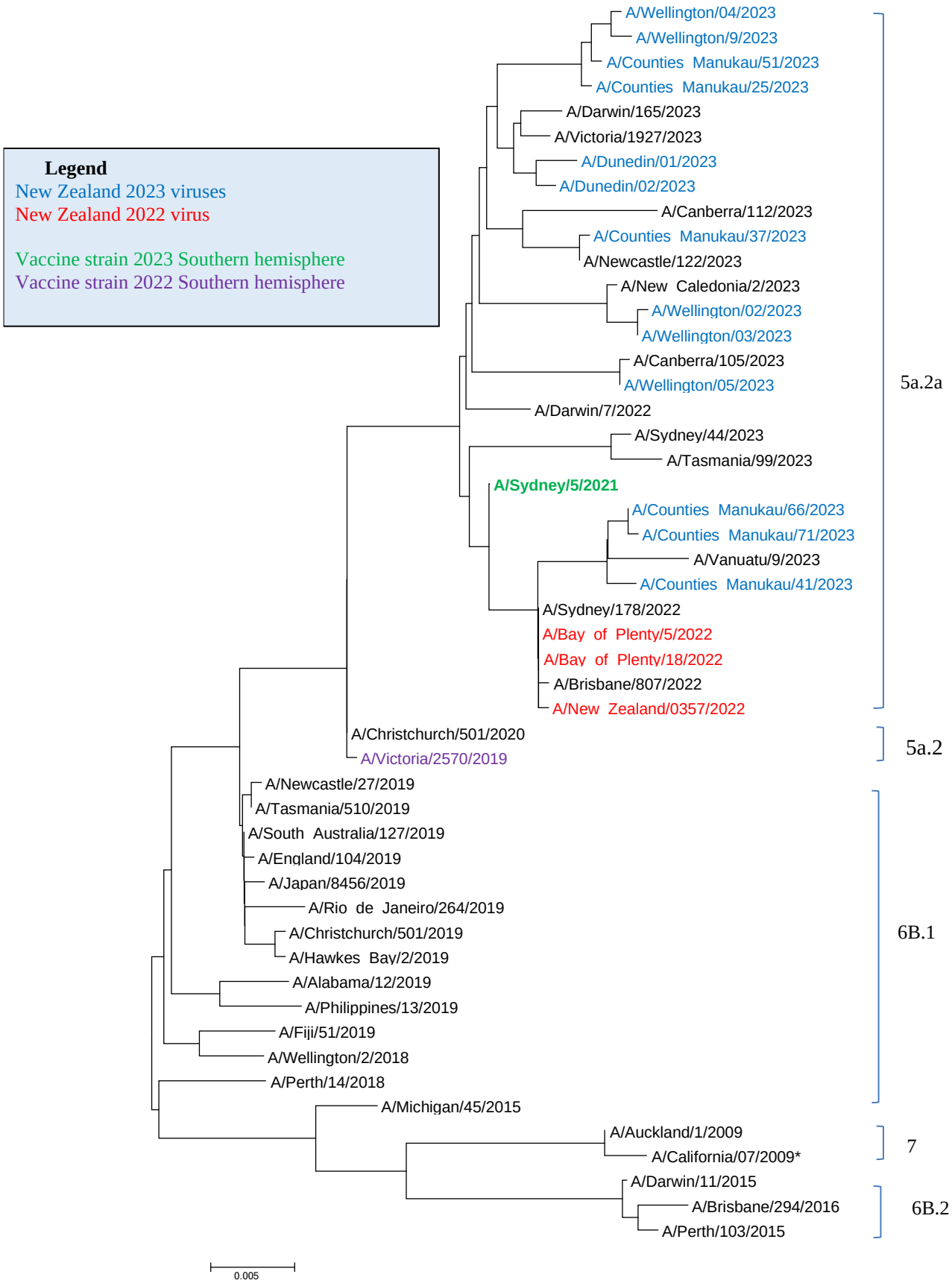


Figure 19. Phylogenetic relationships among influenza A(H3N2) virus haemagglutinin gene

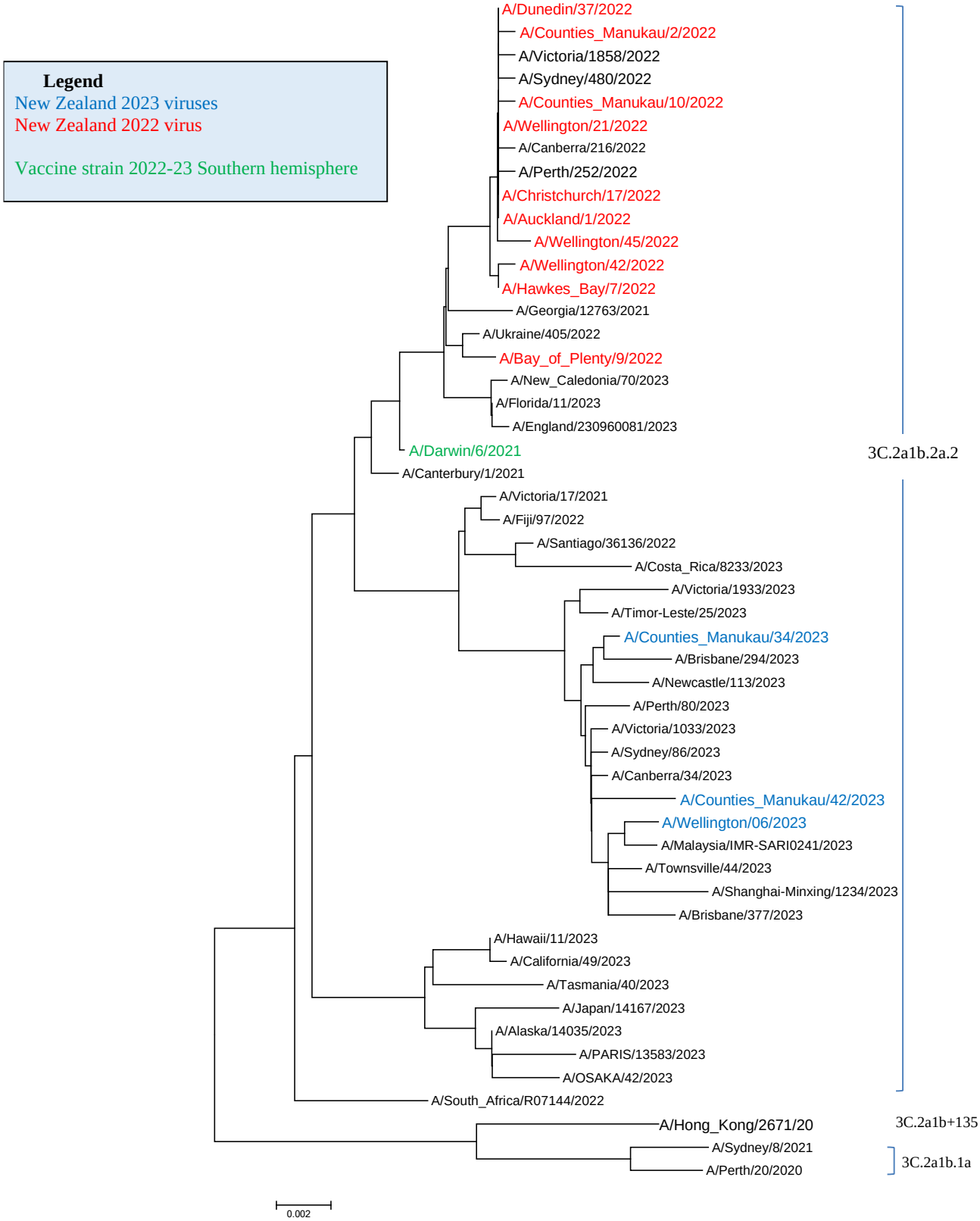
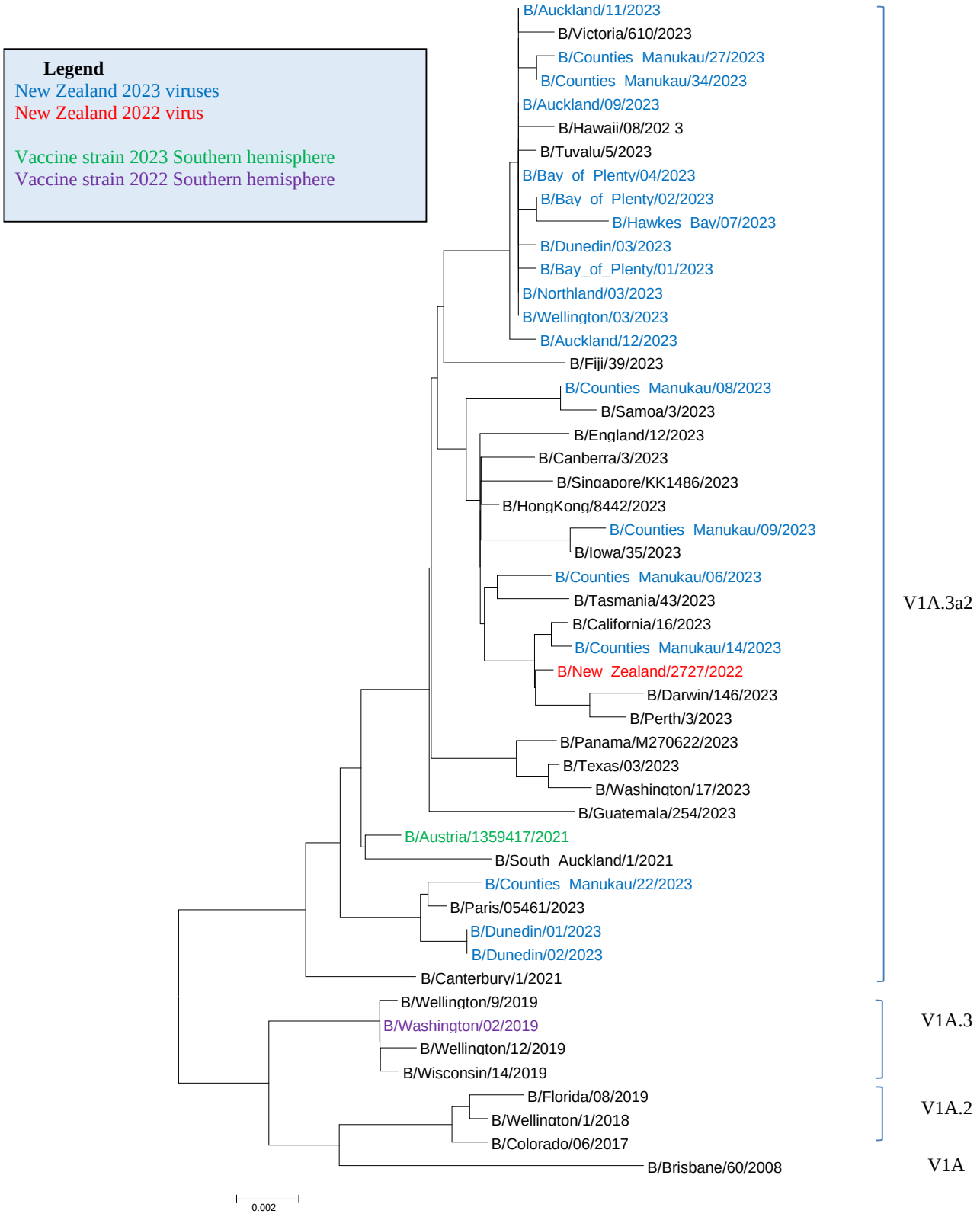


Figure 20. Phylogenetic relationships among influenza B/Victoria lineage virus haemagglutinin gene



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 2023, fluorometric neuraminidase inhibition assay was used to test 189 influenza viruses against oseltamivir and zanamivir. The preliminary results showed that all were sensitive to both oseltamivir and zanamivir (Tables 6 & 7).

Table 6. Antiviral susceptibility to oseltamivir for influenza viruses, 2017–2022^

Influenza	NA inhibition to Oseltamivir	No. of Influenza Viruses					
		2018	2019	2020	2021	2022	2023
A(H1N1)pdm09	Normal	75	12	1	1	5	122
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	6	32	-	3	162	10
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	46	1	-	2	1	57
	Reduced	1	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-

Table 7. Antiviral susceptibility to zanamivir for influenza viruses, 2017–2023^

Influenza	NA inhibition to Zanamivir	No. of Influenza Viruses					
		2018	2019	2020	2021	2022	2023
A(H1N1)pdm09	Normal	75	12	1	1	8	122
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	6	32	-	3	162	10
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	47	1	-	2	2	57
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-

Note: For Tables 6&7, ^Jan-Aug 2023

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. In 2023, influenza vaccine is also freely available for children from 6 months to 12 years.

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, the estimated crude vaccine effectiveness (VE) was 80.4% (95% CI: 72.7 to 86.1). For influenza-confirmed SARI cases, the estimated crude vaccine effectiveness (VE) was 58.6% (95% CI: 31.4 to 76.1).

Table 8. Estimated influenza vaccine effectiveness, by participant age group and by influenza virus type and subtype in New Zealand, 2023 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	52	185	866	604	80.4 (72.7, 86.1)
0–18 years	21	130	358	360	83.8 (73.4, 90.5)
19–64 years	28	55	474	237	74.5 (57.9, 84.8)
65+ years	3	0	34	7	N/A
H1	36	127	882	662	78.7 (68.5, 85.9)
0–18 years	15	86	364	404	80.6 (65.5, 89.8)
19–64 years	18	41	484	251	77.2 (58.4, 87.9)
65+ years	3	0	34	7	N/A
B Vic	12	56	906	733	82.7 (66.9, 91.6)
0–18 years	6	43	373	447	83.3 (59.9, 94.2)
19–64 years	6	13	496	279	74.0 (25.7, 92.0)
65+ years	0	0	37	7	N/A
SARI					
All ages	20	197	142	579	58.6 (31.4, 76.1)
0–18 years	6	123	24	351	28.7 (-84.7, 76.7)
19–64 years	7	50	50	136	61.9 (7.7, 86.3)
65+ years	7	24	68	92	60.5 (-1.8, 86.4)
H1	13	116	149	660	50.4 (8.6, 75.0)
0–18 years	2	62	28	412	52.5 (-96.6, 94.6)
19–64 years	6	32	51	154	43.4 (-48.3, 81.7)
65+ years	5	22	70	94	69.5 (11.5, 91.4)
B Vic	6	78	156	698	65.6 (19.6, 88.0)
0–18 years	4	60	26	414	N/A
19–64 years	1	17	56	169	82.2 (-19.0, 99.6)
65+ years	1	1	74	115	N/A

N/A: not applicable as numbers too low to reach any significance; CI: Confidence interval;

SARI: severe acute respiratory infections.

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