Science for Communities
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RECOMMENDATION FOR SEASONAL INFLUENZA VACCINE COMPOSITION FOR NEW ZEALAND FOR 2023

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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/Sydney/5/2021 (H1N1)pdm09-like virus;
- an A/Darwin/9/2021 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage) - like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage) - like virus.

Cell-based or recombinant-based quadrivalent influenza vaccines:

- an A/Sydney/5/2021 (H1N1)pdm09-like virus;
- an A/Darwin/6/2021 (H3N2)-like virus;
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

The composition of trivalent influenza vaccines is recommended to include the A(H1N1), A(H3N2) and the B/Victoria lineage virus.

Table 1. Influenza vaccine recommendations for New Zealand, 1991–2023

Decision		Use	A H3N2	A H1N1	B (Trivalent)	B (Quadrivalent)
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**	1993–94		A/Beijing/32/92	A/Singapore/6/86	B/Panama/45/90	
NZ	1993	1994	A/Shanghai/24/90	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	
NZ	1992	1993	A/Beijing/353/89	A/Victoria/36/88	B/Yamagata/16/88 or B/Panama/45/90	
WHO**	1991–92		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

New Zealand (NZ), a southern hemisphere country with a temperate climate, has a well-established influenza circulation pattern with peak incidences in the winter months. However, stringent non-pharmaceutical interventions (NPIs) implemented for the control of COVID-19 have eliminated influenza in 2020 (Huang *et al.* Impact of the COVID-19 nonpharmaceutical interventions on influenza and other respiratory viral infections in New Zealand. *Nat Commun* **12,** 1001 (2021). https://doi.org/10.1038/s41467-021-21157-9). This trend continued in the last two years during 2020-2021 when NZ border remained closed overall.

With progressive relaxation of NPIs such as partial border opening since March 2022, we have observed earlier and higher than usual influenza activity in 2022. Overall impact on healthcare use in hospitals was high as measured by influenza-associated severe acute respiratory illness (SARI). Seriousness of disease (i.e. 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 ICU SARI 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 study.

The hospital-based severe acute respiratory illness was moderate in 2022. However, influenza–associated SARI hospitalization in 2022 was at a high level. 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 was higher than 2021 and 2020. The influenza-associated ARI was much higher than previous years. 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 Māori and Pacific peoples than Europeans and Asian ethnic groups.

The newly established SHIVERS-V sentinel general practice based acute respiratory illness surveillance also showed one-third of viral positive specimens were attributable to influenza virus.

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 7080 influenza viruses were detected and reported through this system. Of them, influenza A represented 99.9% (7073) and influenza B 0.1% (7) of all influenza viruses. Among 2607 of subtyped influenza A viruses, 2560 (98.2%) were A(H3N2) and 47 (1.8%) were influenza A(H1N1)pdm09.

WHO National Influenza Centre (NIC) at ESR conducted antigenic typing: 1) 4 influenza A(H1N1)pdm09 viruses were antigenically closely related to the reference strain A/Indiana/02/2020(H1N1) which is closely related to the vaccine strain A/Victoria/2570/2019 (H1N1)pdm09; 2) 170 influenza A(H3N2) viruses were antigenically closely related to the cell-based vaccine strain A/Darwin/6/2021 (H3N2). Genetically, most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2

3. EPIDEMIOLOGY - NEW ZEALAND INFLUENZA SEASON IN 2022

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 acute respiratory illness surveillance).

3.1 Hospital-based surveillance

3.1.1 HOSPITAL-BASED SEVERE ACUTE RESPIRATORY ILLNESS (SARI) SURVEILLANCE

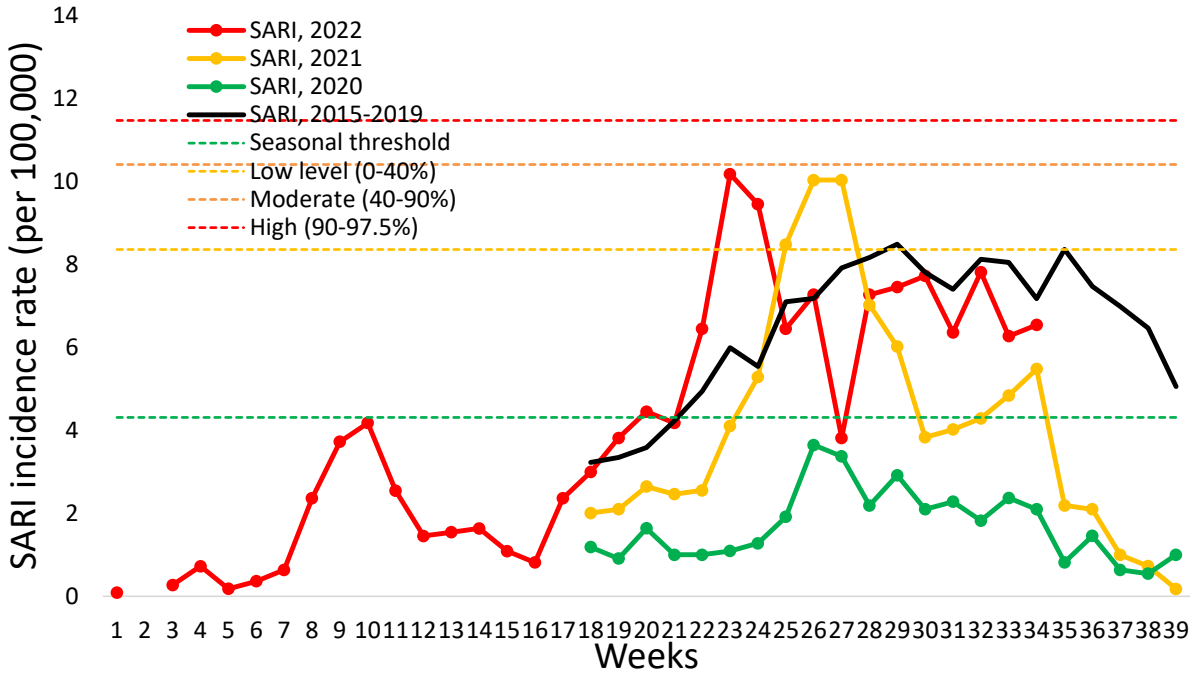
Inpatients with suspected respiratory infections admitted overnight to any of the four hospitals (Auckland City Hospital and the associated Starship Children's Hospital, Middlemore Hospital and the associated Kidz First Children's Hospital) in the Auckland District Health Board (ADHB) and Counties Manukau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

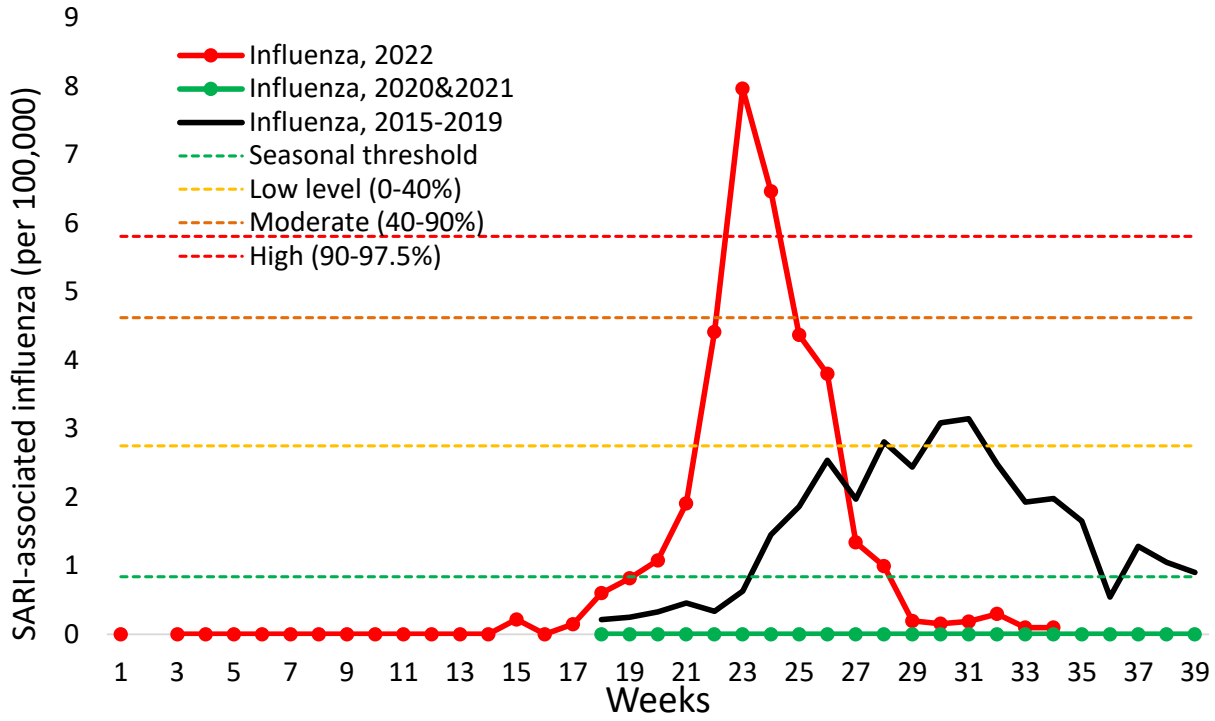
From week 1 (commencing 1 January 2022) through week 34 (ending 29 August 2022), severe acute respiratory illness (SARI) hospitalization rates were below baseline during weeks 1-20, then had a sharp increase and peaked at week 23 and then declined (Figure 1). SARI hospitalization rates in 2022 was similar to 2021.

Figure 1. Weekly hospitalisation rates for SARI in 2022 compared to 2015-2019, 2020 and 2021



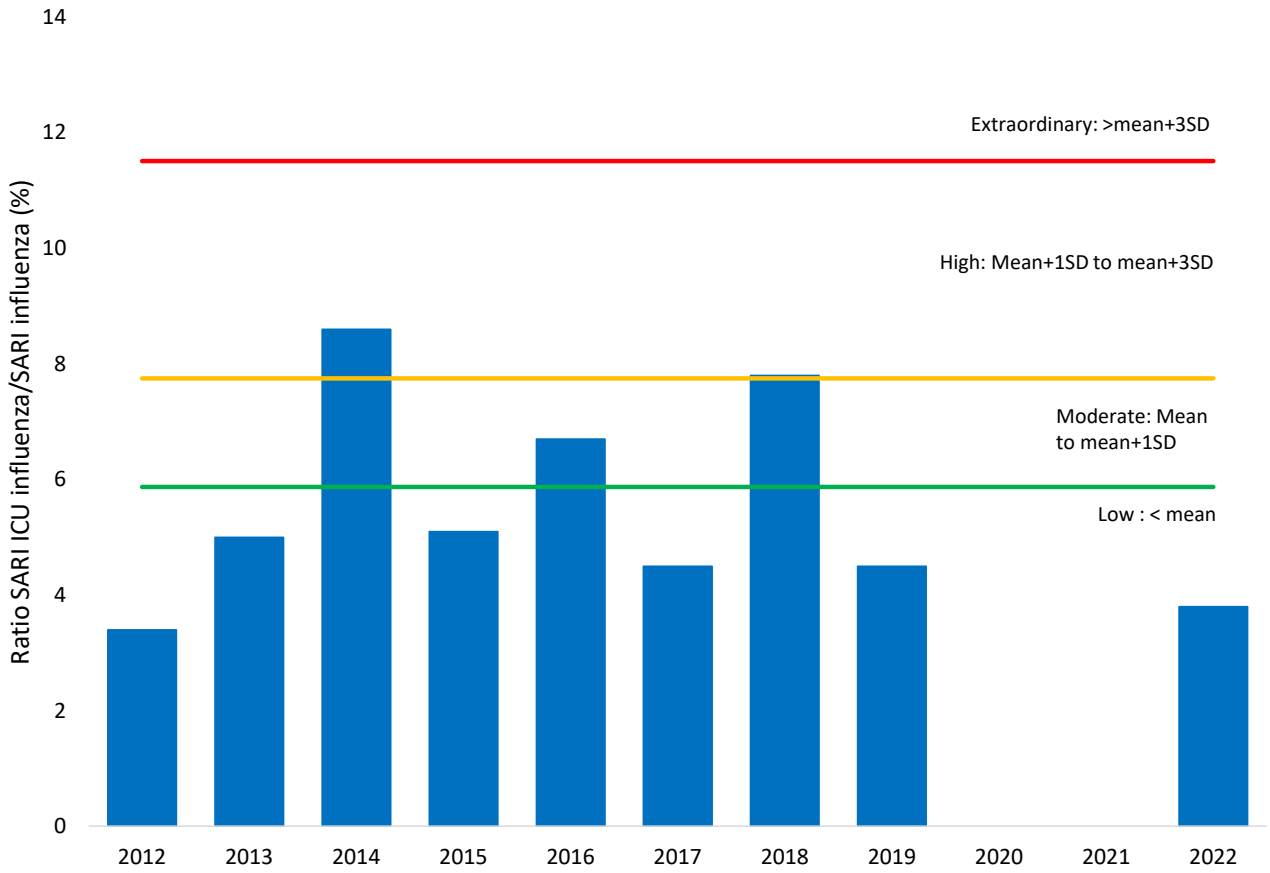
Overall impact on healthcare use in hospitalizations was high as measured by influenza-associated SARI hospitalizations. SARI-associated influenza hospitalizations were at a high level in 2022 (Figure 2). The peak of influenza hospitalizations in 2022 was 2.5 times higher than the median peak during 2015-2019.

Figure 2. SARI-associated influenza hospitalizations in 2022 compared to 2015-2019, 2020 and 2021



Seriousness of disease (i.e. severity) that indicates the extent to which individuals get sick when infected with the influenza virus was low in 2022 as measured by the ratio of influenza-associated ICU SARI admission over influenza-associated SARI hospitalization (Figure 3).

Figure 3. Seriousness of disease indicator in 2022 compared to 2012–2021



From 1 January to 28 August 2022, a total of 1458 hospitalized patients with severe acute respiratory illness (SARI) met the SARI case definition. Among these, 1143 were residents of ADHB and CMDHB, giving the SARI incidence rate of 103.6 per 100 000 population (78.6 per 100,000 in 2021 and 116.6 per 100 000 in 2019) (Table 1). Among the SARI cases who were ADHB and CMDHB residents, 302 (26.4%) had positive influenza virus results. This gives a SARI related influenza incidence of 27.4 per 100 000 population (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 2022

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	**1458**	**552**	**1143**	**103.6**	**302**	**27.4**	**523**	**47.4**
Age group (years)								
<1	162	25	150	1117.7	12	89.4	24	178.8
1–4	207	44	188	370.2	23	45.3	38	74.8
5–19	77	51	65	30.4	28	13.1	43	20.1
20–34	122	76	115	40.6	56	19.7	73	25.7
35–49	105	58	100	45.6	34	15.5	56	25.5
50–64	164	97	157	84.1	52	27.9	93	49.8
65–79	2232	133	227	217.7	69	66.2	129	123.7
>80	144	68	141	449.6	28	89.3	67	213.6
Unknown	0	0	0	0.0	0	0.0	0	0.0
Ethnicity								
Māori	197	128	181	126.8	65	45.6	116	81.3
Pacific peoples	492	242	473	244.7	145	75.0	237	122.6
Asian	112	39	111	31.2	19	5.3	39	10.9
European and Other	408	143	377	91.6	73	17.7	131	31.8
Unknown	249		1		0	0.0		
Hospitals								
ADHB	684	274	596	119.9	140	28.2	253	50.9
CMDHB	565	278	547	90.2	162	26.7	270	44.5
Sex								
Female	600	313	571	103.2	167	30.2	298	53.8
Male	610	239	572	104.0	135	24.5	225	40.9
Unknown	0	0	0	0.0	0	0.0	0	0.0

From 1 January to 28 August 2022, 1032 SARI specimens have been tested and 319 (30.9%) were positive for influenza viruses (Table 2). Of the 81 specimens collected from ICU admitted patients with acute respiratory illness (SARI and non-SARI), 15 (18.5%) were positive for influenza viruses. Of the 43 specimens collected from fatal cases with acute respiratory illness (SARI and non-SARI), 6 were positive for influenza viruses. Influenza A(H3N2) was the predominant strain.

Additionally, 1211 SARI specimens were tested for non-influenza respiratory viruses (Table 2).

Table 2. Influenza and non-influenza respiratory viruses among SARI cases, 2022

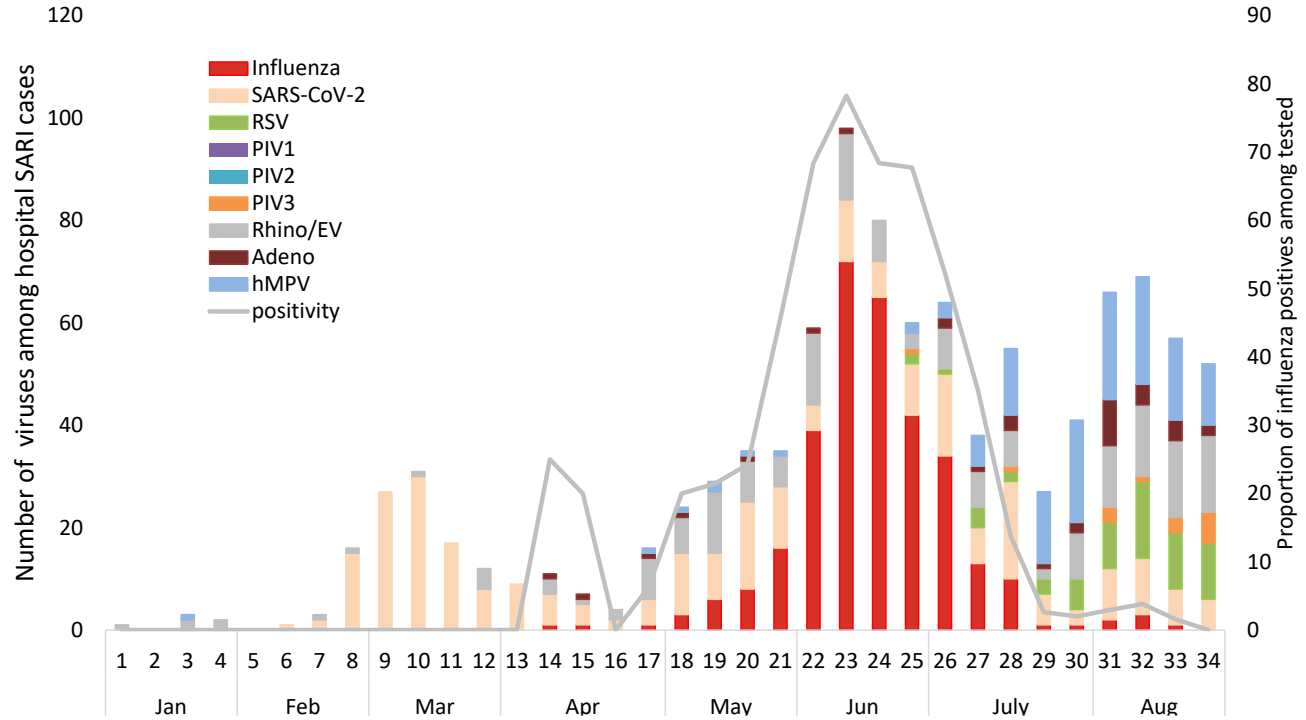
Influenza viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	1032	81	43
No. of positive specimens (%)[1]	319 (30.9)	15 (18.5)	6 (14.0)
Influenza A	318	15	6
A (not subtyped)	179	4	3
A(H1N1)pdm09	2	1	0
A(H1N1)pdm09 by PCR	2	1	0
A/Victoria/2570/2019 (H1N1)pdm09 - like	0	0	0
A(H3N2)	137	10	3
A(H3N2) by PCR	137	10	3
A/Darwin/9/2021 (H3N2)-like	0	0	0
Influenza B	2	0	0
B (lineage not determined)	2	0	0
B/Yamagata lineage	0	0	0
B/Yamagata lineage by PCR	0	0	0
B/Phuket/3073/2013 - like	0	0	0
B/Victoria lineage	0	0	0
B/Victoria lineage by PCR	0	0	0
B/Austria/1359417/2021-like	0	0	0
Influenza and non-influenza co-detection (% +ve)	34 (10.6)	3 (20.0)	0 (-)

Non-influenza respiratory viruses	SARI	SARI and non-SARI	
	Cases (%)	ICU (%)	Deaths (%)
No. of specimens tested	1211	81	66
No. of positive specimens (%)[1]	641 (52.9)	46 (56.8)	34 (51.5)
Respiratory syncytial virus (RSV)	64	4	0
Parainfluenza 1 (PIV1)	0	0	0
Parainfluenza 2 (PIV2)	0	0	0
Parainfluenza 3 (PIV3)	15	1	0
Rhinovirus (RV)/Enterovirus	186	30	2
Adenovirus (AdV)	35	4	1
Human metapneumovirus (hMPV)	135	11	0
SARS-Cov-2	295	5	33
Single virus detection (% of positives)	535 (83.5)	32 (69.6)	32 (94.1)
Multiple virus detection (% of positives)	106 (16.5)	14 (30.4)	2 (5.9)

[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 during June-July 2022. Around the middle of April 2022, NZ provided free quarantine travel to vaccinated Australians and other visa-waiver countries. This may have contributed to community-wide influenza outbreak in NZ in 2022.

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



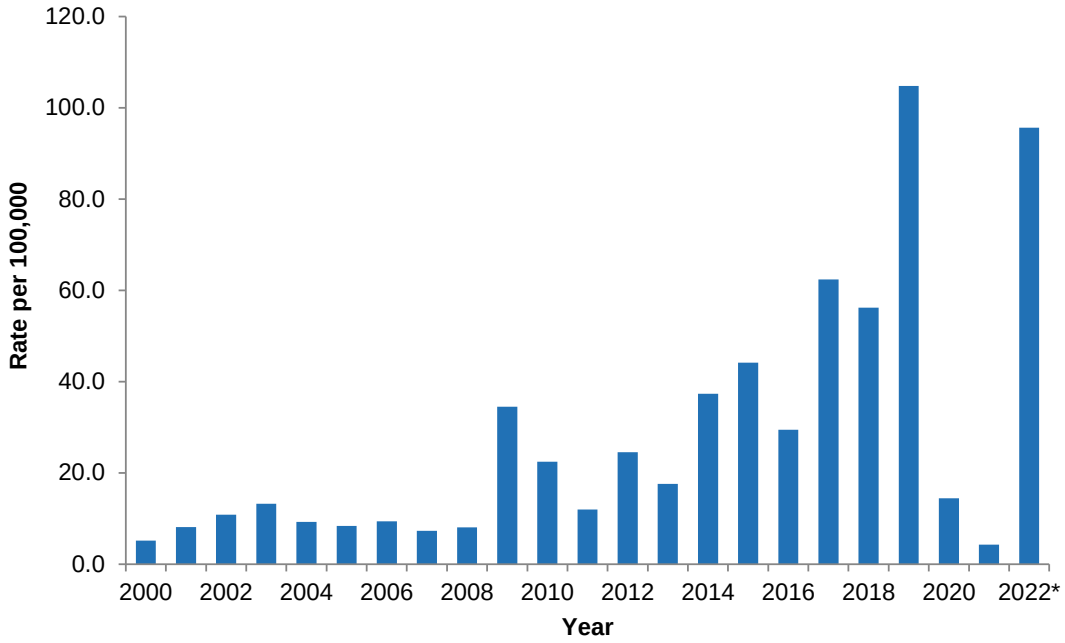
[1]Figures for recent weeks will be underestimates due to time lag in receiving laboratory test results

3.1.2 MINISTRY OF HEALTH DATA ON PUBLICLY FUNDED HOSPITAL DISCHARGES

Hospitalisation data for influenza (ICD-10AM-VI code I (J09-J11) for 2022 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 2000–2022. 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 Aug 2022, there were a total of 4899 hospitalisations (95.6 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 2022.

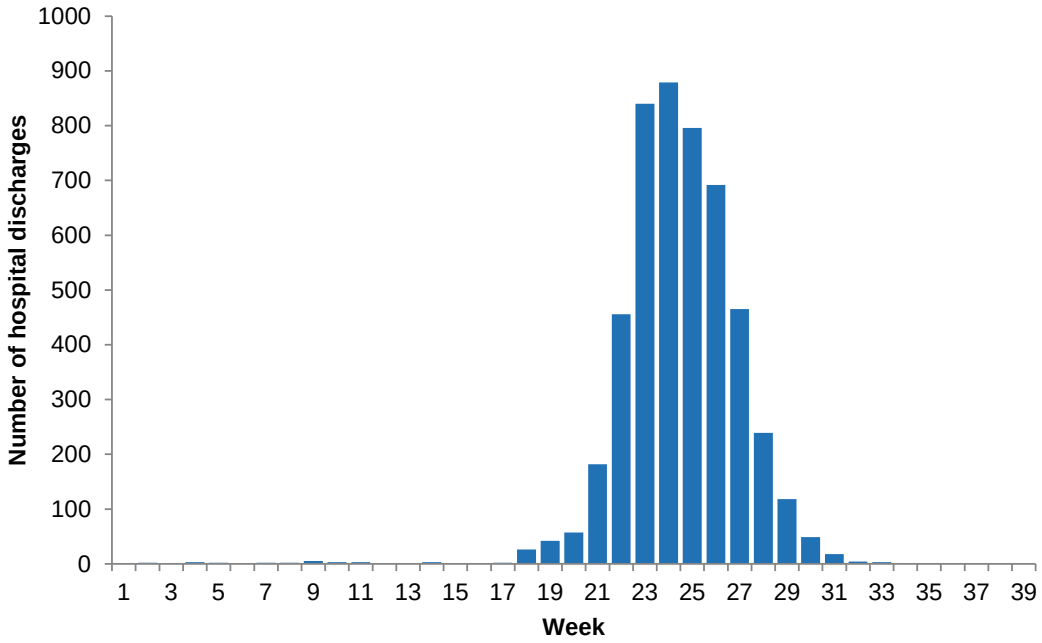
Figure 5. Influenza hospital discharge rates, 2000–2022*



*2022 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 (879) occurred in week 24 (week ending 19 June 2022).

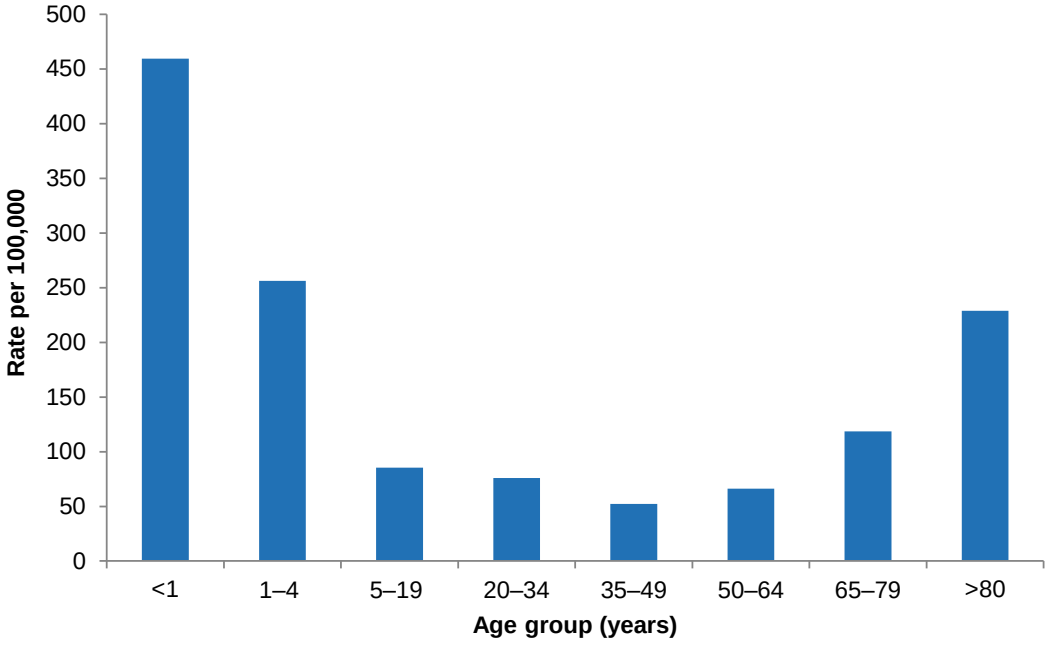
Figure 6. Influenza hospital discharges by week, 2022*



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

From 1 January to 16 Aug, the highest influenza hospitalisation rates were recorded among infants <1 year (459.6 per 100,000) followed by young children aged 1-4 years (256.2 per 100,000) and those 80 years and over (229.0 per 100,000) (Figure 7).

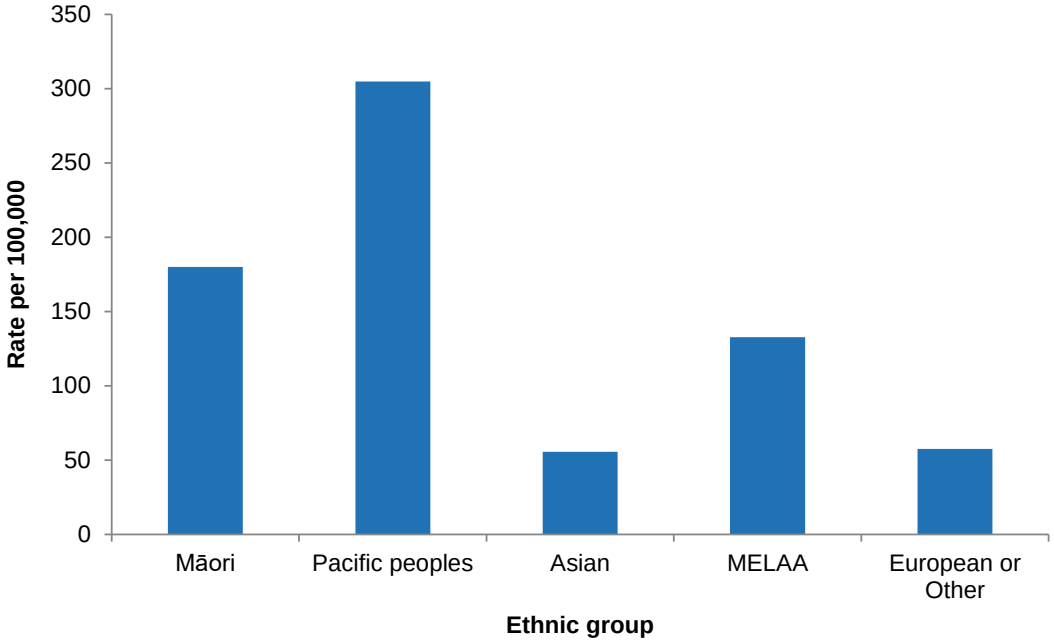
Figure 7. Influenza hospital discharge rates by age group, 2022*



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

The ethnic distribution of influenza hospitalisations in 2022 is shown in Figure 8. Pacific peoples had the highest hospitalisation rate (304.8 per 100,000) followed by Māori (180.0 per 100,000), and MELAA (132.7 per 100,000). Asian (55.6 per 100,000) and European or Other (57.5 per 100,000) ethnic groups had the lowest rates of hospitalisations.

Figure 8. Hospital discharge rates by prioritised ethnic group, 2022*



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

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 primarycare management system. In 2022, SHIVERS-II study staff followed these participants (~1000) and monitored their ILIs and acute respiratory illness (ARI)s.

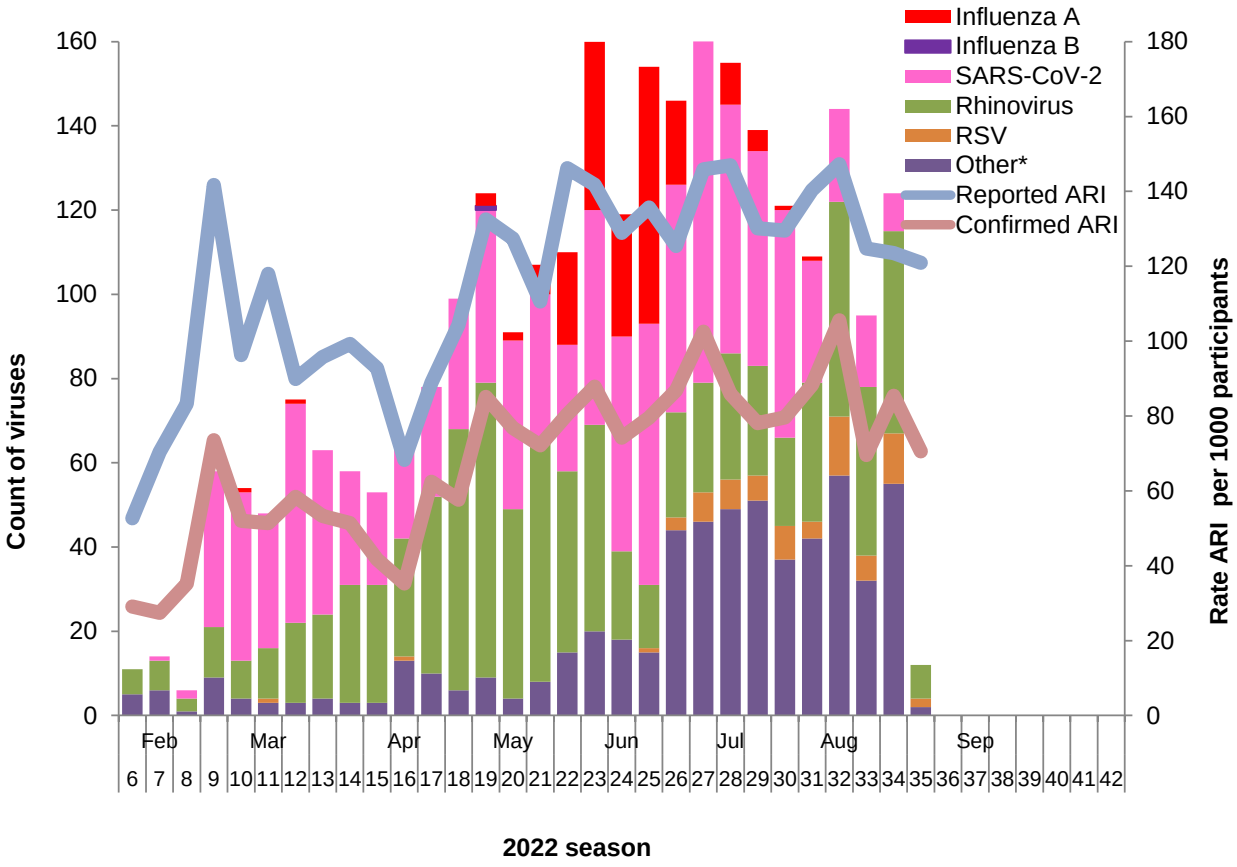
SHIVERS-III (i.e. WellKiwis Infant) is a prospective Wellington infant cohort aiming to recruit 600 infant-mother pairs from Oct 2019-Sept 2022 (200 pairs a year) and follow them until 2026. In 2022, the study staff followed up ~400 infants and monitored their ILIs and ARIs.

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 2022, the study staff followed up ~1800 household members and monitored their ILIs and ARIs.

During 7-Feb to 4-September 2022, SHIVERS-II, III and IV study staff sent weekly surveys to participants regarding their respiratory illness. Due to COVID-19, the ARI case definition in 2022 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 the same as before: “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 and ARI, research nurses visited the participant and take a nasopharyngeal or nasal or throat swab to test for influenza, RSV and other respiratory viruses and SARS-CoV-2.

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 2022. SARS-CoV-2 and influenza were the dominant viruses in 2022. NZ has not had any influenza outbreaks in communities for two years since May-2020. Since March 2022, NZ border has been progressively relaxed and quarantine free travel was offered to those vaccinated Australian and vaccinated individuals from ~60 visa-waiver countries. This may have contributed to community-wide influenza outbreak in NZ in 2022 due to importation of influenza viruses from travellers across NZ border.

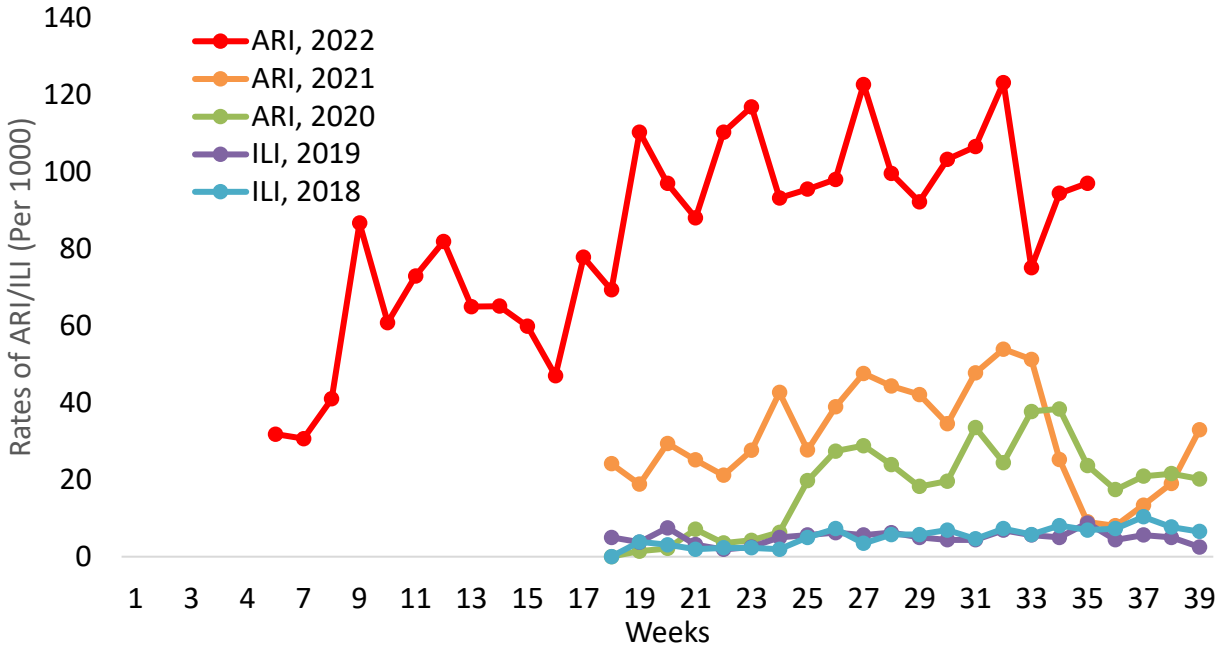
Figure 9. Weekly incidence rate of acute respiratory illness and associated viruses in 2022



*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 2022 was higher than the previous years of 2021 and 2020 (Figure 10).

Figure 10. Weekly ARI/ILI incidence rates in 2022, compared to 2018-2021



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

Figure 11. Weekly influenza associated ARI rates in 2022, compared to 2018-2021

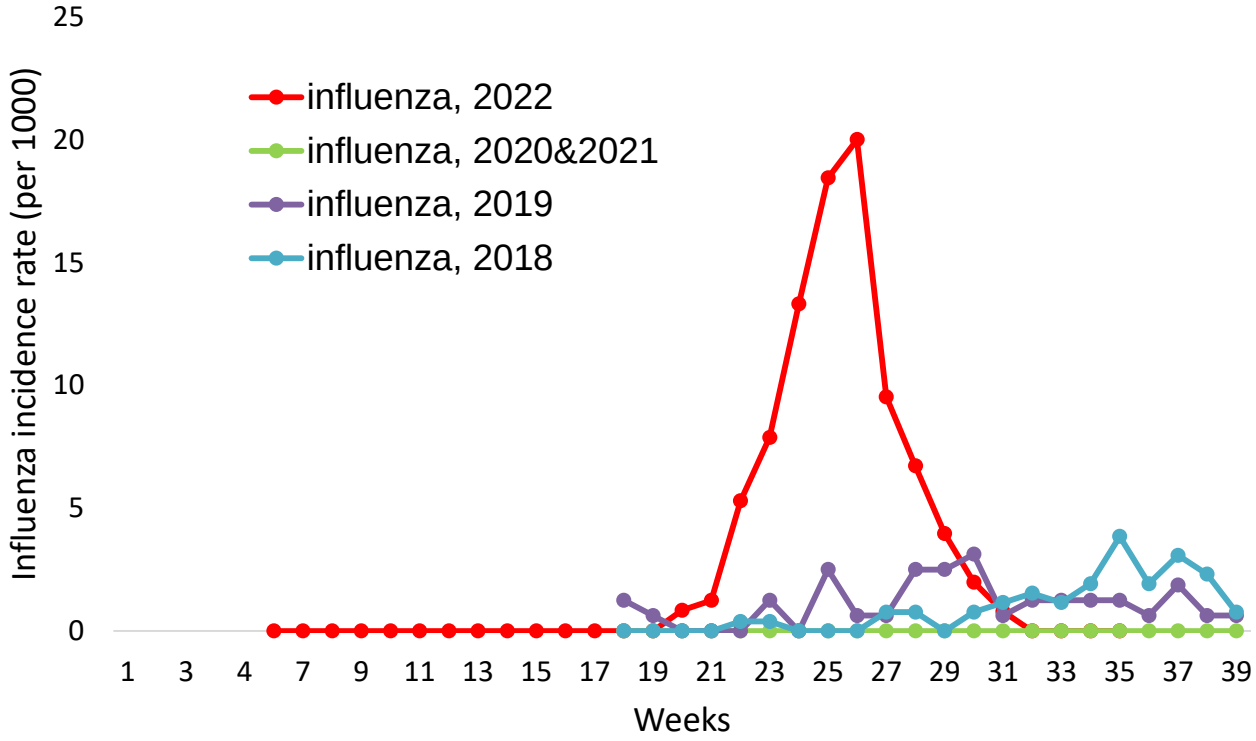


Table 3. Demographic characteristics of ARI cases and related influenza cases, during 7-Feb to 4-Sept 2022

Characteristics	ARI & influenza cases among WellKiwis cohort participants			
	ARI cases	ARI incidence (per 100)	Influenza Cases	Influenza associated ARI incidence (per 100)
Overall	**4114**	**138.8**	**221**	**7.5 (6.5, 8.5)**
Age group (years)				
<1	625	138.0	25	5.5 (3.6, 8.0)
1–4	837	263.2	63	19.8 (15.6, 24.6)
5–19	513	136.8	71	18.9 (15.1, 23.3)
20–34	631	178.2	22	6.2 (3.9, 9.3)
35–49	1009	145.8	35	5.1 (3.5, 7.0)
50+	499	65.5	5	0.7 (0.2, 1.5)
Unknown	0	0.0		0.0 (0.0, 28.5)
Ethnicity				
Māori	466	150.3	50	16.1 (12.2, 20.7)
Pacific peoples	118	147.5	7	8.8 (3.6, 17.2)
Asian	260	105.7	16	6.5 (3.8, 10.3)
European and Other	3257	143.4	147	6.5 (5.5, 7.6)
Unknown	13	22.8	1	1.8 (0.0, 9.4)
Sex				
Female	2348	138.9	106	6.3 (5.2, 7.5)
Male	1757	141.4	115	9.3 (7.7, 11.0)
Unknown	9	28.1	0	0.0 (0.0, 10.9)

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

From 7-Feb to 4-Sept 2022, 4268 respiratory specimens have been tested and 233 (5.5%) were positive for influenza viruses. Of which, 206 A(H3N2) were detected and was the predominant strain (Table 4). Additionally, 4219 specimens were tested for non-influenza respiratory viruses (Table 4).

Table 4 Influenza and Non-influenza respiratory viruses among ILI cases, since 7 Feb 2022

Influenza viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	2273	1088	907	4268
No. of positive specimens (%)[1]	162 (7.1)	60 (5.5)	11 (1.2)	233 (5.5)
Influenza A	161	60	11	232
A (not subtyped)	14	6	4	24
A(H1N1)pdm09	2	0	0	2
A(H1N1)pdm09 by PCR	2	0	0	2
A/Victoria/2570/2019 (H1N1)pdm09 - like	0	0	0	0
A(H3N2)	145	54	7	206
A(H3N2) by PCR	144	54	7	205
A/Darwin/6/2021 (H3N2)-like virus	1	0	0	1
Influenza B	1	0	0	1
B (lineage not determined)	1	0	0	1
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)	1 (0.6)	0 (0.0)	0 (0.0)	1 (0.4)

Non-influenza respiratory viruses	WellKiwis Households	Wellkiwis Infants	WellKiwis Adults	Total
No. of specimens tested	2237	1081	901	4219
No. of positive specimens (%)[1]	1046 (46.8)	743 (68.7)	488 (54.2)	2277 (54.0)
Respiratory syncytial virus (RSV)	36	34	2	72
Parainfluenza 1 (PIV1)	4	0	0	4
Parainfluenza 2 (PIV2)	2	0	0	2
Parainfluenza 3 (PIV3)	33	56	5	94
Rhinovirus (RV)	411	422	52	885
Adenovirus (AdV)	57	95	10	162
Human metapneumovirus (hMPV)	85	61	10	156
Enterovirus	29	49	4	82
SARS-CoV-2	467	137	415	1019
Single virus detection (% of positives)	977 (93.4)	642 (86.4)	479 (98.2)	2098 (92.1)
Multiple virus detection (% of positives)	69 (6.6)	101 (13.6)	9 (1.8)	179 (7.9)

3.2.2 SENTINEL GENERAL PRACTICE ACUTE RESPIRATORY ILLNESS SURVEILLANCE

Prior to 2020, influenza-like illness (ILI) surveillance through sentinel general practices was the main means of identifying seasonal influenza activity in New Zealand communities. The COVID-19 pandemic has changed the landscape at the primary care level through intensive screening for COVID-19 both at general practices and community-based assessment centres for patients presenting with any acute respiratory illness. However, this situation also creates new opportunity of tracking influenza and other respiratory viruses by testing those samples already collected for COVID-19 with no additional effort from practices.

During 2021-2022, we piloted a sentinel general practice-based Acute Respiratory Illness (ARI) surveillance using routine swabs indicated for COVID-19 testing (i.e. no change in practice) among voluntary sentinel general practices. Our aim is to identify an efficient, fit-for-purpose public health surveillance system which does not impact on clinical workload in a new and rapidly evolving environment where respiratory viral infections may be caused by COVID-19, influenza and non-influenza respiratory viruses. This pilot is called SHIVERS-V, the fifth iteration of SHIVERS (Southern Hemisphere Influenza and Vaccine Effectiveness Research and Surveillance).

Acute respiratory illness is manifested by a range of symptoms such as cough, fever, sore throat, and runny nose. Many respiratory viruses can cause ARI including SARS-CoV-2 (causing COVID-19), influenza and other non-influenza respiratory viruses.

The specific aims of ARI surveillance in primary care are to:

1. Align with the current COVID-19 clinical guidelines in general practices while expanding testing to include influenza and non-influenza respiratory viruses in addition to COVID-19.
2. Utilise the current mechanism for COVID-19 data collection through use of the routine laboratory electronic order/specimen request form:
    - No extra work is required during the standard clinical consultation, beyond ticking the correct box in the existing request form (i.e. testing request for COVID-19/influenza/non-influenza virus).
    - Patient demographic information pre-populated from the Practice Management System as usual.
3. Provide valuable information on influenza disease burden, epidemiology, etiology, risk factors and vaccine effectiveness in the COVID-19 era to guide early detection of influenza epidemics/pandemics, inform vaccination policy, vaccine strain selection and other public health measures.

ARI case definition: it is consistent with the current Ministry of Health definition on COVID-19 when to take swabs in primary care (https://www.health.govt.nz/our-work/diseases-and-conditions/covid-19-novel-coronavirus/covid-19-information-health-professionals/case-definition-and-clinical-testing-guidelines-covid-19#guidance) (updated on 7 May 2021)

Any acute respiratory infection with at least one of the following symptoms (with or without fever):

- *new or worsening cough,*
- *fever (at least 38˚C),*
- *shortness of breath,*
- *sore throat,*
- *coryza (runny nose),*
- *anosmia (loss of sense of smell),*
- *dysgeusia (altered sense of taste).*

People meeting the above clinical criteria should be tested.

Some people may present with less typical symptoms such as only fever, diarrhoea, headache, myalgia (muscle aches), nausea/vomiting, or confusion/irritability. For people with less typical symptoms, if there is not another more likely diagnosis, they should also be tested.

Eligibility criteria for sample collection: All consultation-seeking patients with symptoms consistent with COVID-19 are eligible for ARI swabbing. Patients who do not have symptoms consistent with COVID-19 but are required or are seeking COVID-19 testing for other reasons (eg. travel, routine testing of border workers, or asymptomatic contacts etc.) are not eligible for ARI testing.

Electronic order/Specimen request form: Wellington Southern Community Laboratory (WSCL) and Labtests to provide additional testing option on their electronic order/specimen (e-order) form. GPs or nurses can choose to: either test for COVID-19/influenza/non-influenza for those patients agreeing ARI testing or test for COVID-19 alone for those patients declining ARI testing. Patient demographic information will be pre-populated from PMS to this form.

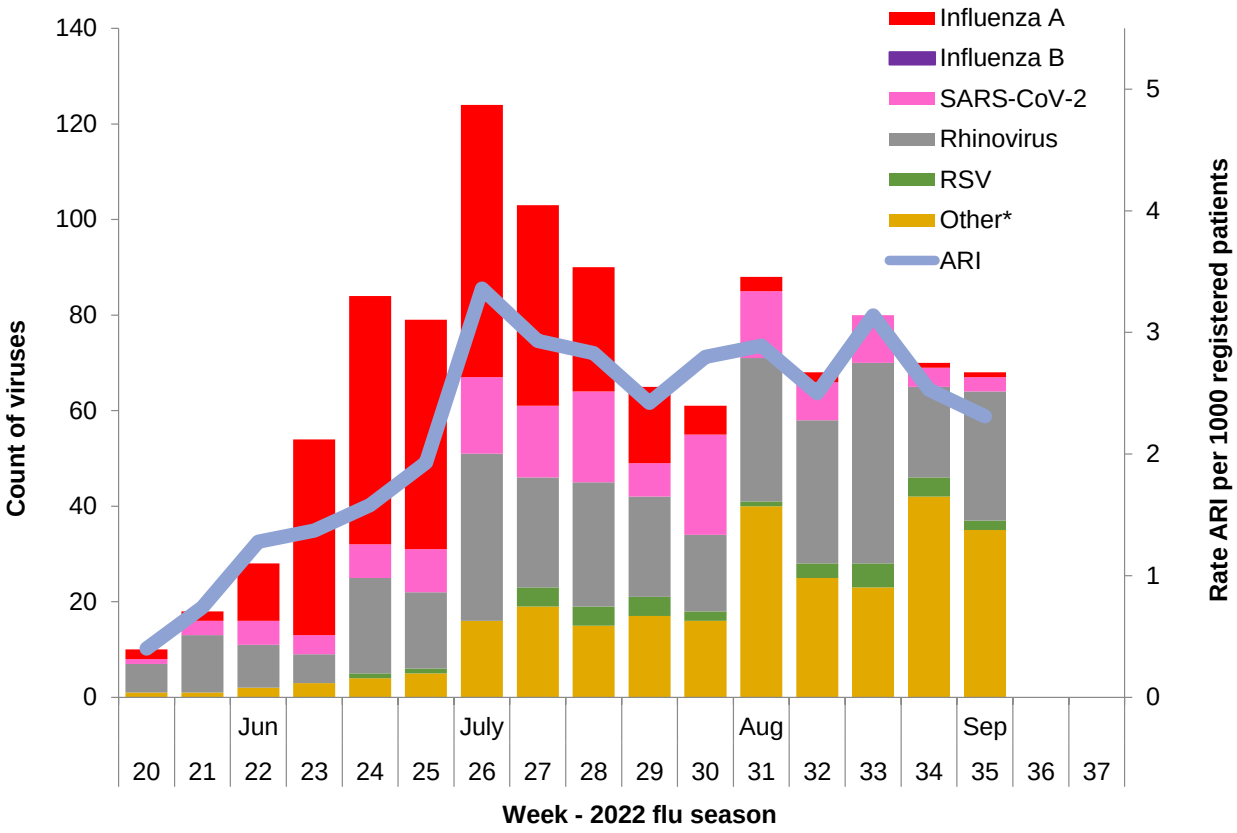
Laboratories: WSCL in Wellington and Labtests in Auckland and ESR's WHO National Influenza Centre are involved in testing. Laboratory identification included molecular detection using the polymerase chain reaction (PCR) for SARS-CoV-2, influenza A&B, and non-influenza respiratory viruses (respiratory syncytial virus, parainfluenza virus types 1, 2, 3 and 4, rhinovirus, adenovirus, human metapneumovirus).

Practice denominator: The number of the enrolled patients, including age, sex, ethnicity (and addresses to allow geocoding for the NZ Deprivation index). This will be collected once the practice agrees to take part in this pilot. Consultation rates were calculated using the registered patient populations of the participating practices as a denominator.

Data from Practice Management system: At the end of the influenza season, additional data will be collected on ARI patients, including respiratory symptoms or illness, underlying conditions, travel history, vaccination status etc

Figure 12 shows the weekly rate of acute respiratory illness and associated viruses detected in this sentinel general practice-based ARI surveillance between Week 20 (starting 16 May) to week 35 (ending 4 Sept) 2022. Influenza was the dominant virus during June-July 2022.

Figure 12. Weekly incidence rate of acute respiratory illness and associated viruses in 2022



*Note: other viruses include enterovirus, adenovirus, parainfluenza virus types 1-3 and human metapneumovirus. The left axis indicates number of respiratory viruses detected among registered patients with acute respiratory illnesses 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 purple line is the weekly rate of ARI reported by registered patients (per 100,0000), meeting the case definition). **: The 2021 national lockdown at Level 4 may lead to health seeking behaviour changes among consultation seeking patients which may contribute to a higher than usual ARI rate.

From 16 May to 4 Sept 2022, 1823 respiratory specimens have been tested and 311 (54.9%) were positive for influenza viruses (Table 5).

Table 5 Non-influenza respiratory viruses among GP consultation seeking patients with ARI, since 16 May 2022

Respiratory viruses	Total
No. of specimens tested	1823
No. of positive specimens (%)	1001 (54.9)
Influenza A	311
Influenza B	0
Respiratory syncytial virus (RSV)	31
Parainfluenza 1 (PIV1)	0
Parainfluenza 2 (PIV2)	3
Parainfluenza 3 (PIV3)	71
Rhinovirus (RV)	338
Adenovirus (AdV)	32
Human metapneumovirus (hMPV)	158
Enterovirus	0
SARS-CoV-2	146
Single virus detection (% of positives)	918 (91.7)
Multiple virus detection (% of positives)	83 (8.3)

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 2022

A total of 7080 influenza viruses were detected and reported through any surveillance system in 2022, with influenza A representing 99.9% (7073/7080) and influenza B 0.1% (250/2129) of all influenza viruses (Table 6). Among A sub-typed, 98.2% (2560/2607) were A(H3N2) virus and 1.8% (47/2607) were A(H1N1)pdm09 virus. None of 7 influenza B were lineage typed.

Table 6. Influenza virus identifications by type and sub-type and lineage-typed, 2022

Viruses	All viruses		Sub-typed and lineage-typed	
	N.	Col%	N.	%
Influenza virus	**7080**	**100.0**	**2607**	**100.0**
Influenza A	**7073**	**99.9**	**2607**	**100.0**
Influenza A (not sub-typed)	4466	63.1		
Influenza A(H1N1)pdm09	47	0.7	47	1.8
A(H1N1)pdm09 by PCR	45	0.6		
A/Victoria/2570/2019 (H1N1)pdm09-like	2	0.0		
Influenza A(H3N2)	2560	36.2	2560	98.2
A(H3N2) by PCR	2512	35.5		
A/Darwin/6/2021 (H3N2)-like	48	0.7		
Influenza B	**7**	**0.1**		
Influenza B (not lineage-typed)	7			
B/Victoria lineage	0		0	
B/Victoria lineage by PCR	0			
B/Austria/1359417/2021-like	0			
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 for each week throughout 2022. A(H3N2) was the predominant subtype throughout the season.

Figure 13. Total influenza viruses by type and week specimen taken, 2022

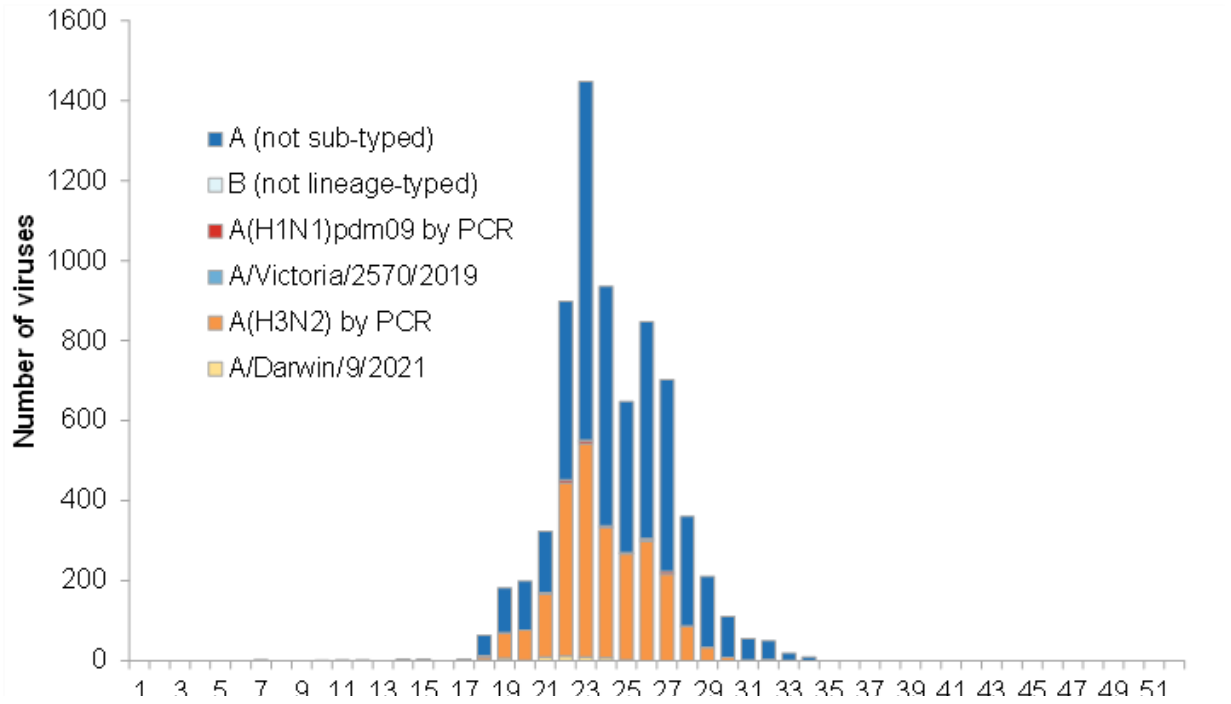
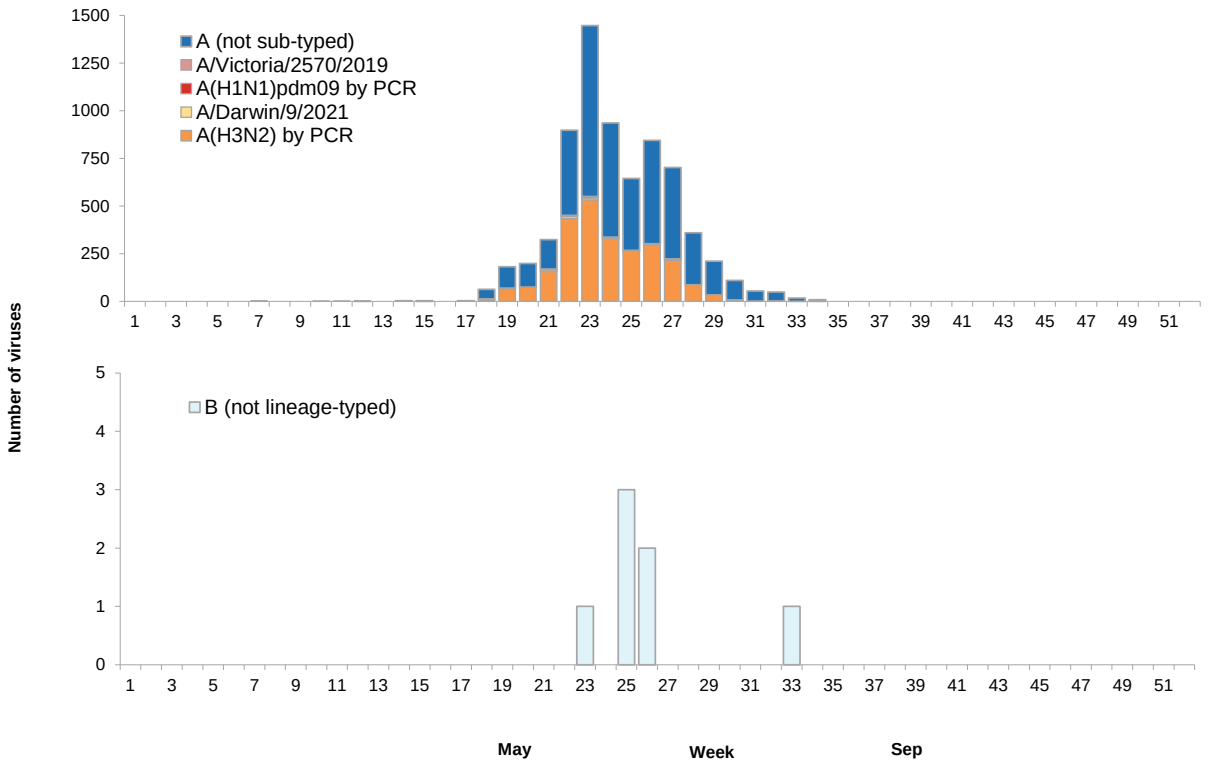


Figure 14 shows the general pattern of influenza virus identifications. Influenza A and B viruses co-circulated throughout the season.

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



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 and CDC-Atlanta. During 1 January to 9 September 2022, a total of 4 influenza A(H1N1)pdm09 isolates were antigenically typed using antisera against A/Indiana/02/2020(H1N1)-like virus. All of them were antigenically closely related to the reference strain A/Indiana/02/2020(H1N1) which is closely related to the vaccine strain A/Victoria/2570/2019 (H1N1)pdm09.

890 A(H1N1)pdm09 viruses with collection dates between February to September 2022 were characterized at the Melbourne WHOCC from 5 countries. All A(H1N1)pdm09 viruses belonged to phylogenetic subclade 6B.1A.5a (5a). It grouped in two major subclades: 5a.1 and 5a.2. Subclade 5a.2 viruses have further diversified.

The antigenic characteristics of A(H1N1)pdm09 viruses were assessed in haemagglutination inhibition (HI) assays with post-infection ferret antisera (*Table 1*). HI results for viruses with collection dates after January 2022 showed that the majority of 5a.1 viruses were recognized well by antisera raised against the previous vaccine virus (egg- and cell culture-propagated A/Guangdong-Maonan/SWL1536/2019-like 5a.1 viruses). Viruses in subclade 5a.2 were recognized poorly by these 5a.1 antisera. Ferret antisera raised against cell culture- and egg-propagated A/Victoria/2570/2019 vaccine viruses recommended for the NH 2021-2022 and 2022-2023, and the SH 2022 seasons, recognized 5a.2 viruses well despite substitutions at known antigenic sites compared with the vaccine viruses. These ferret antisera recognized 5a.1 viruses poorly. However, a pool of sera from adults who had received the SH 2022 egg- based vaccine generally showed good recognition of both 5a.1 and 5a.2 viruses, though a subgroup of 5a.2 viruses that have HA1 K142R and P137S substitutions was recognized less well.

Human serology studies used 3 serum panels from adults (18–64 years) and elderly adults (≥65 years) who had received egg-based quadrivalent inactivated vaccines (standard or adjuvanted) or cell culture- based quadrivalent inactivated vaccine formulated for the SH 2022 season. SH 2022 egg-based vaccines contained antigens from A/Victoria/2570/2019 (H1N1)pdm09-like, A/Darwin/09/2021 (H3N2)-like, B/Austria/1359417/2021- like (B/Victoria lineage) and B/Phuket/3073/2013-like (B/Yamagata lineage) viruses; cell-based vaccines contained antigens from A/Wisconsin/588/2019 (H1N1)pdm09-like, A/Darwin/6/2021 (H3N2)-like, B/Austria/1359417/2021-like (B/Victoria lineage) and B/Phuket/3073/2013 (B/Yamagata lineage)-like viruses.

Human serology studies using serum panels against SH 2022 and NH 2021-2022 vaccines showed minor reductions in post-vaccination HI geometric mean titres (GMTs) for the majority of recently circulating, representative A(H1N1)pdm09 5a.1 viruses when compared to cell culture-propagated A/Wisconsin/588/2019-virus. However, significant reductions in HI GMTs were observed for some 5a.2 viruses with additional HA1 amino acid substitutions A186T, Q189E, T216A and E224A, notably so for those with additional amino acid substitutions P137S and K142R (e.g. A/South Africa/R06166/2022). When measured against egg-propagated A/Victoria/2570/2019, most recent A(H1N1)pdm09 viruses showed significantly reduced GMTs.

In summary, Influenza A(H1N1)pdm09 viruses collected since 1 February 2022 with HA genes that belonged to 2 subclades, 6B.1A.5a.1 (5a.1) and 6B.1A.5a.2 (5a.2), circulated in different geographic locations. Viruses in the 5a.2 subclade continue to diversify and recently circulating viruses (represented by A/Sydney/5/2021) share substitutions in antigenic site Sb. Post-infection ferret antisera raised against the NH 2021-2022 and SH 2022 A(H1N1)pdm09 vaccine components (egg-propagated A/Victoria/2570/2019 and cell culture-propagated A/Wisconsin/588/2019 (5a.2)) recognized 5a.2 viruses well, but 5a.1 viruses poorly. However, human serology assays

showed markedly reduced post-vaccination GMTs against a substantial number of recent cell culture-propagated 5a.2 viruses in most serum panels when compared to titres against cell culture-propagated A/Wisconsin/588/2019 or egg-propagated A/Victoria/2570/2019 A(H1N1)pdm09-like vaccine viruses.

Based on all of the available data, the WHO consultation recommended to use an A/Sydney/5/2021 (H1N1)pdm09-like strain for 2023. The AIVC accepted this recommendation.

(*Abridged from the Weekly Epidemiological Record (WER), 2022 97(43):537-566 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 and CDC-Atlanta. During 1 January to 9 September 2022, a total of 170 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 cell-based vaccine strain A/Darwin/6/2021 (H3N2). Genetically, most of influenza A(H3N2) viruses fell into group 3C.2a1b.2a.2 (CDC designations) (Figure 15)

5158 A(H3N2) viruses with collection dates between February to September 2022 were characterized at the Melbourne WHOCC from 10 countries with most coming from Australia. Phylogenetic analysis of the HA gene of A(H3N2) viruses collected since 1 February 2022 showed that viruses belonging to genetic subclade 3C.2a1b.2a.2 (2a.2) with the HA1 substitutions Y159N, T160I (resulting in the loss of a glycosylation site), L164Q, G186D, D190N, F193S and Y195F predominated globally and were detected in all regions. The 2a.2 HA further diversified into 4 genetic groups containing H156Q or H156S and D53G or H156S and D53N or D53G, that circulated in different proportions in different regions. However, viruses belonging to 3C.2a1b subclade 2a.1 (HA1 substitutions G186S, F193S, Y195F and S198P) predominated in China and early in 2022 in Timor-Leste. Viruses reported from China had additional substitutions K171N and I48T in HA1.

Antigenic characterisation of A(H3N2) viruses was performed by HI and virus neutralization (VN) assays. Ferret antisera raised against cell culture-propagated A/Darwin/6/2021-like viruses and egg-propagated A/Darwin/9/2021-like viruses (2a.2), representing the vaccine viruses for the SH 2022 and NH 2022-2023 influenza seasons, recognized recent 2a.2 viruses possessing the HA1 substitution H156S well. However, a small number of 2a.2 viruses without the H156S substitution reacted less well with these antisera. Recent 2a.1 viruses, including those with additional HA1 substitutions, were recognized well by ferret antisera raised against cell culture-propagated A/Cambodia/ e0826360/2020-like viruses (2a.1), but were recognized less well by ferret antisera raised against 2a.2 viruses (cell culture-propagated A/Darwin/6/2021-like and egg- propagated A/Darwin/9/2021-like viruses)

Human serology studies were conducted with human serum panels from the SH 2022 season, using HI and virus neutralization (VN) assays. Geometric mean HI and VN titres against most recent representative A(H3N2) viruses from genetic groups 2a.2 and 2a.1 were not significantly reduced compared to titres against the cell culture-propagated A/Darwin/6/2021 vaccine virus. Reductions of VN GMTs were more pronounced when compared to egg-propagated A/Darwin/9/2021-like reference viruses.

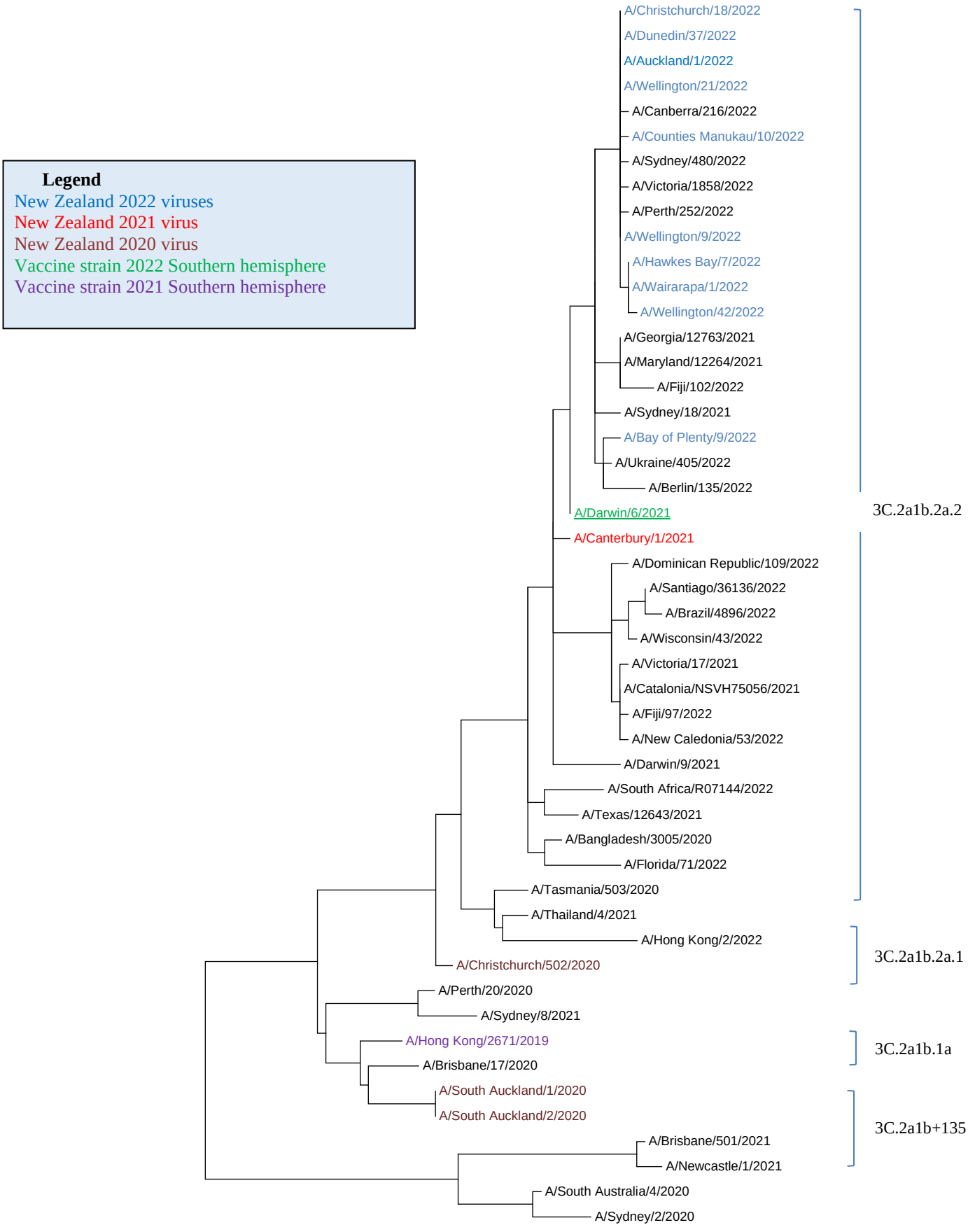
In summary, the vast majority of A(H3N2) viruses collected since 1 February 2022 had HA genes that belonged to genetic group 3C.2a1b.2a.2 (2a.2). The majority of recently circulating viruses were recognized well by ferret anti- sera raised against 2a.2 viruses, such as cell culture-propagated A/Darwin/6/2021 and egg-propagated A/Darwin/9/2021. Human serology assays

showed that post-vaccination GMTs against most recent representative A(H3N2) viruses from genetic groups 2a.2 and 3C.2a1b.2a.1 were not significantly reduced compared to titres against the cell culture-propagated A/Darwin/6/2021 vaccine virus.

Based on all available data, the WHO Consultative Group recommended to continue to use the same vaccine strain containing a cell culture-propagated A/Darwin/6/2021 or egg-propagated A/Darwin/9/2021-like strain. AIVC accepted this recommendation.

(*Abridged from the Weekly Epidemiological Record (WER), 2022 97(43):537-566 and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

Figure 15. Phylogenetic relationships among influenza A(H3N2) haemagglutinin genes



4.2.3 INFLUENZA B

Two distinct lines of influenza B have co-circulated in many countries during recent years. This dates from the late 1980s when the B/Panama/45/90 variant of influenza B was first observed. This strain and its further variants of the Yamagata/16/88 lineage (most recently representative strain-B/Phuket/3073/2013) spread worldwide, whereas strains of the previous B/Victoria/2/87-like viruses continued to circulate in Asia and subsequently underwent independent evolution as an antigenically distinct lineage (most recent representative strain-B/Colorado/6/2017). For reasons not wholly understood, these remained geographically restricted to Asia until 2001. In 2002 the B/Victoria/2/87 lineage viruses were the predominant viruses worldwide.

In 2022, the WHO National Influenza Centre at ESR received 3 influenza B clinical samples and one influenza B virus was isolated by cell culture. Antigenic typing was conducted using rabbit antisera raised against B/Washington/02/2019 supplied by the WHO Collaborating Centre (WHOCC) in Melbourne. It was antigenically closely related to B/Washington/02/2019.

A total of 155 influenza B isolates with collection dates between February to September 2022 were characterized at the Melbourne WHOCC. Globally, influenza B viruses represented 4.7% of the viruses detected since 1 February 2022, and all of those tested 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 substitution K136E and a triple amino acid deletion in HA1 (positions 162-164). The 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 belong to group 1A.3a. The 1A.3a HA diversified into 2 main subgroups, one with additional HA1 substitutions V220M and P241Q (3a.1) and the other with HA1 substitutions A127T, P144L and K203R (3a.2). HA subgroup 3a.1 represented a small proportion of the viruses circulating in early 2022 in China. The 3a.2 HA subgroup has predominated in Africa, Asia (including China), Europe, North America, Oceania, and South America. The majority of viruses in the 3a.2 HA subgroup have the additional substitution D197E in HA1.

Antigenic analysis showed that post-infection ferret antisera raised against B/Austria/1359417/2021-like viruses (3a.2) recognized the predominant 3a.2 subgroup well but recognized other viruses less well. Ferret antisera raised against B/Sichuan-Jingyang/12048/2019-like viruses (3a.1) recognized viruses in subgroup 3a.1 well but subgroup 3a.2 viruses less well. The viruses in subclade 1A.3 that have continued to evolve were not 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, using the serum panels from the SH 2022 season, did not show significant reductions in post-vaccination HI GMTs against the majority of recent representative B/Victoria lineage viruses from the 3a.2 subgroup when compared to the egg or cell culture-propagated B/Austria/1359417/2021 vaccine viruses. Significant reductions were detected with most serum panels for viruses from clade 1A.3 with additional amino acid substitutions K75E, E128K, T155A and G230N. Due to the lack of available recent viruses, human serology studies were not performed for the B/Yamagata lineage.

In summary, all circulating influenza B viruses collected since 1 February 2022 were of the B/Victoria/2/87 lineage. Most recent viruses belonged to genetic subgroups 1A.3a.1 (3a.1) or 1A.3a.2 (3a.2), and the latter predominated. The great majority of the circulating viruses were recognized well by 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 most recent representative B/Victoria lineage viruses from genetic subgroup 3a.2 were not significantly reduced

compared to titres against the 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 B/Austria/1359417/2021-like virus (B/Victoria/2/87-lineage) and B/Phuket/3073/2013-like virus (B/Yamagata/16/88-lineage) as quadrivalent vaccine strains. AIVC accepted this recommendation.

(*Abridged from the Weekly Epidemiological Record (WER), 2022 97(43):537-566 and a report to AIVC by Dr Ian Barr, WHO Collaborating Centre for Influenza, Melbourne).*

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 2022, fluorometric neuraminidase inhibition assay was used to test 72 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, 2017–2022^

Influenza	NA inhibition to Oseltamivir	No. of Influenza Viruses					
		2017	2018	2019	2020	2021	2022
A(H1N1)pdm09	Normal	103	75	12	1	1	3
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	254	6	32	-	3	69
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	548	46	1	-	2	
	Reduced	-	1	-	-	-	-
	Highly reduced	-	-	-	-	-	-

^ Jan-Aug 2022

Neuraminidase inhibition was defined as:

Normal inhibition = IC_{50} values which are within or close to the median IC_{50} of the type/subtype matched viruses as detailed in the table above.

Reduced inhibition = IC_{50} 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 = IC_{50} values which are greater than 100 fold above the median value of viruses with normal inhibition (above 50 fold for influenza B viruses)

Table 8. Antiviral susceptibility to zanamivir for influenza viruses, 2017–2022^

Influenza	NA inhibition to Zanamivir	No. of Influenza Viruses					
		2017	2018	2019	2020	2021	2022
A(H1N1)pdm09	Normal	125	75	12	1	1	3
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
A(H3N2)	Normal	284	6	32	-	3	69
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-
Influenza B	Normal	641	47	1	-	2	-
	Reduced	-	-	-	-	-	-
	Highly reduced	-	-	-	-	-	-

^ Jan-Aug 2022

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), among GP-consultation seeking patients with influenza-like illness (ILI), 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 and ILI 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 75.5% (95% CI: 65.7 to 82.7). For influenza-confirmed SARI cases, the estimated crude vaccine effectiveness (VE) among adults aged 19-64 years was 63.5% (95% CI: 2.3, 87.9). For influenza-confirmed ILI cases, the estimated VE was 58.7% (95% CI: 26.9 to 77.6) (Table 9).

Table 9. Estimated influenza vaccine effectiveness, by participant age group and by influenza virus type and subtype in New Zealand, 2022 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	50	173	993	842	75.5 (65.7, 82.7)
0-18 years	23	135	189	467	57.9 (31.6, 75.0)
19-64 years	27	36	697	339	63.5 (37.0, 79.1)
65+ years	0	0	97	11	N/A
H3	48	169	995	847	75.8 (66.0, 83.0)
0-18 years	22	133	190	470	59.1 (33.0, 75.9)
19-64 years	26	34	698	341	62.6 (34.7, 78.8)
65+ years	0	0	97	11	N/A
SARI					
All ages					
0-18 years	2	33	6	233	N/A
19-64 years	7	41	25	53	63.5 (2.3, 87.9)
65+ years	20	9	39	23	N/A
H3					
0-18 years	2	28	6	233	N/A
19-64 years	3	27	25	53	76.2 (11.1, 95.8)
65+ years	7	2	39	23	N/A
ILI					
All ages	18	144	78	258	58.7 (26.9, 77.6)
0-18 years	1	50	1	86	N/A
19-64 years	9	91	50	160	68.4 (30.9, 86.9)
65+ years	8	3	27	12	N/A

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

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