NIPH
Norwegian Institute of Public Health

REPORT

2023

NORWAY:

IInfluenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2024

September 2023

NORWAY:

Norwegian Institute of Public Health

Influenza Virological and Epidemiological season report

prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2024,

October 2023

Division of Infection Control

Department of Virology

Section for Influenza and other respiratory viruses

and

Department of Infection Control and Vaccines

Section for Respiratory, Blood-borne and Sexually transmitted infections

Authors:

Olav Hungnes
Trine Hessevik Paulsen
Andreas Rohringer
Elina Seppälä
Håkon Bøås
Jesper Dahl
Even Fossum
Jeanette Stålcrantz
Birgitte Klüwer
Kjersti Rydland
Torstein Aune
Karoline Bragstad

ISBN: 978-82-8406-397-3

The 2022-2023 influenza season, Norway

Summary

- The preceding 2021-2022-influenza season developed unusually late, only after the distancing measures against COVID-19 were lifted in February, and at a time when the Omicron-variant driven main pandemic wave was on its decline. The influenza outbreak peaked around week 15, was of low-to medium magnitude, and influenza A(H3N2) viruses in the 3C.2a1b.2a.2 group predominated.
- Seroprevalence against A/Victoria/2570/2019(H1N1) was at a moderate level in sera collected in August 2022. However, there was significantly less antibodies against the A/Norway/25089/2022 strain, which became a prominent subvariant during the H1 outbreak seen in early winter. Seroprevalence against A/Darwin/9/2021 (H3N2) was low in the general population (22 %), although higher in the age groups 5-14 and 15-24 years potentially due to late H3N2-epidemic in spring 2022. Seroprevalence against recent B/Victoria-lineage virus was at a low level, especially in the younger age groups, suggesting a high degree of susceptibility.
- The current season started early with outbreak threshold of 10 % positives in week 48 (sentinel)/week 49 (comprehensive) and had a sharp first peak in weeks 51-52/2022 with 46 % positives in the sentinel and 25 % positives in the comprehensive surveillance. The positivity rate fell markedly in the following few weeks before it recovered and went through two smaller peaks in weeks 6 and 12, respectively. After this, the numbers declined gradually, falling below 10 % positives in overall testing in week 15 and in sentinel testing in week 18. The positivity rate has been very low (below 1%) since midsummer but with sporadic detections in every week.
- Influenza A(H1N1) viruses predominated in the first and largest peak around New Year. With subsequently declining numbers, the frequencies of H1N1 and H3N2 also became more even. Influenza B/Victoria lineage viruses started to rise after New Year, passed influenza A in week 8, and were predominant in the last wave that peaked in week 12. Since midsummer, influenza A viruses have again been in majority among the few detections with a large proportion being H1N1. All circulating influenza B viruses that have been tested for lineage have belonged to the B/Victoria/2/1987 lineage.
- The age group representing school-age children has had the highest proportion of influenza positives throughout the period and has shown rising numbers earlier than the other age groups.
- The proportion of influenza-like illness (ILI) consultations in primary health care gradually increased from week 40/2022, with a rapid increase from week 48/2022, crossing the epidemic threshold the week after. It peaked in week 52/2022, several weeks earlier than normal. After a steep decrease until week 3/2023, the decrease was more gradual, including two minor peaks corresponding to the pattern in the virological surveillance. It crossed below the epidemic threshold in week 14/2023, resulting in a 14-week-long influenza outbreak, two weeks longer than average, before decreasing further down toward and through the summer.
- The numbers of hospitalisations and ICU admissions with influenza began to increase around week 46-2022, reaching a peak in week 52-2022. As of week 34-2023, 5462 hospital admissions and 193 ICU admissions have been reported, clearly exceeding

numbers reported for the preceding season 2021-2022. The weekly number of influenza-associated deaths peaked during weeks 52-2022 – 2-2023, coinciding with the highest rate of all-cause mortality in Norway since 2017.

- 30% (1378/4546) of all influenza positive samples received for surveillance have been whole genome sequenced. Both the H1N1 A/Sydney/5/2021 6B.1A.5a.2 lineage and its A/Norway/25089/2022 6B.1A.5a.2.1 sublineage with the HA P137S substitution have been circulating, but by mid-season the A/Sydney-lineage viruses predominated with several separate clusters. The H3N2 viruses are all categorized as 3C.2a.1b.2a.2 belonging to the A/Slovenia/8720/2022 group of viruses with the R299K substitution. All influenza B viruses sequenced were B/Victoria lineage, belonging to the B/Austria/1359417/2021 clade, but several subgroups were detected with some mutation differences and dominated the late season.
- Vaccination coverage among risk groups younger than 65 years and health care workers decreased compared to the 2021/2022 season. The coverage rate for individuals above 65 years was 64 %, which is at the same level as last season. The number of distributed doses decreased by 9 % compared to the 2021/22 season. 1.2 million doses intended for use in risk groups and health care workers were distributed.
- Highly pathogenic avian influenza viruses (H5N1, H5N5) belonging to clade 2.3.4.4b continued to be detected in wild birds in Norway. During autumn 2022 there were two outbreaks of H5N1 in commercial poultry flocks. In the summer of 2023, there was a mass mortality event among seagulls (particularly black-legged kittiwakes) along the northern coastline of Norway, caused by HPAI H5N1. This virus was also detected in a young red fox found dead in the same area. No human cases have been detected, and the risk of human infection has been assessed as very low.

Influensasesongen 2022-2023 i Norge (Norwegian)

Hovedbudskap

- Influensautbruddet i den foregående 2021-2022-sesongen kom uvanlig sent. Utbruddet begynte å vokse seg stort først i mars, etter at smitteverntiltakene mot covid-19 ble hevet i midten av februar. Det store covid omikronutbruddet var også i sterk nedgang på denne tiden. Influensatoppen ble nådd rundt uke 15 og var av lavt til middels omfang. Influensavirus A(H3N2) i gruppen 3C.2a1b.2a.2 dominerte.
- Seroprevalensen mot influensa A/Victoria/2570/2019(H1N1)-virus var moderat i et panel av serumprøver innsamlet i august 2022. Det var imidlertid signifikant færre som hadde beskyttende antistoff mot den nyere undervarianten A/Norway/25089/2022(H1N1), som har utgjort en stor andel av vinterens influensautbrudd. Andelen med beskyttende antistoff mot A/Darwin/9/2021(H3N2) var lav i befolkningen generelt (22%). Det var noe høyere grad av beskyttelse i aldersgruppene 5-14 og 15-24 år, hvilket kan skyldes H3N2 epidemien på våren 2022. Beskyttende antistoffer mot nyere influensa B/Victoria-virus var lav, særlig blant de yngste, noe som kan indikere lav befolkningsimmunitet.
- Influensasesongen 2022-2023 startet tidlig. Terskelen for utbrudd (10 % av de testede influensapositive) ble nådd i uke 48 basert på fyrtårnprøver og uke 49 basert på alle testede i landets laboratorier. Det økte deretter raskt mot en skarp topp i uke 51/52, med et påfølgende raskt fall over nyttår. Påvisningene gikk ned etter nyttår, men stabiliserte seg og ga deretter to mindre influensatopper i uke 6 og uke 12. Deretter var det et jevnt fall, og andelen influensapositive falt under 10% blant alle testede i uke 15 og blant fyrtårnprøver i uke 18. Svært lav andel (under 1 %) har fått påvist influensa i sommerukene, men det har forekommet funn hver uke.
- Under hovedutbruddstoppen ved nyttår var det klar dominans av influensavirus A(H1N1). Deretter avtok andelen med influensa A gradvis, samtidig som andelen av influensa A med subtype H1N1 og H3N2 jevnet seg ut. Influensavirus B begynte å øke rundt nyttår, kom i flertall i uke 8, og dominerte under den siste toppen i uke 12 og fram til sent i juni. Deretter har det vært klart mest influensavirus A blant de få påvisningene i sommerukene, med H1N1 i flertall blant disse. Alle de influensavirus B som har blitt testet for genotype har tilhørt B/Victoria/2/1987 slektslinjen.
- Gjennom hele sesongen har aldersgruppen med høyest andel influensapositive av de testede vært barn i skolealder (5-14 år). Denne gruppen hadde også tidligere økning enn de øvrige aldersgruppene.
- Andelen legekonsultasjoner i primærhelsetjenesten for influensalignende sykdom (ILS) økte gradvis fra uke 40/2022, med en rask økning fra uke 48 slik at utbruddsterskelen ble krysset uken deretter. Toppen ble nådd i uke 52/2022, flere uker tidligere enn normalt. Etter en kraftig nedgang frem til uke 3/2023, var nedgangen mer gradvis og inkluderte to mindre topper, tilsvarende mønsteret i den virologiske overvåkningen. ILS krysset under utbruddsterskelen igjen i uke 14/2023 slik at vinterens influensautbrudd fikk en varighet på 14 uker, to uker mer enn gjennomsnittet. Andelen ILS sank deretter videre og holdt seg på et stabilt svært lavt nivå frem mot og gjennom sommeren.
- Antallet sykehusinnleggelser og intensivinnleggelser med influensa begynte å øke rundt uke 46-2022, og nådde en topp i uke 52-2022. Frem t.o.m. uke 34-2023 har det foreløpig blitt rapportert om 5462 innleggelser i sykehus og 193 innleggelser i intensivavdeling. Disse tallene er betydelig høyere enn antallet rapporterte innleggelser under sesongen

2021-2022. Ukentlige antall influensa-assosierte dødsfall toppet seg i perioden uke 52-2022 til 2-2023, og sammenfalt med den høyeste raten av dødsfall uavhengig av årsak i Norge siden 2017.

- 30 % av influensaovervåkingsprøvene innkommet til FHI har blitt helgenomsekvensert. Blant A(H1N1) virus har både A/Sydney/5/2021 (subclade 6B.1A.5a.2) og A/Norway25089/2022 (subclade 6B.1A.5a.2.1 med HA-substitusjonen P137S) sirkulert, men fra midten av sesongen har det vært mest av A/Sydney-gruppen, fordelt på flere ulike undergrupper. Influensa A(H3N2)-virusene har alle blitt kategorisert som 3C.2a.1b.2a.2 tilhørende A/Slovenia/8720/2022 gruppen som har HA-substitusjonen R299K. Alle sekvenserte influensavirus B tilhører B/Victoria slektslinjen og den nyere genetiske gruppen representert av B/Austria/1359417/2021. Blant de sekvenserte virusene er det imidlertid flere undergrupper med ytterligere mutasjoner som har vært vanligst mot slutten av utbruddet.
- Vaksinasjonsdekningen i risikogrupper og blant helsepersonell gikk ned sammenlignet med fjorårssesongen, selv om dekningen blant personer over 65 år holdt seg på omtrent samme nivå (64 %) som i fjor. Vaksinasjonsdekningen blant personer over 65 år var 64 prosent på landsbasis. Antallet distribuerte doser gikk ned med 9 prosent fra sesongen 2021/22. Forbruket i programmet var omtrent 1,2 millioner doser.
- Høypatogene fugleinfluensavirus (H5N1 og H5N5) tilhørende undergruppen 2.3.4.4b fortsatte å bli påvist hos ville fugler i Norge. Høsten 2022 var det to utbrudd av H5N1 i kommersielle fjørfebesetninger. Sommeren 2023 forårsaket slike virus massedød blant krykkjer i Troms og Finnmark, med funn av virus i mindre skala også mange andre steder i Norge. Tilsvarende virus ble også påvist i en revevalp funnet død i fylket. Det har ikke blitt ikke påvist smitte til mennesker, og risiko for smitte til mennesker er vurdert som svært lav.

A look back at the preceding 2021/2022 season

The 2021/22 season in Norway saw the return of influenza after its almost total absence during the preceding 2020/21 winter. The outbreak was, however, unusually late, peaking only in April.

It is likely that public health and social measures against COVID-19 were holding influenza back, with most measures being lifted in February 2022 and influenza indicators rising from early March.

The proportion of influenza-like illness (ILI) increased from mid-March and only reached low-level intensity at its peak in week 15, with 5 weeks above the outbreak threshold. Similarly, the frequency of influenza virus detections in non-sentinel and sentinel specimens peaked in week 14.

The trends of influenza hospitalisations and ICU admissions reflected the trends in influenza detections well, with a late peak around week 14-16 in 2022. Between week 40-2021 and 39-2022, a total of 2737 patients were admitted to hospital with influenza, and 64 patients were admitted to ICU, indicating a low-to moderate severity level of the epidemic compared to previous seasons. The weekly number of influenza-associated deaths also peaked during weeks 14-19 in 2022, with a total of 143 influenza-associated deaths being reported between week 40-2021 and 39-2022.

Influenza A(H3N2) viruses predominated. Out of more than 600 000 specimens tested for influenza, 14 706 type A and 140 type B viruses were detected. 95% of subtyped A viruses were H3and 5% were H1pdm09. All lineage typed influenza B viruses belonged to the B/Victoria/2/1987 lineage.

The influenza A(H3N2) viruses driving the 2021/22 influenza outbreak were characterized as A/Bangladesh/4005/2020-like viruses, i.e., belonging to the genetic group 3C.2a1b.2a.2. The majority of the viruses possessed the antigen drift substitution H156*S* in the HA protein. These viruses corresponded well to the H3 vaccine component for the Northern hemisphere 2022/23 season, A/Darwin/6/2021.

Highly pathogenic avian influenza viruses (HPAIVs) belonging to H5 clade 2.3.4.4b were detected in wild birds all across Norway, including Spitzbergen and Jan Mayen. A/H5N1 and A/H5N5 predominated. During summer 2022, H5N1 was detected in a large number of sick or dead seabirds found along the Norwegian coast, and in a few wild red foxes that probably fed on such birds. This was the first detection of the virus in mammals in Norway. In November 2021, Norway experienced the first ever outbreak of HPAI in a commercial poultry, when HPAI H5N1 was detected in two flocks. No cases of avian influenza were detected in humans and the risk of human infection was assessed as very low.

The 2022/2023 season

The components of the surveillance system are briefly described in Appendices.

Influenza-like illness (ILI) in primary health care

The proportion of ILI consultations began to rise gradually from week 40/2022, increasing rapidly from week 48/2022, a few weeks earlier than normal. The present-season epidemic threshold, defined by the Moving Epidemic Method (MEM), was crossed in week 49 (Figure 2). Influenza activity peaked in week 52 when 2,7 % of the consultations were due to influenza-like illness, at medium intensity level, where the ILI indicator resided for only two weeks. The outbreak reached its peak earlier than most previous influenza outbreaks in Norway, which in most seasons peak in late February or early March (Figure 1).

In all age groups, the ILI proportion peaked in week 52/2022, however the ILI proportion among the younger age groups (5-14 and 15-19 years) seem to be affected by the circulating virus types later in the season as ILI in these groups had several waves while influenza B viruses dominated (for more information, see "Influenza hospitalisations based on registry data", and "Laboratory confirmed influenza: Virological surveillance").

There was a gradual decrease in the proportion of ILI from week 3/2023 until it crossed below the epidemic threshold in week 14/2023. The 2022/23 influenza outbreak lasted for 14 weeks according to ILI and the MEM, two weeks longer than an average influenza outbreak in Norway.

Comparing proportion ILI to proportion positive laboratory tests for influenza virus, ILI seems to reflect the trend, and also the beginning and end of the outbreak. However, the top week at medium intensity seems too low compared to both proportion positive tests and the number of influenza hospitalizations. Also, the level of ILI among children does not seem to reflect the high admission rates throughout the season.

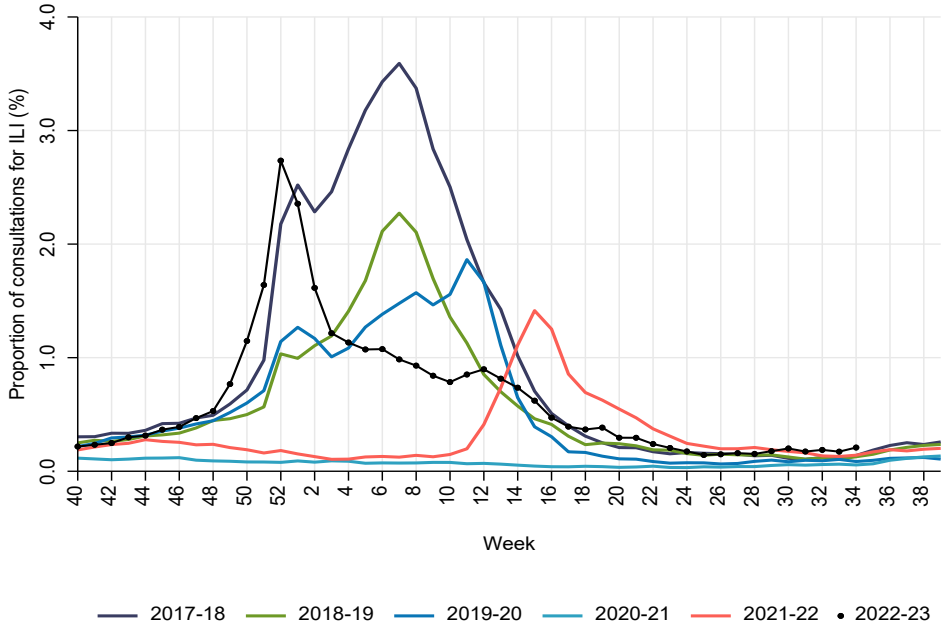

Figure 1. Weekly proportion of consultations for ILI, Norway 2022-2023 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the five previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH.

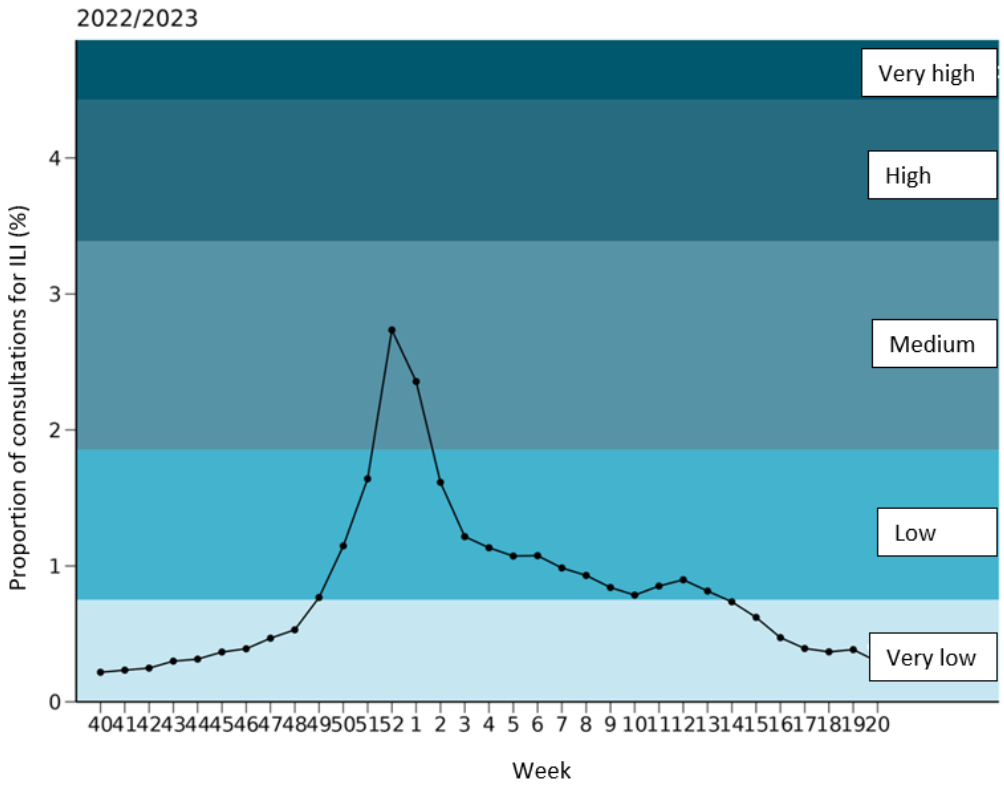

Figure 2. MEM intensity levels, Norway 2022-2023 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSyss with data from KUHR, NIPH.

Influenza hospitalisations based on registry data

Between week 40/2022 and 34/2023, 5462 (99.5 per 100 000 inhabitants) new hospital admissions with influenza, based on influenza diagnosis code and positive influenza test, have been reported, with a peak of 863 new admissions in week 52/2022 (figure 2). The median age of the patients was 64 years, and 49 % (2664) of the admissions were among females. The admission rates were highest in the age groups 65-79 and 80+ years, followed by children aged 0-4 years (table 1). However, the admission rates were strongly affected by the circulating influenza virus types (table 2). While the admissions among the elderly peaked around week 52/2022 when influenza A viruses dominated, admissions among children and adolescents had several peaks, the last of which occurred while influenza B viruses dominated (Figure 4; see "Laboratory confirmed influenza: Virological surveillance" for more information). Thirty-two percent of all patients hospitalised with influenza were vaccinated ≥14 days before testing positive for influenza virus.

In comparison, in season 2021-2022 the influenza epidemic started late, with hospital admission peaking in week 15 (424 new admissions). By week 1/2023, the number of admissions reported in season 2022-2023 already exceeded the number of new admissions reported during the entire one-year period from weeks 40/2021 through 39/2022 (2736).

While registry data on influenza-positive PCR tests have been available only since the start of the COVID-19 pandemic, registry data based on hospital discharge codes alone can be used for comparing seasons from 2017-2018 onward. In comparison to the previous 5 seasons for which

data are available, the weekly number of hospitalisations in week 52/2022 (n=920) was significantly higher than during the top weeks in the other seasons (n=280-625). Furthermore, in the current season, the hospitalisation rate has been higher among the 0-4- and 5-14-year-olds than during any of these previous seasons (figure 3).

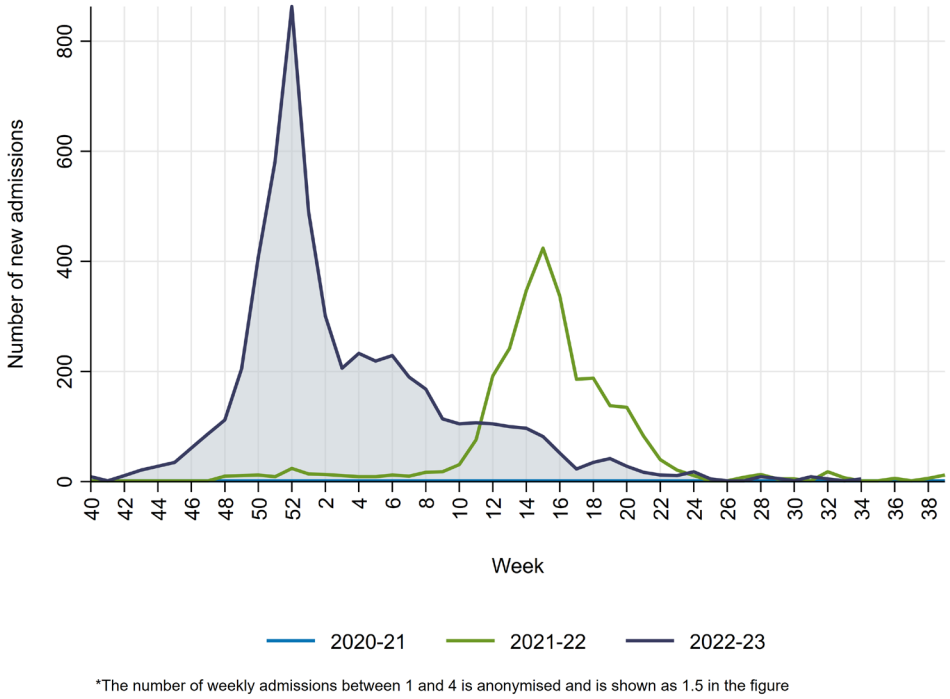

Figure 3. Weekly number of new hospital admissions with influenza by week and season, Norway, 28 September 2020 – 27 August 2023. Source: The Norwegian Emergency Preparedness Registry (Beredt C19) with data from the Norwegian Surveillance System form Communicable Diseases laboratory database and the Norwegian Patient Registry.

Table 1. Number of new hospital admissions with influenza by age group, Norway, 2 October 2022 – 29 January 2023. Source: The Norwegian Emergency Preparedness Registry (Beredt C19) with data from the Norwegian Surveillance System for Communicable Diseases laboratory database and the Norwegian Patient Registry.

	Weeks 40/2022 to 34/2023		
Age group	Admissions	Admissions per 100000	Proportion (%)
0-4 years	466	167.8	8.5
5-14 years	385	60.3	7.0
15-29 years	377	36.7	6.9
30-64 years	1532	60.5	28.0
65-79 years	1610	210.4	29.5
80+ years	1092	443.3	20.0
Total	5462	99.5	100.0

Table 2. Number of new hospital admissions with influenza by virus type and age group, Norway, 2 October 2022 – 27 August 2023. Source: The Norwegian Emergency Preparedness Registry (Beredt C19) with data from the Norwegian Surveillance System for Communicable Diseases laboratory database and the Norwegian Patient Registry.

	Weeks 40/2022 to 34/2023			
	Influenza A		Influenza B	
Age group	Admissions	Admissions per 100000	Admissions	Admissions per 100000
0-4 years	354	127.4	112	40.3
5-14 years	192	30.1	193	30.2
15-29 years	222	21.6	151	14.7
30-64 years	1217	48.0	291	11.5
65-79 years	1540	201.3	48	6.3
80+ years	1037	420.9	45	18.3
Totalt	4562	83.1	840	15.3

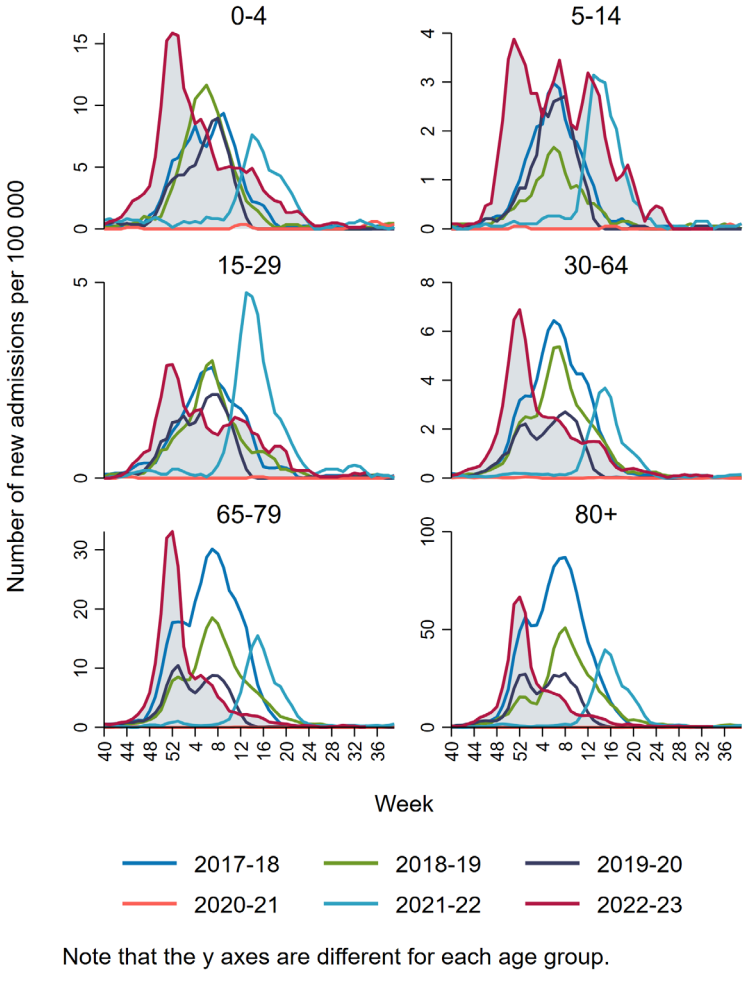

Figure 3. Weekly number of new hospital admissions with influenza by week and season, Norway, 28 September 2020 – 27 August 2023. Source: The Norwegian Emergency Preparedness Registry (Beredt C19) with data from the Norwegian Patient Registry.

Influenza patients in intensive care units

Between week 40/2022 and 20/2023, a total of 193 patients (3.5 per 100 000 inhabitants) were admitted to ICU with confirmed influenza, with a peak of 37 patients admitted in week 52. The median age of the patients was 62 years, and 50 % (97) are female.

In comparison, 63 patients were admitted to ICU with influenza in Norway between weeks 40 and 24 in 2021-2022.

Influenza-associated deaths

Influenza-associated deaths were counted as any death with ICD-10 diagnosis codes J09-J11 stated as one of the causes of death on the death certificate. Between week 40-2022 and 34-2023 there were 265 recorded influenza-associated deaths in Norway, compared to 131 (2021/22), 7 (2020/21), 130 (2019/20), 214 (2018/19), 414 (2017/18) and 309 (2016/17) for the same time period in the preceding seasons. The highest weekly rates of influenza-associated deaths occurred during weeks 52, 1, and 2. This coincided with the highest weekly rate of all-cause death in Norway (during week 52-2022) since week 2-2017. The total number deaths caused by influenza is most likely underestimated, since the influenza-specific ICD-codes are generally used when concurrent laboratory test results are also available, while testing for influenza in e.g. nursing homes is not comprehensive.

Laboratory confirmed influenza: Virological surveillance

Altogether, 260,715 patients in Norway were tested for influenza during weeks 40/2022-34/2023, resulting in 18,084 recorded detections of influenza A virus (71% of the influenza detections) and 7,508 influenza B virus (29% of influenza detections) (Figure 4, Table 2).

Of these, 2,143 influenza A and 1,517 influenza B positive specimens have been referred to the NIC for further identification and characterisation. Among these 2,121 type A viruses were subtyped (1,342 H1(63 %) and 779 H3 (37%). Five type A virus specimens were too weak for successful subtyping and 14 could not be confirmed as influenza A in the NIC. All 1,491 lineage-typed influenza B viruses belonged to the B/Victoria/2/1987 lineage, 13 were confirmed as influenza B but contained too little viral RNA for lineage determination, and 11 initially influenza B positive specimens could not be verified in the NIC.

In addition to this, primary testing laboratories have identified 2,008 type A viruses as H1 and 73 as H3, of which 139 H1 and 14 H3 specimens were forwarded to the NIC. This testing is biased by several laboratories testing for H1pdm09 but not H3.

The number of detections started to rise in early November and increased more and more rapidly until reaching a peak in weeks 51-52/2022, when approx. 25 % of samples in the comprehensive surveillance and 46 % (week 52) in the sentinel surveillance tested positive for influenza. There was a marked drop after New Year, which soon levelled out and then there were two smaller peaks, one mixed influenza A and B peak around week 6, and at last a predominantly influenza B dominated peak around week 12 (Figure 4, 6). This triple-peak pattern may be seen as a composite of declining influenza A rates after New Year and growing

rates of influenza B beginning at the same time and that at some points more than compensated for the influenza A drop. The final peak around week 12 consisted mainly of influenza B infections. After this, there was a steady decline with overall positivity rate going below 10% in week 15 and continuing to drop until domestic circulation had more or less subsided around midsummer.

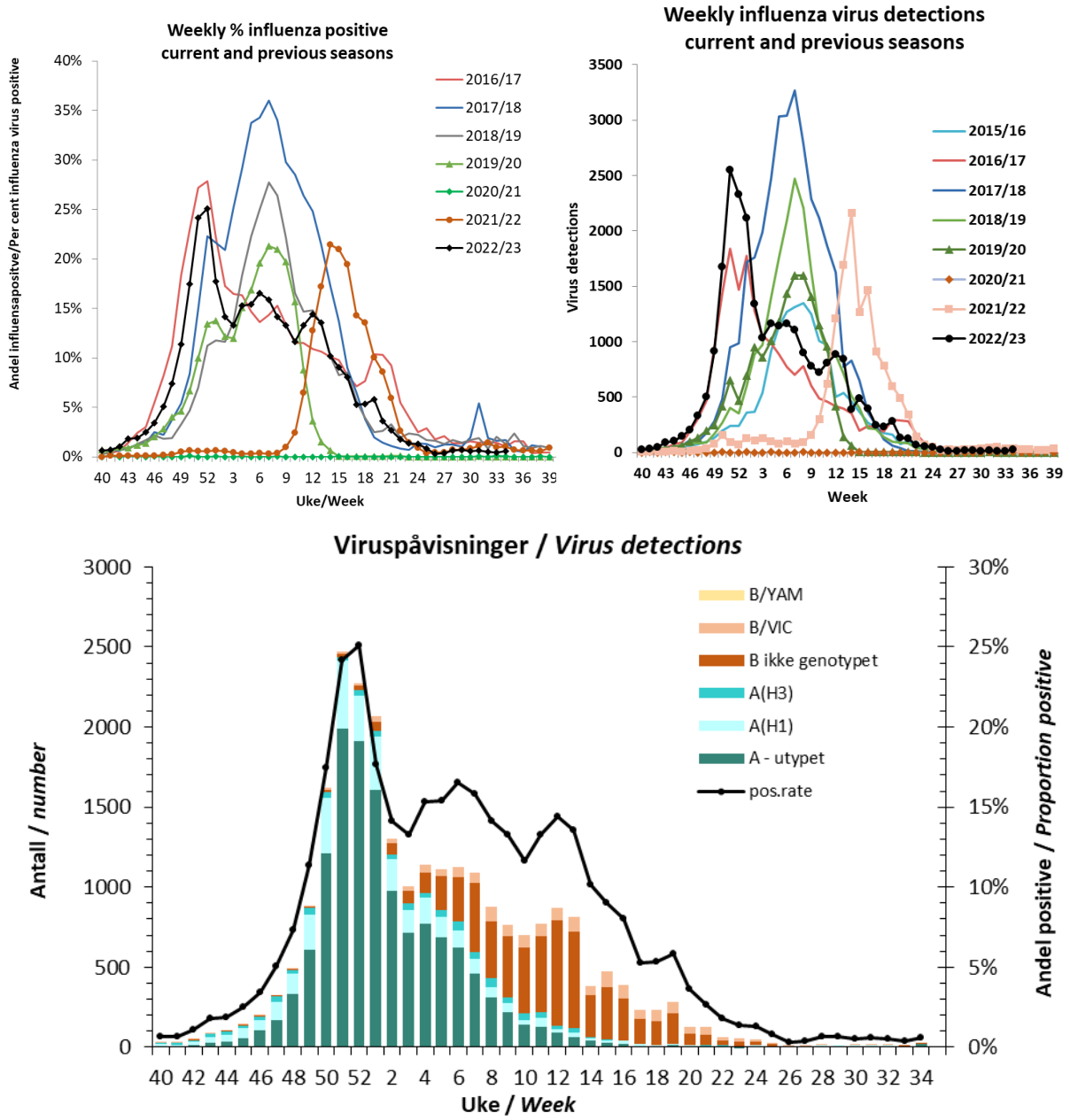

Figure 4. Laboratory detections, Norway 2022-2023. Upper left-hand panel: Weekly proportion of influenza virus positive specimens, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. Seasons impacted by Covid-19 are marked with symbols.
Lower panel: Weekly number of the different influenza viruses, displayed as stacked bars.

During the main peak around New Year, A(H1N1) viruses predominated. During late winter and spring the dwindling number of influenza A infections were more evenly distributed between subtypes H1N1 and H3N2 (Figure 5). Influenza B viruses were exclusively B/Victoria/2/87-lineage. There was some regional heterogeneity in the proportions of the different influenza types and subtypes, particularly in the beginning. The subtype analysis is limited to viruses that have been tested for both H1 and H3, since many laboratories test only for H1 and not H3, thus producing a strong subtype bias.

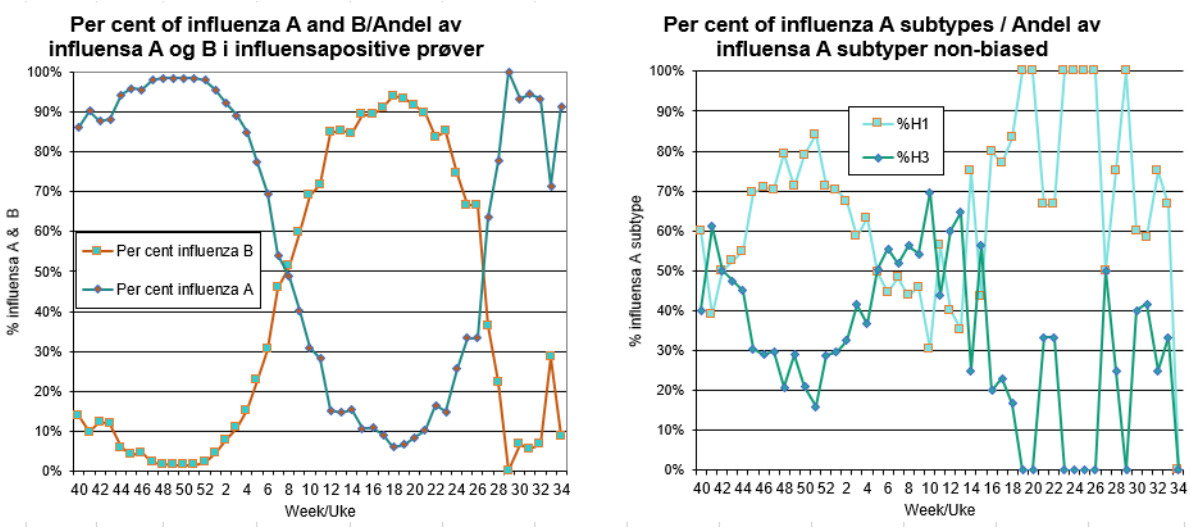

Figure 5. Influenza virus detections since week 40/2022, proportions per type A and B (left panel) and influenza A subtypes H1 and H3 (right panel). Only viruses tested for both subtypes are counted in the subtype analysis.

False positives due to vaccine contaminating sampling workstations?
Similar to earlier seasons, in a few instances in the autumn trace amounts of virus RNA representing three or four different subtypes/lineages were detected in the same sample; this has been interpreted as likely contamination with tetravalent influenza vaccine and they have not been counted as infections in the surveillance. In one case there was sufficient virus to obtain partial sequence, and the genetic profile was indicating the genetic backbone of live attenuated vaccine strains. However, the use of LAIV in Norway has been extremely low, and in most cases the source is believed to be environmental contamination with inactivated vaccine in settings where administration of vaccine and respiratory specimen collection is done at the same workstation.

Table 2. Weekly total number of specimens tested for influenza, proportion of specimens positive for influenza virus, and influenza virus detections per type/subtype/lineage, in Norway from week 40/2022 through week 34/2023 (sentinel and non-sentinel data combined).

	Viruspåvisninger/*Virus detections*							
UKE/ *week*	Prøver/ *Specimens*	% positive	A(utypet) *not subtyped*	A(H1)	A(H3)	B ikke genotypet *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
40	4392	0,7 %	7	12	6	2	2	0
41	4489	0,7 %	8	9	11	2	1	0
42	4623	1,1 %	15	18	10	5	1	0
43	5176	1,8 %	27	36	19	5	6	0
44	5545	1,9 %	33	42	23	6	0	0
45	5881	2,5 %	54	67	21	4	2	0
46	5882	3,4 %	107	67	18	7	2	0
47	6520	5,1 %	174	117	33	7	0	0
48	6863	7,4 %	329	146	22	5	3	0
49	8056	11,4 %	614	236	51	7	7	0
50	9598	17,5 %	1210	394	46	13	12	0
51	10546	24,2 %	1994	482	32	23	17	0
52	9277	25,1 %	1923	306	50	29	20	0
1	11937	17,7 %	1609	365	46	58	35	0
2	9482	14,1 %	974	224	41	69	33	0
3	7811	13,3 %	713	161	49	76	36	0
4	7610	15,3 %	772	180	36	129	47	0
5	7415	15,4 %	687	134	61	209	50	0
6	7054	16,5 %	628	116	66	279	76	0
7	6982	15,8 %	457	97	44	434	74	0
8	6365	14,2 %	309	72	58	351	111	0
9	5887	13,2 %	222	53	39	382	84	0
10	6216	11,6 %	138	38	48	408	92	0
11	6057	13,3 %	124	68	35	476	102	0
12	6178	14,4 %	90	21	24	661	93	0
13	6209	13,5 %	65	26	33	599	118	0
14	3836	10,2 %	42	14	4	264	66	0
15	5381	9,0 %	28	11	13	326	107	0
16	4975	8,0 %	24	16	3	266	90	0
17	4648	5,3 %	8	11	3	158	65	0
18	4369	5,3 %	8	5	1	149	70	0
19	4890	5,8 %	11	8	0	196	70	0
20	3595	3,6 %	4	7	0	74	45	0
21	4729	2,7 %	2	8	3	65	49	0
22	3753	1,8 %	6	4	1	34	22	0
23	3946	1,4 %	0	8	0	26	20	0
24	3582	1,3 %	3	9	0	22	13	0
25	3348	0,8 %	4	5	0	10	8	0
26	3219	0,3 %	1	2	0	2	4	0
27	2893	0,4 %	4	2	1	2	2	0
28	2725	0,7 %	8	5	1	2	2	0
29	2699	0,7 %	9	9	0	0	0	0
30	2773	0,5 %	7	5	2	0	1	0
31	2877	0,6 %	5	7	5	0	1	0
32	2992	0,5 %	4	8	2	0	1	0
33	3414	0,4 %	6	3	1	4	0	0
34	4020	0,6 %	20	1	0	2	0	0
Total	260715		13487	3635	962	5848	1660	0
UKE/ *week*	Prøver/ *Specimens*	% positive	A(utypet) *not subtyped*	A(H1)	A(H3)	B ikke genotypet *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
		Type A: 18084			Type B: 7508			

Sentinel-based surveillance

From week 40/2022 through week 34/2023, 3566 sentinel specimens have been tested, with 463 detections of influenza virus A (314 subtype H1, 132 subtype H3, and 17 not subtyped), and 195 influenza virus B (of which 187 were Victoria-lineage and 8 were not lineage identified and none were Yamagata-lineage). In addition, 396 SARS-CoV-2, 182 RSV, 499 rhinovirus, 119 human metapneumovirus (hMPV), 184 parainfluenza virus and 146 other human coronaviruses were detected (Fig 6, Table 3). Influenza detections increased and peaked simultaneously to the detections in the non-sentinel virological surveillance.

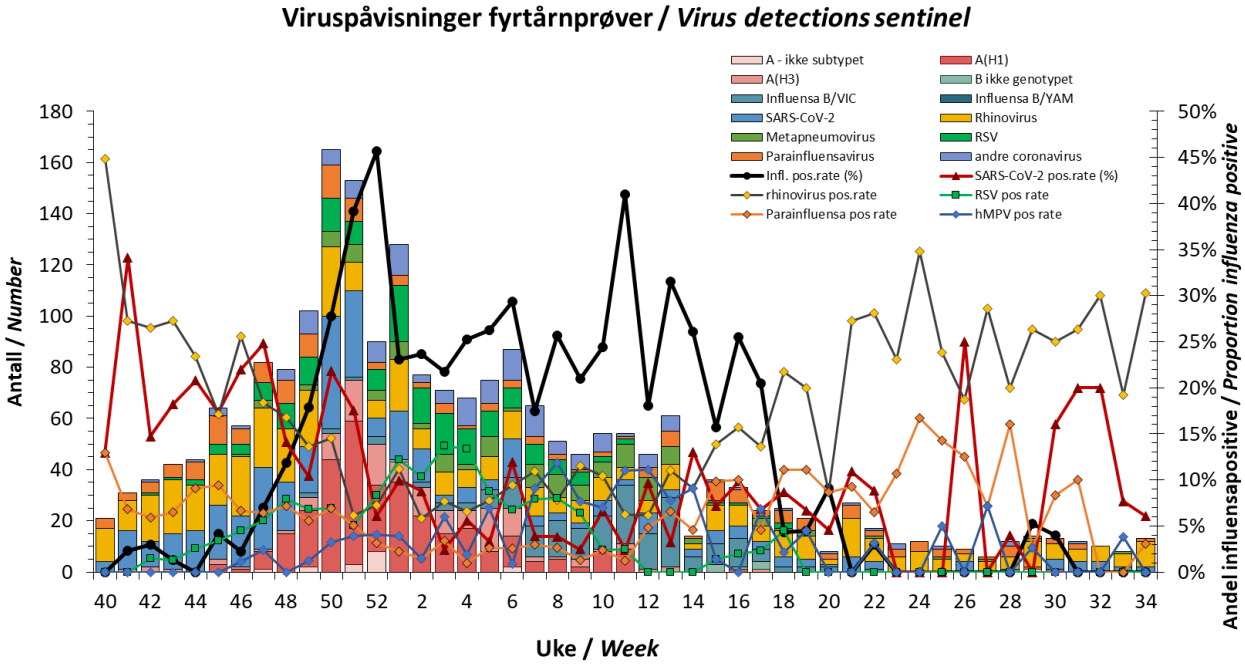

Figure 6. Weekly numbers of detections and per cent positives of respiratory viruses in the respiratory sentinel surveillance.

Table 3. Weekly virus detections in the virological sentinel system (fyrtårnsystemet)

Week	Specimens tested	Influenza A - not subtyped	A(H1)	A(H3)	Influenza B untyped	B/Victoria	B/Yamagata	Influenza % positive	Influenza A % positive	Influenza B % positive	SARS-CoV-2 antall	% positive	RSV	% positive	Rhinovirus	% positive	Parainfluensa 1	Parainfluensa 2/4	Parainfluensa 3	All parainfl. % positive	Metapneumovirus	% positive	Andre coronavirus	% positive
41	44	0	0	1	0	0	0	2 %	2 %	0 %	15	34 %	0	0 %	12	27 %	1	0	2	7 %	0	0 %	0	0 %
42	68	0	0	2	0	0	0	3 %	3 %	0 %	10	15 %	1	1 %	18	26 %	2	2	0	6 %	0	0 %	1	1 %
43	77	0	0	1	0	0	0	1 %	1 %	0 %	14	18 %	1	1 %	21	27 %	2	2	1	6 %	0	0 %	0	0 %
44	77	0	0	0	0	0	0	0 %	0 %	0 %	16	21 %	2	3 %	18	23 %	3	3	1	9 %	0	0 %	1	1 %
45	121	0	3	2	0	0	0	4 %	4 %	0 %	21	17 %	4	3 %	20	17 %	4	4	3	9 %	0	0 %	3	2 %
46	91	0	1	1	0	0	0	2 %	2 %	0 %	20	22 %	4	4 %	23	26 %	2	2	2	7 %	1	1 %	1	1 %
47	129	1	7	1	0	0	0	7 %	7 %	0 %	32	25 %	7	6 %	23	18 %	3	3	2	6 %	3	2 %	0	0 %
48	135	0	15	1	0	0	0	12 %	12 %	0 %	19	14 %	10	8 %	21	17 %	3	3	3	7 %	0	0 %	4	3 %
49	173	2	22	5	0	2	0	18 %	17 %	1 %	18	10 %	11	7 %	22	14 %	5	3	1	6 %	2	1 %	9	5 %
50	202	0	44	10	0	2	0	28 %	27 %	1 %	44	22 %	13	7 %	27	15 %	8	5	0	7 %	6	3 %	6	3 %
51	194	3	56	16	0	1	0	39 %	39 %	1 %	34	18 %	9	5 %	11	6 %	4	3	2	5 %	7	4 %	7	4 %
52	116	8	26	16	0	3	0	46 %	43 %	3 %	7	6 %	8	8 %	7	7 %	0	1	2	3 %	4	4 %	8	7 %
1	191	0	35	8	1	0	0	23 %	23 %	1 %	19	10 %	22	12 %	20	11 %	2	1	1	2 %	7	4 %	12	6 %
2	148	0	22	11	0	2	0	24 %	22 %	1 %	13	9 %	14	10 %	8	6 %	1	1	0	1 %	2	1 %	3	2 %
3	124	0	15	9	0	3	0	22 %	19 %	2 %	3	2 %	16	14 %	9	8 %	2	0	2	3 %	7	6 %	5	4 %
4	107	0	17	7	0	3	0	25 %	22 %	3 %	6	6 %	14	13 %	7	7 %	0	0	1	1 %	2	2 %	11	10 %
5	122	0	8	17	0	7	0	26 %	20 %	6 %	4	3 %	10	9 %	9	8 %	0	2	1	3 %	8	7 %	9	7 %
6	126	2	12	11	0	12	0	29 %	20 %	10 %	15	12 %	8	7 %	11	9 %	1	0	2	3 %	1	1 %	12	10 %
7	103	0	4	2	0	12	0	17 %	6 %	12 %	4	4 %	8	8 %	11	11 %	0	1	2	3 %	9	9 %	12	12 %
8	78	0	5	1	0	14	0	26 %	8 %	18 %	3	4 %	6	8 %	6	8 %	0	1	1	3 %	9	12 %	5	6 %
9	81	0	2	3	0	12	0	21 %	6 %	15 %	2	2 %	5	6 %	9	12 %	0	0	1	1 %	6	8 %	6	7 %
10	90	0	8	1	0	13	0	24 %	10 %	14 %	6	7 %	2	2 %	9	10 %	1	0	1	2 %	6	7 %	7	8 %
11	83	0	9	2	0	23	0	41 %	13 %	28 %	2	2 %	2	2 %	5	6 %	0	0	1	1 %	9	11 %	1	1 %
12	83	0	0	1	0	14	0	18 %	1 %	17 %	8	10 %	0	0 %	5	6 %	0	1	3	5 %	9	11 %	5	6 %
13	92	0	0	2	0	27	0	32 %	2 %	29 %	3	3 %	0	0 %	10	11 %	0	1	5	7 %	7	8 %	6	7 %
14	23	0	0	0	0	6	0	26 %	0 %	26 %	3	13 %	0	0 %	2	9 %	0	0	1	5 %	2	9 %	0	0 %
15	70	0	0	0	3	8	0	16 %	0 %	16 %	5	7 %	1	1 %	10	14 %	0	1	6	10 %	1	1 %	1	1 %
16	51	0	1	0	1	11	0	25 %	2 %	24 %	5	10 %	1	2 %	8	16 %	0	0	5	10 %	0	0 %	1	2 %
17	44	0	0	1	3	5	0	20 %	2 %	18 %	3	7 %	1	2 %	6	14 %	0	1	1	5 %	3	7 %	0	0 %
18	46	0	0	0	0	2	0	4 %	0 %	4 %	4	9 %	2	4 %	10	22 %	0	0	5	11 %	1	2 %	1	2 %
19	45	0	0	0	0	2	0	4 %	0 %	4 %	3	7 %	0	0 %	9	20 %	0	1	4	11 %	2	4 %	0	0 %
20	22	0	0	0	0	2	0	9 %	0 %	9 %	1	5 %	0	0 %	2	9 %	0	0	2	9 %	0	0 %	1	5 %
21	55	0	0	0	0	0	0	0 %	0 %	0 %	6	11 %	0	0 %	15	27 %	0	1	4	9 %	0	0 %	1	2 %
22	34	0	0	0	0	1	0	3 %	0 %	3 %	3	9 %	0	0 %	9	28 %	0	0	2	6 %	1	3 %	1	3 %
23	28	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	6	23 %	0	0	3	11 %	0	0 %	2	7 %
24	24	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	8	35 %	0	0	4	17 %	0	0 %	0	0 %
25	21	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	5	24 %	0	1	2	14 %	1	5 %	1	5 %
26	16	0	0	0	0	0	0	0 %	0 %	0 %	4	25 %	0	0 %	3	19 %	0	1	1	13 %	0	0 %	0	0 %
27	14	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	4	29 %	0	1	0	7 %	1	7 %	0	0 %
28	25	0	0	0	0	0	0	0 %	0 %	0 %	1	4 %	0	0 %	5	20 %	0	0	4	16 %	0	0 %	2	8 %
29	38	1	1	0	0	0	0	5 %	5 %	0 %	0	0 %	0	0 %	10	26 %	0	1	0	3 %	1	3 %	0	0 %
30	25	0	1	0	0	0	0	4 %	4 %	0 %	4	16 %	0	0 %	6	25 %	0	2	0	8 %	0	0 %	0	0 %
31	20	0	0	0	0	0	0	0 %	0 %	0 %	4	20 %	0	0 %	5	26 %	0	2	0	10 %	0	0 %	1	5 %
32	20	0	0	0	0	0	0	0 %	0 %	0 %	4	20 %	0	0 %	6	30 %	0	0	0	0 %	0	0 %	0	0 %
33	26	0	0	0	0	0	0	0 %	0 %	0 %	2	8 %	0	0 %	5	19 %	0	0	0	0 %	1	4 %	0	0 %
34	33	0	0	0	0	0	0	0 %	0 %	0 %	2	6 %	0	0 %	10	30 %	0	1	0	3 %	0	0 %	0	0 %
Sum	3566	17	314	132	8	187	0				396		182		499		45	52	87		119		146	

Genetic characterization of Influenza viruses in Norway

This season NIPH has received 4546 influenza viruses for analysis and 30.0 % of these has been characterized further with whole genome sequencing. This season 72 clinical isolates have so far been shared with the WHO Collaborating Centre in the UK (Worldwide Influenza Centre, Francis Crick Institute) and 1120 HA gene sequences have been submitted to GISAID.

H1N1 viruses

This season, all characterized H1N1 viruses are classified as 6B.1A.5a.2, as shown in Figure 7 and Table 4. During the summer and fall of the previous season 2021-22, new strains of H1N1 virus emerged and constituted a larger proportion of the H1 viruses. These H1 viruses are this season defined by the WHO as A/Norway/25089/2022-like viruses, NextClade classified as 6B.1.A.5a.2.1 and are being closely monitored due to the emergence of immune evasion mutations. At the beginning of the 2022/23 influenza season, these viruses made up about half of all detections in Norway together with the A/Sydney/5/2021 viruses. The A/Norway-like viruses (circulating in Norway) carry haemagglutinin mutations P137S, K142R and T277A. Two clusters of the H1 A/Sydney/5/2021 lineage are defined by the N129D and T185I mutation and are related to the earlier A/Victoria/2570/2019 line, both clusters continued to grow through the season as seen in Figure 8B and Figure 9. Although 6B.1.A.5a.2.1 A/Norway/25089/2022-like viruses dominated at the beginning of the season, A/Sydney/5/2021 viruses have been dominant since the end of December among the H1N1 detections. For the neuraminidase no reassortment between the clades have been observed as seen in Figure 10.

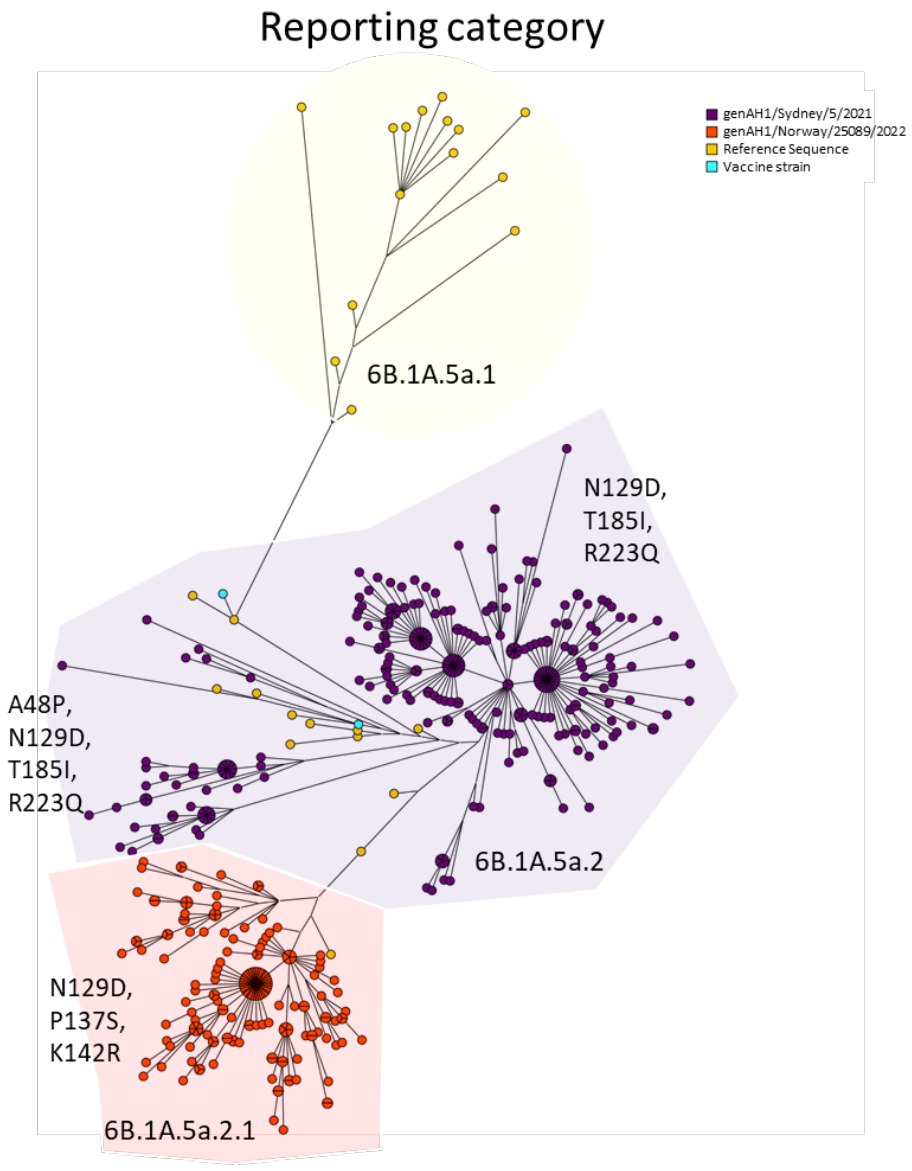

Figure 7 H1N1 Maximum Parsimony tree: The figure shows how the haemagglutinin sequences of H1N1 influenza genomes from viruses in Norway group genetically with reference viruses and vaccine strains from the northern and southern hemispheres, colour coded by ECDC/EuroFlu reporting category.

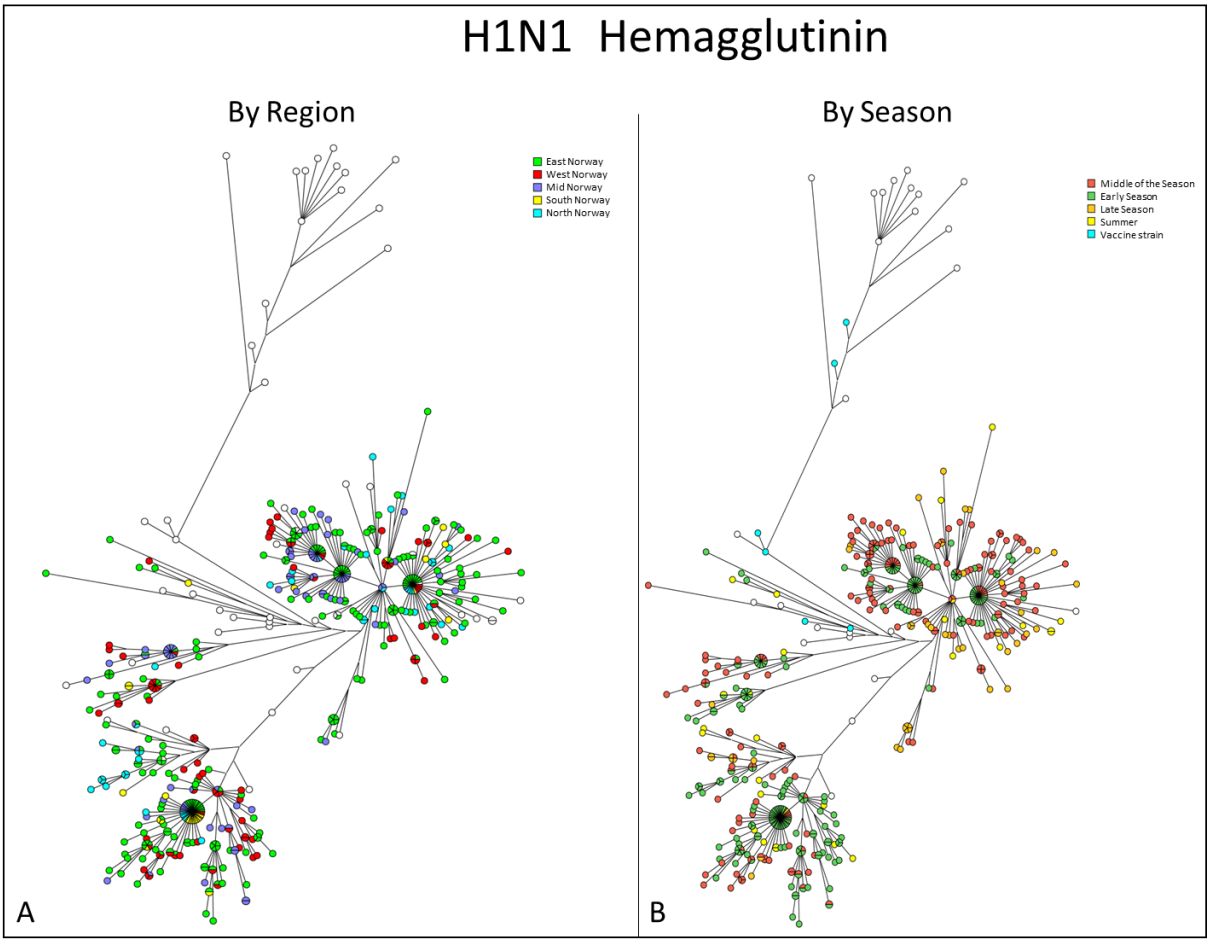

Figure 8 H1N1 Maximum Parsimony tree: The figure shows how the haemagglutinin sequences of H1N1 influenza genomes from viruses in Norway group genetically with reference viruses and vaccine strains from the northern and southern hemispheres, colour-coded by region of detection (A) or Season of detection (B). Early Season defines the period between week 40 and week 50 in 2022, Mid-Season is between 50 2022 and week 12 2023), Late season week 12 – week 19 and summer period between weeks week 19 and 40.

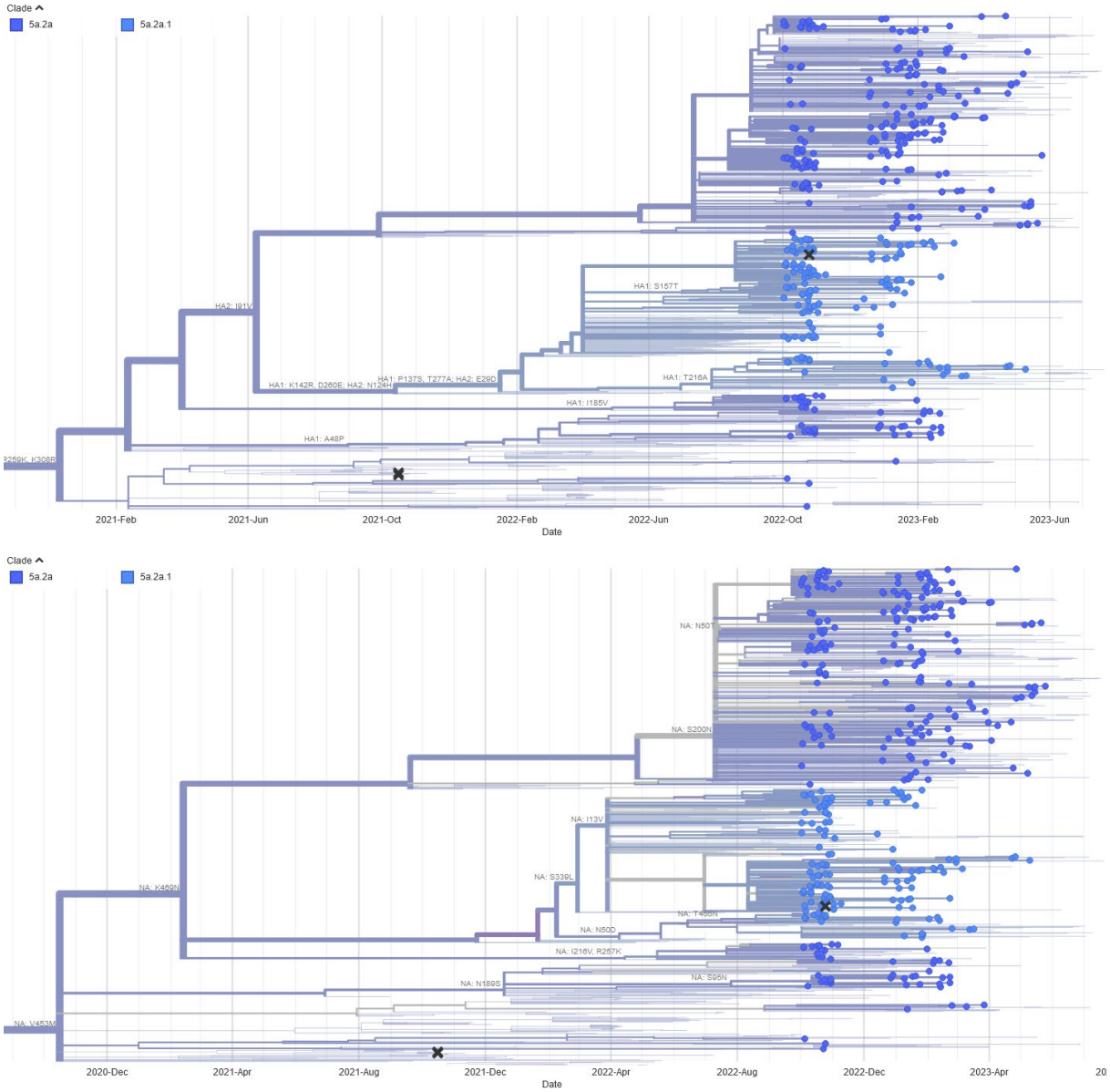

Figure 9. H1N1 Phylogenetic tree: NextClade phylogenetic tree of the haemagglutinin (Top) and neuraminidase (Bottom) of the H1N1 viruses from Norway compared with other international strains. Clade defining amino acids indicated on key nodes.

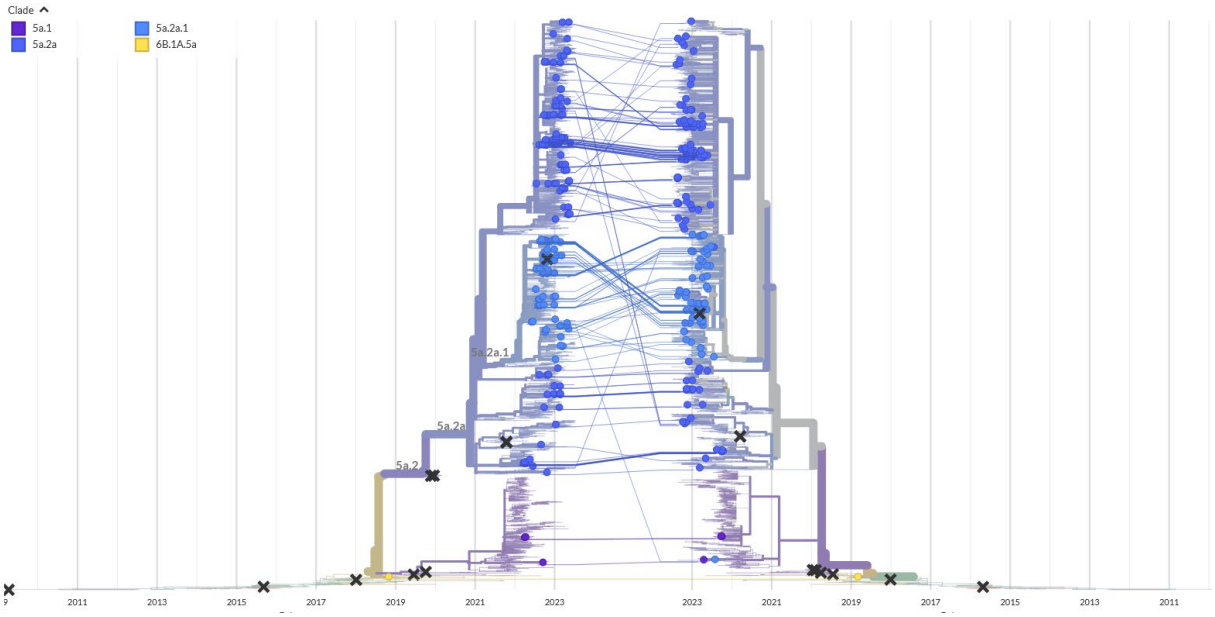

Figure 10. H1N1 Phylogenetic tree: NextClade phylogenetic tree of the haemagglutinin (left) and neuraminidase (right) of the H1N1 viruses from Norway compared with other international strains. Clades indicated on key nodes.

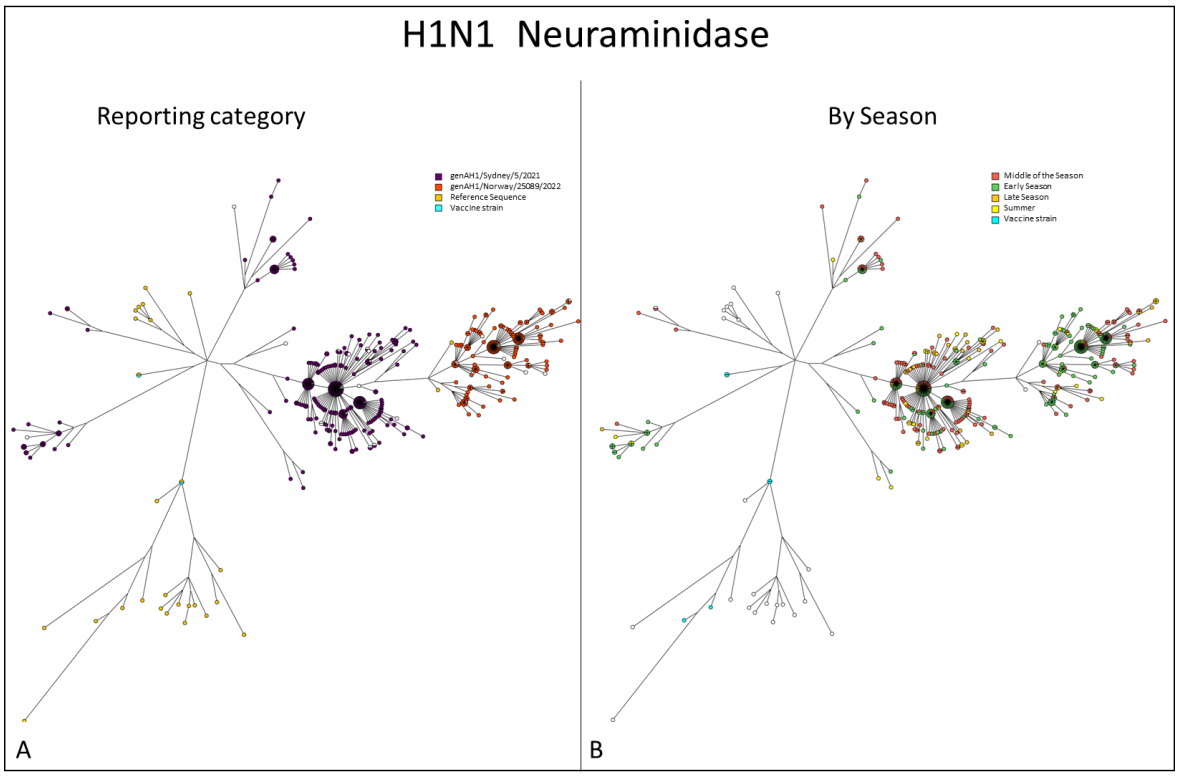

Figure 11. H1N1 Maximum Parsimony tree: The figure shows how the neuraminidase sequences of H1N1 influenza genomes from viruses in Norway group genetically with reference viruses and vaccine strains from the northern and southern hemispheres, color-coded by Sequence (A) or Season of detection (B). Early Season defines the period between week 40 and week 50 in 2022, Mid-Season is between 50 2022 and week 12 2023), Late season week 12 – week 19 and summer period between weeks week 19 and 40.

H3N2 viruses

This season the H3N2 viruses have been classified as belonging to the 3C.2a.1b.2a.2 group of H3 viruses, as shown in Figure 12 and Table 4. Most of the viruses belonged to the A/Slovenia/8720/2022 group of viruses and carry mutations I140K, G186D and G225D in HA. Other viruses were characterized as A/Bangladesh/4005/2020-like (I137K, S153H, N186D and G225D) and A/Darwin/9/2021 group of viruses defined by N96S, I140K, G186D, I192F and G225D mutations are also detected. All subvariants appear to be genetically well covered by the vaccine. All genetic clusters had detections since week 51 2022 and are continuing to grow although slower than the H1N1 lineages (Figure 12A, Table 4). Interestingly, the NA gene shows many reassortment events between the A/Bangladesh/4005/2020-like and the A/Slovenia/8720/2022 like viruses. While the A/Darwin/9/2021-like NA genes mainly cluster like the HA based clusters (Figure 13A).

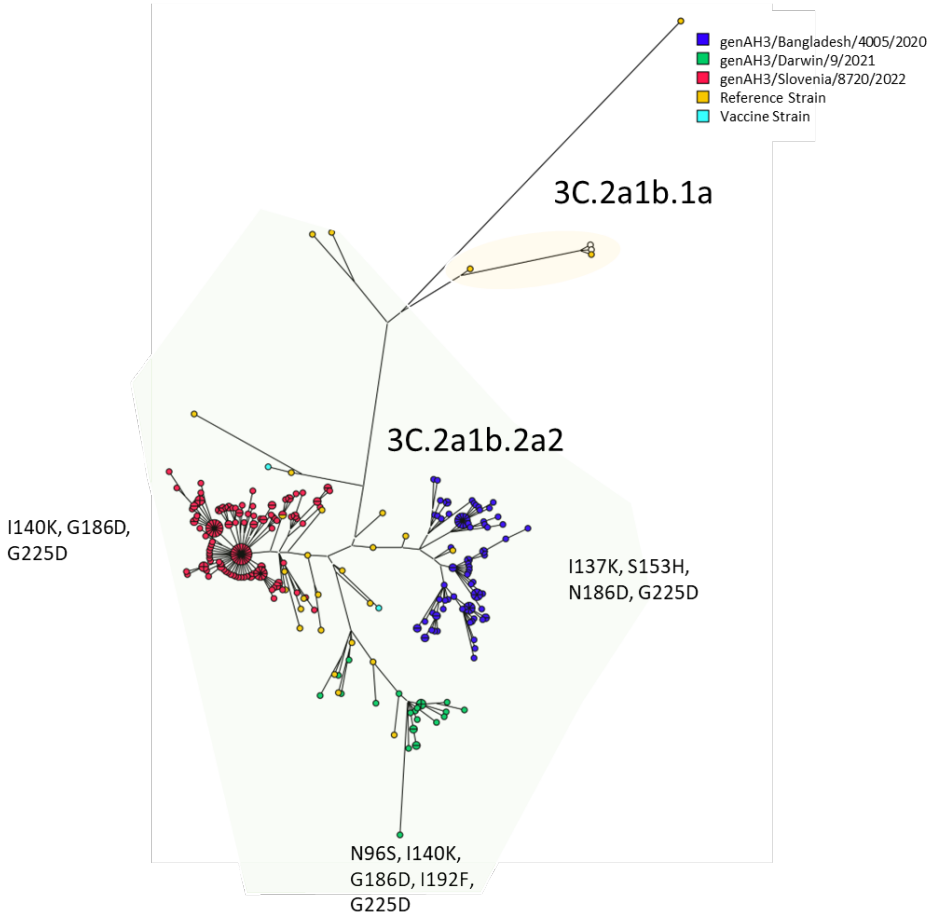

Figure 12. The H3N2 Maximum Parsimony Tree: The figure shows how the hemagglutinin sequence of the H3N2 viruses from Norway genetically groups with reference Viruses and vaccine strains from the northern and southern hemisphere, color-coded by ECDC/EuroFlu reporting category.

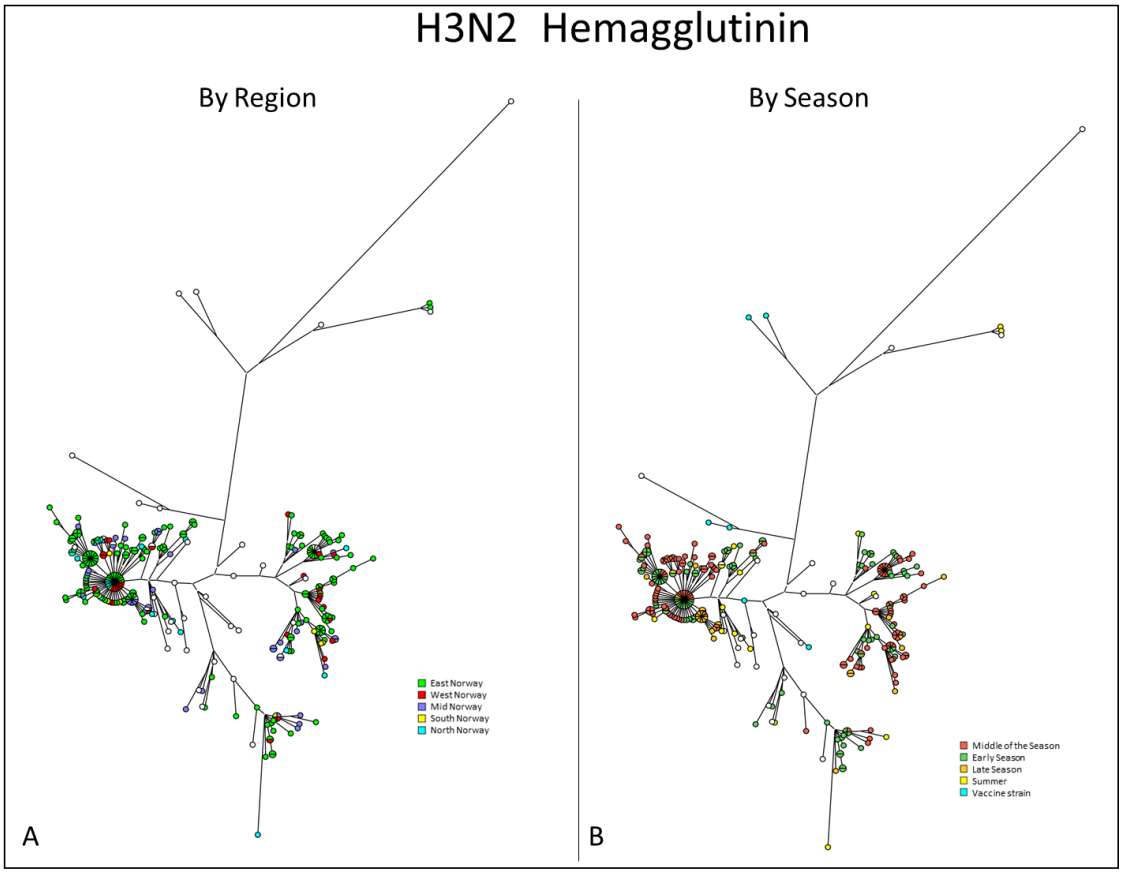

Figure 13. H3N2 Maximum Parsimony tree: The figure shows how the hemagglutinin sequences of H3N2 influenza genomes from viruses in Norway group genetically with reference viruses and vaccine strains from the northern and southern hemispheres, color-coded by Sequence (A) or Season of detection (B). Early Season defines the period between week 40 and week 50 in 2022, Mid-Season is between 50 2022 and week 12 2023), Late season week 12 – week 19 and summer period between weeks week 19 and 40.

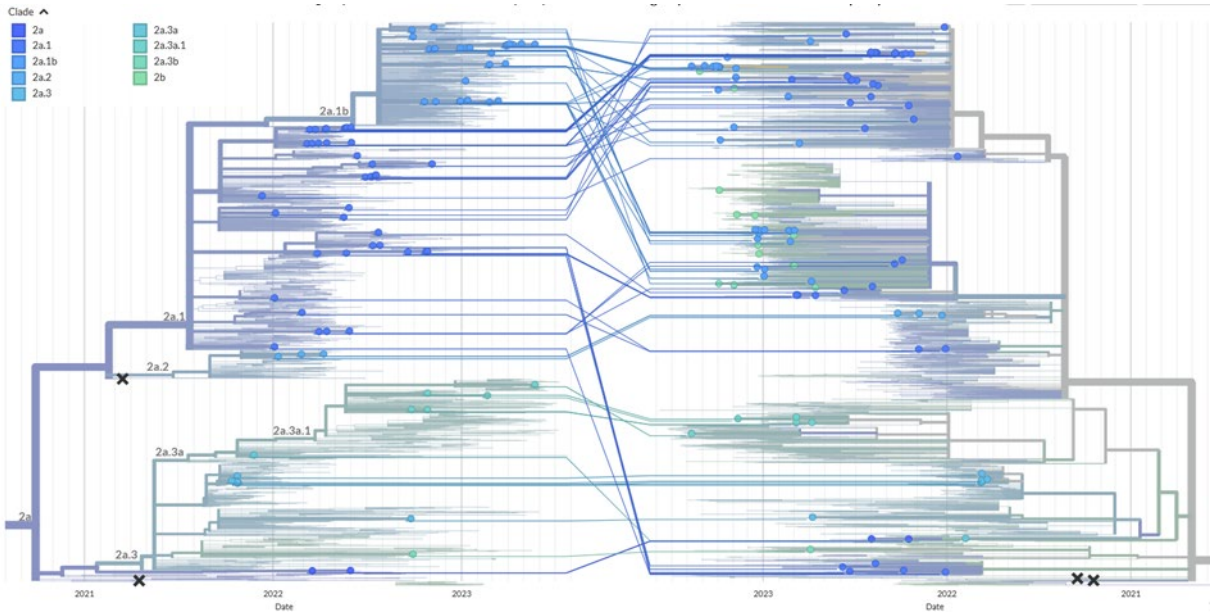

Figure 14 *H3N2 Phylogenetic tree: NextClade phylogenetic tree of the haemagglutinin (left) and neuraminidase (right) of the H3N2 viruses from Norway compared with other international strains. Clades indicated on key nodes.*

B/Victoria-lineage viruses

The B/Victoria virus sequences fall under the B/Austria/1359417/2021-like virus group (Figure 14). Viruses with a number of additional mutations have also been detected, such as viruses with A127T, N129D, N197E, Y586C/R, S208P and D209E. 341 B/Victoria strains have been sequenced over the whole season, the frequency is increased in 2023 and overtook the weekly H1N1 numbers the early weeks of 2023. However, all variants appear to be genetically well covered by the vaccine.

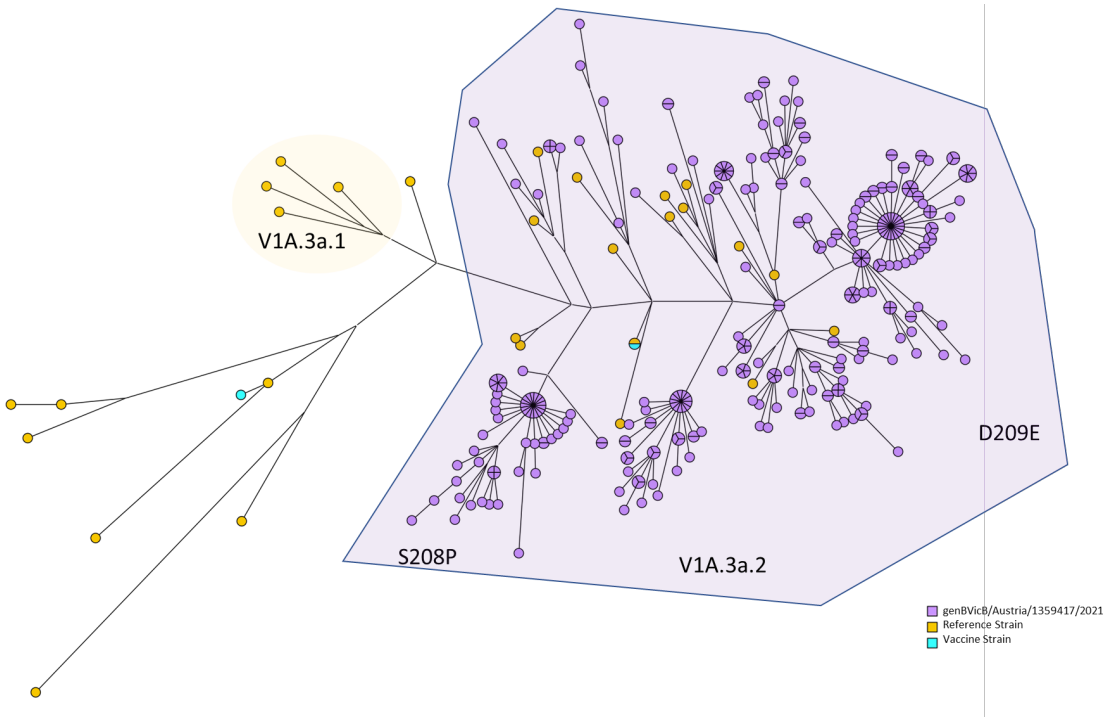

Figure 15. B/Victoria Maximum Parsimony tree: The figure shows how the hemagglutinin sequence of B/Victoria influenza genome sequences from viruses in Norway genetically groups with reference viruses and vaccine strains from the northern and southern hemispheres, color-coded according to the ECDC reporting category.

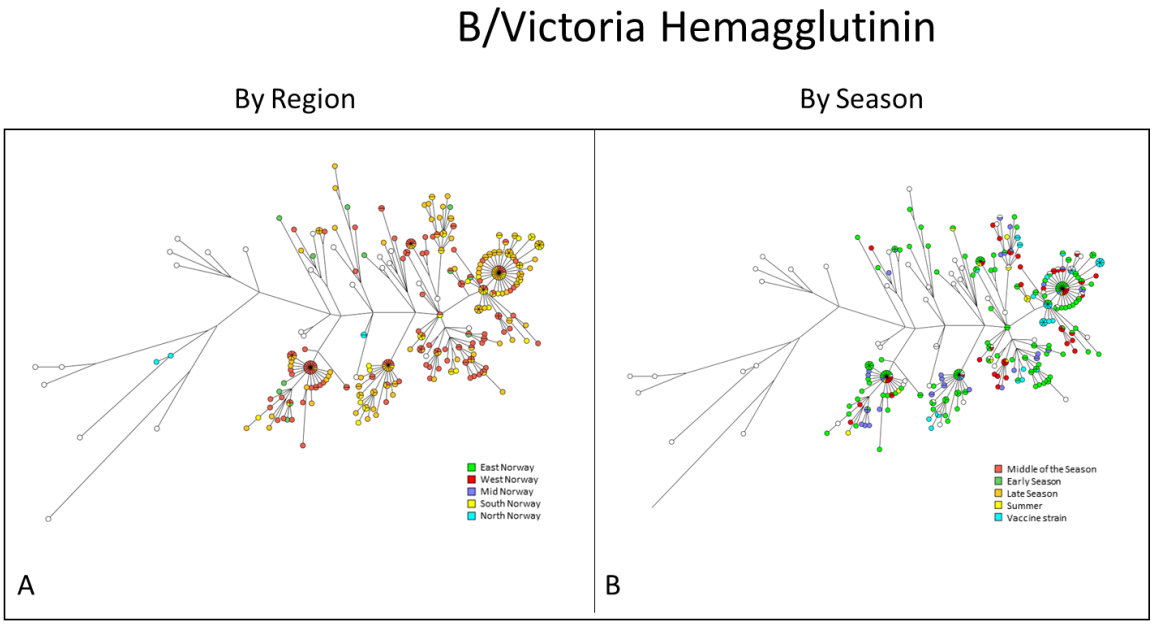

Figure 16. B/Victoria Maximum Parsimony tree: The figure shows how the hemagglutinin sequences of B/Victoria influenza genomes from viruses in Norway group genetically with reference viruses and vaccine strains from the northern and southern hemispheres, color-coded by Sequence (A) or Season of detection (B). Early Season defines the period between week 40 and week 50 in 2022, Mid-Season is between 50 2022 and week 12 2023), Late season week 12 – week 19 and summer period between weeks week 19 and 40.

Table 4. Genetic characterization results for influenza viruses detected in Norway in the past four weeks and in total. Source: National Influenza Centre at FHI.

Strain	2022 W40	2022 W41	2022 W42	2022 W43	2022 W44	2022 W45	2022 W46	2022 W47	2022 W48	2022 W49	2022 W50	2022 W51	2022 W52	2023 W01	2023 W02	2023 W03	2023 W04	2023 W05	2023 W06	2023 W07	2023 W08	2023 W09	2023 W10	2023 W11	2023 W12	2023 W13	2023 W14	2023 W15	2023 W16	2023 W17	2023 W18	2023 W19	2023 W20	2023 W21	2023 W22	2023 W23	2023 W24	2023 W25	2023 W27	2023 W28	Total
6B.1A.5a.2.1	3	0	6	6	11	17	7	12	11	27	14	3	5	10	6	5	6	1	4	2	4	2	1	3	1	0	1	1	1	2	0	1	1	0	0	0	2	1	0	0	177
genAH1/Norway/25089/2022	3	0	6	6	11	17	7	12	11	27	14	3	5	10	6	5	6	1	4	2	4	2	1	3	1	0	1	1	1	2	0	1	1	0	0	0	2	1	0	0	177
6B.1A.5a.2	3	2	4	6	7	14	11	20	15	26	7	8	7	11	20	11	19	16	13	4	15	5	5	4	0	5	6	5	7	3	2	8	3	2	1	1	2	1	1	1	301
genAH1/Sydney/5/2021	3	2	4	6	7	14	11	20	15	26	7	8	7	11	20	11	19	16	13	4	15	5	5	4	0	5	6	5	7	3	2	8	3	2	1	1	2	1	1	1	301
3C.2a1b.2a.2	3	8	6	9	10	16	10	13	6	25	7	2	3	11	14	20	10	18	9	7	20	11	7	3	1	10	2	7	3	2	1	0	0	2	0	0	0	0	1	0	277
genAH3/Bangladesh/4005/2020	1	3	3	1	3	5	4	2	1	4	5	2	0	5	5	7	3	5	8	5	5	5	5	1	0	3	0	1	1	1	1	0	0	0	0	0	0	0	0	0	95
genAH3/Slovenia/8720/2022	1	4	1	6	4	11	6	8	5	18	1	0	3	5	8	12	6	13	1	2	14	6	2	2	1	6	2	6	2	1	0	0	0	1	0	0	0	0	0	0	158
genAH3/Darwin/9/2021	1	1	2	2	3	0	0	3	0	3	1	0	0	1	1	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	0	24
V1A.3a.2	1	1	0	3	0	0	2	0	0	2	3	2	6	9	10	9	9	10	7	7	28	18	12	15	2	21	7	11	26	23	24	21	11	18	12	7	4	0	0	0	341
genBVicB/Austria/1359417/2021	1	1	0	3	0	0	2	0	0	2	3	2	6	9	10	9	9	10	7	7	28	18	12	15	2	21	7	11	26	23	24	21	11	18	12	7	4	0	0	0	341
genBYamB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	10	11	16	24	28	47	30	45	32	80	31	15	21	41	50	45	44	45	33	20	67	36	25	25	4	36	16	24	37	30	27	30	15	22	13	8	8	2	2	1	1096

Surveillance of antiviral resistance in Influenza viruses

For Influenza infections, especially for people belonging to risk groups, the attending physician should consider the need for use of antivirals. This applies to both vaccinated and unvaccinated individuals. Treatment should be initiated as early as possible in the course of the infection. Patients who are so sick that they are admitted to the hospital should always be assessed for antiviral drugs, even later in the course of the disease. Preventive treatment may be appropriate in nursing homes with outbreaks.

So far this season, 496 Influenza viruses have been tested for resistance (150 H3N2, 303 H1N1, 43 B-Victoria) to neuraminidase inhibitors such as oseltamivir and polymerase inhibitor Baloxavir. No resistance mutations have been detected and all viruses tested are sensitive to treatment with Tamiflu® and XOFLUZA®.

Population immunity against recent influenza viruses, August 2022

In August each year, the National Influenza Seroepidemiology Programme solicits approximately 2000 anonymised residual sera from clinical/microbiological laboratories across Norway. The sera, aimed to be representative of the Norwegian population geographically and by age composition, are tested by the haemagglutination-inhibition assay (HAI) to determine the antibody immunity against relevant circulating influenza viruses. Due to continued increased workload related to COVID-19, a subset of ca. 1200 sera collected in August 2022 were analysed. The main findings are shown in figure 15, table 5, and summarised as follows:

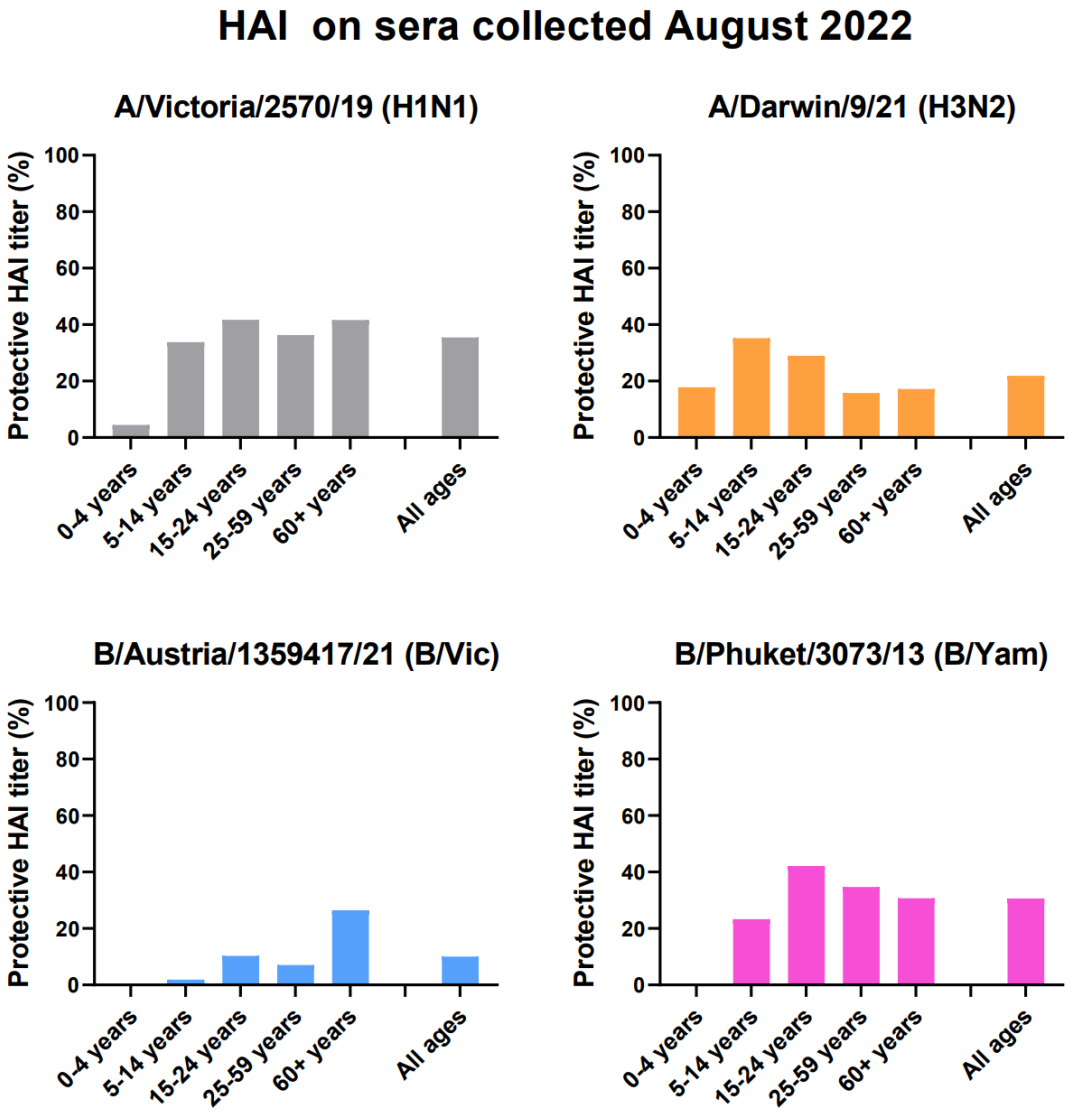

Figure 15. Seroprevalence in August 2022 against current influenza A and B strains for 'All ages' and in various age groups. HAI was performed against A/Victoria/2570/2019 (H1N1, clade 6B.1A.5a.2), A/Darwin/9/2021 (H3N2, 3C.2a1b.2a.2), B/Austria/1359417/2021 (Victoria lineage, V1A.3a.2) and B/Phuket/3073/2013 (Yamagata lineage). Protective HAI titres were defined as ≥40 for influenza A and ≥80 for ether treated influenza B.

For A/Victoria/2570/2019 (H1N1), the seroprevalence was approx. 30-40 % for all age groups, with the exception of the 0-4 age group which had a seroprevalence of 4.4 %. The A/Victoria/2570/2019 strain was included in the 2021/22 influenza vaccine for the Northern Hemisphere, which may have contributed to the seroprevalence seen in the serum samples collected in August 2022.

For A/Darwin/9/2021 (H3N2), the seroprevalence was 35 % for the age groups 5-14 years, ca. 30 % for the age group 15-24 years and just above 15 % for the remaining age groups. The higher seroprevalence seen in the younger age groups may reflect the H3N2 outbreak seen in March/April 2022. Vaccination has had a lesser contribution to H3 seroprevalence, as the A/Darwin/9/2021 strain was first included in the 2022/2023 vaccine administered after collection of sera.

The seroprevalence against contemporary B/Austria/1359417/2021 (Victoria lineage) was generally low; only 10% of the serum samples had a protective HAI titre. The seroprevalence was highest in the 60+ age group (ca 26%), and very low in the youngest age groups.

For the B/Phuket/3073/2013 strain (Yamagata lineage) which has been included in the tetravalent influenza vaccine since the 2015/16 season, there was a ca. 30% seroprevalence in the sera from August 2022. The prevalence varied from 23% in 5–14-year age group up to 42% in the 15-24 years age group, with the exception of 0–4-year-olds for whom the seroprevalence was zero.

Up until the end of January 2023, the 2022/2023 influenza season in Norway was dominated by H1N1 virus belonging to the A/Sydney/5/2021 and A/Norway/25089/2022 lineages. Both lineages belong to the 6B.1A.5a.2 clade, which also contains the A/Victoria/2570/2019 vaccine strain. However, the A/Norway/25089/2022 sublineage of viruses have acquired several additional HA1 mutations that are thought to mediate escape from existing antibody responses, including P137S, K142R and T277A. To evaluate if sera collected in August 2022 had reduced protection against the Norway-lineage of viruses, 75 sera with HAI titers of ≥160 against A/Victoria/2570/2019 were evaluated against A/Norway/25089/2022. We observed a significant reduction in HAI titers towards the Norway-lineage with geometric mean titers dropping from 187 towards A/Victoria/2570/2019 to 50 against A/Norway/25089/2022 (Fig. 16). When dividing the serum samples into different age groups there was a significant reduction in HAI titers in the older age groups (25-59 and 60+ years). There was also a reduction in HAI titer in the 5-24 years age group, but the difference was not significant.

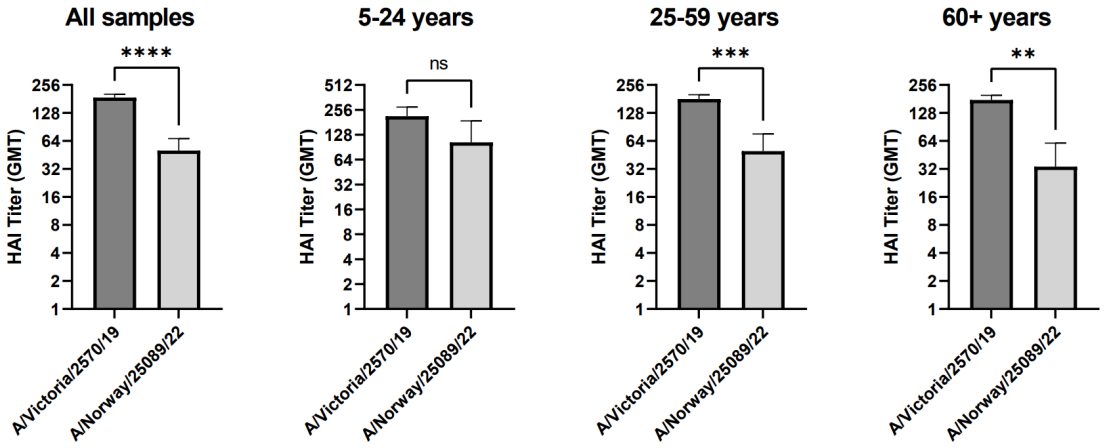

Figure 16: Reduction in HAI titre against A/Norway/25089/22, relative to A/Victoria/2570/2019. Residual serum samples from August 2022 with HAI titre of ≥160 against A/Victoria/2570/19 were evaluated in an HAI assay against A/Norway/25089/22. Data presented is geometric mean titre (GMT) with error bars representing 95% confidence interval. Significance was determined using a Wilcoxon matched-paired signed rank test, and ** = p < 0.01, ** = p<0.001 and **** = p < 0.0001.

Table 5. Influenza seroepidemiology results in August 2022 – Seroprevalence* in age groups.

For comparison data from studies performed for the preceding years 2017-2021 are also included. Due to the covid-19 pandemic, no HAI assays were performed in 2020.

	Age groups						
Influenza strains (Year$)	**0-4**	**5-14**	**15-24**	**0-24**	**25-59**	**60+**	**All ages**
H1 X-179A/A(H1N1)pdm09 (2017)	25	79	77	67	52	46	57
H1 Michigan/45/15 (2017)	26	79	79	68	50	42	56
H1 Michigan/45/15 (2018)	17	67	71	58	48	41	51
H1 Michigan/45/15 (2019)	38	68	75	64	46	41	53
H1 Brisbane/2/18 (2019)	34	62	58	54	37	32	44
H1 Victoria/2570/19 (2021)**	8	37	47	36	22	20	27
H1 Victoria/2570/19 (2022)	***4***	***34***	***42***	***32***	***36***	***42***	***35***
H3 Hong Kong/5738/14 (2017)	28	78	59	60	30	43	45
H3 Norway/3806/16 (2017)	28	77	68	63	36	45	49
H3 Hong Kong/5738/14 (2018)	25	78	72	63	36	43	50
H3 Sing/INFIMH-16-19/2016 (2018)	19	70	54	52	23	32	38
H3 Switzerland/8060/17(2018)	25	71	47	51	29	34	40
H3 Sing/INFIMH-16-19/2016 (2019)	22	72	53	53	27	34	40
H3 Kansas/14/17 (2019)	6	15	13	12	7	8	10
H3 Cambodia/e0826360/20 (2021)	13	61	61	52	51	32	48
H3 Darwin/9/21 (2021)**	20	39	18	28	18	20	23
H3 Darwin/9/21 (2022)*	***18***	***35***	***29***	***30***	***16***	***17***	***22***
B/Vic Brisbane/60/08 (2017)	11	27	27	23	13	26	20
B/Vic Brisbane/60/08 (2018)	3	23	31	22	15	21	19
B/VicΔ2 Norway/2409/17 (2018)	1	4	15	7	18	23	14
B/Vic Brisbane/60/08 (2019)	7	24	36	24	15	25	21
B/VicΔ2 Norway/2409/17 (2019)	4	6	18	10	15	22	14
B/VicΔ3B Wash/02/19 (2019)	6	10	20	13	15	19	15
B/Wash/02/19 (Vic-Δ3B) (2021)	6	4	5	5	12	13	10
B/Cote d'Ivoire/948/20 (Vic-Δ3B) (2021)	8	3	7	6	8	23	10
B/Austria/1359417/21 (Vic-Δ3B) (2022)*	***0***	***2***	***10***	***5***	***7***	***26***	***10***
B/Yam Phuket/3073/13 (2017)**	4	28	33	25	23	19	23
B/Yam Phuket/3073/13 (2018)**	17	37	50	38	30	24	32
B/Yam Phuket/3073/13 (2019)**	17	48	46	39	36	25	35
B/Yam Phuket/3073/13 (2021)**	0	20	27	19	28	18	22
B/Yam Phuket/3073/13 (2022)*	***0***	***23***	***42***	***27***	***35***	***31***	***31***
Sera analysed (n): 2016 Aug	188	351	333	874	745	411	2028
Sera analysed (n): 2017 Aug	189	318	353	860	797	436	2093
Sera analysed (n): 2018 Aug	155	251	236	642	501	275	1418
Sera analysed (n): 2019 Aug	113	187	171	471	375	208	1054
Sera analysed (n): 2021 Aug	48	107	114	269	250	137	656
Sera analysed (n): 2022 Aug	***90***	***210***	***204***	***504***	***455***	***238***	***1197***

$Year of serum collection and HI analysis.

*All entries are per cent of sera having HI titres ≥ 40 for the A strains and ≥ 80 for the ether-treated B strains.

**(Corresponding to) components of the Northern hemisphere influenza vaccine (trivalent/quadrivalent) for the season 2022-2023.

B/Yam: B/Yamagata/16/1988 lineage; **B/Vic**: B/Victoria/2/1987 lineage

Vaccine distribution and coverage

A total of 1.63 million influenza vaccine doses have been distributed in the 2022/23 season; 1.2 million of these were distributed from the NIPH specifically intended for persons in medical risk groups and health care workers (HCW) involved in direct patient care. The number of distributed doses decreased by 9 % compared to the 2021/22 season. This is probably largely due to a withdrawal of funding for vaccination of risk groups this season, in combination with vaccine fatigue in the population and specifically among HCWs. (Figure 17).

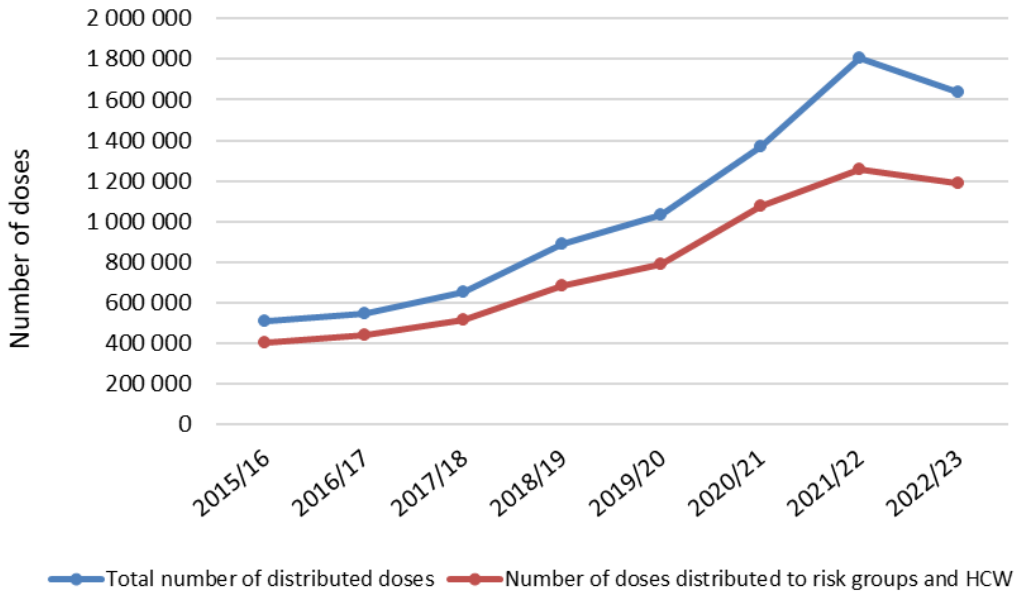

Figure 17. Influenza vaccine doses distributed in Norway, September 2015 through May 2023. HCW = Health Care Workers.

According to the Norwegian Immunization Registry SYSVAK (SYSVAK), at least 64 % of the population above 65 years of age received an influenza vaccine this season (Figure 18).

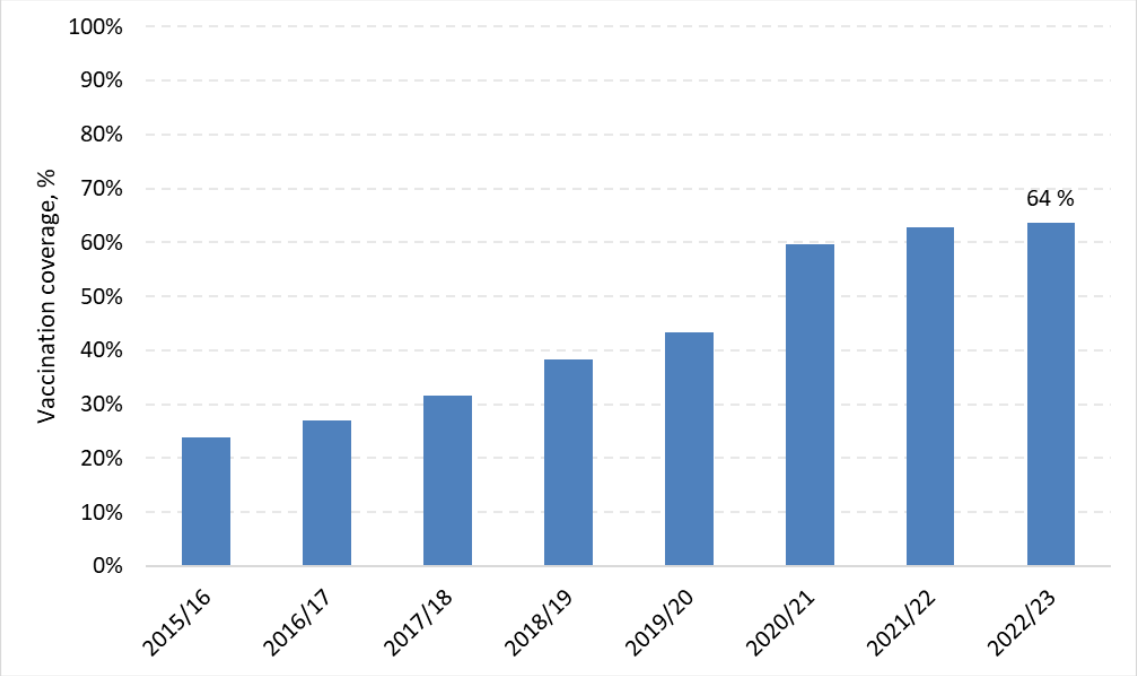

Figure 18. Vaccination coverage among residents above 65 years in Norway, 2015/16 season through to 2022/23 season as of May 2023.

According to the Emergency preparedness register for COVID-19 (Beredt C19), vaccination coverage in risk groups 18-64 years and 0-17 years per 17th of May 2023 was 36% and 8%, respectively. Vaccination coverage among HCWs was 55% in the specialist health care services (mainly hospitals) and 31% in primary healthcare. Coverage decreased in all these groups compared to the previous season, except for the children in risk groups. The coverage rates for the 2021/2022 season being 38%, 8%, 59% and 38%, respectively. Approximately 83% of the distributed doses are registered in SYSVAK, due to underreporting and technical issues. Vaccination coverage is therefore also estimated by survey data from Statistics Norway for the various risk groups and HCWs. However, these estimates will not be available until October 2023.

Animal influenza

A panzootic of highly pathogenic avian influenza (HPAI) A(H5N1) virus clade 2.3.4.4.b is ongoing in birds in Europe, Africa, Asia and the Americas. Since 2021, there have been four outbreaks of HPAIV A(H5N1) in commercial poultry flocks in Norway, of which two occurred in October-November 2022 (1). During autumn 2022 and winter 2023, H5N1 has predominated in wild birds, and the Norwegian Veterinary Institute has reported several detections in anseriform species (swans, ducks), gulls and raptors (2). During summer 2023, there was a mass mortality event among sea gulls (black-legged kittiwakes) along the northern coastline of Norway, caused by HPAI H5N1. This virus was also detected in a young red fox found dead in the same area. More sporadic detections have been made in wild birds elsewhere in the country. No cases have been detected in humans in Norway.

The Norwegian Institute of Public Health has assessed the risk for human infection as very low (3), but increased awareness and precautionary infection control measures are recommended to prevent zoonotic infection.

References

1 Granstad, Silje, Rømo, Grim, Helberg, Morten, Gjerset, Britt, Åkerstedt, Johan. Fugleinfluensa (høypatogen aviær influensa – HPAI) i Norge og Europa: Statusrapport per 11.01.2023. Veterinærinstituttet 2023. Available from: https://www.vetinst.no/nyheter/fugleinfluensaviruset-fortsetter-a-herje

2 Norwegian Veterinary Institute. Avian Influenza in Wild Birds in Norway. Available from: https://www.vetinst.no/dyr/vilt/fugleinfluensa-i-norge

3 Folkehelseinstituttet. Vurdering av risiko for smitte til mennesker med høypatogen fugleinfluensa A (H5Nx) 2.3.4.4b i Norge. Available from: https://www.fhi.no/publ/2023/vurdering-av-risiko-for-smitte-til-mennesker-med-hoypatogen-fugleinfluensa-/

Previous **Norwegian reports prepared for the WHO vaccine consultation meeting:**

WHO-rapporter - FHI (https://www.fhi.no/sv/influensa/influensaovervaking/who-rapporter/)

Acknowledgements

The work presented relies heavily on the essential contributions by the Norwegian medical microbiology laboratories, physicians in the virological sentinel network, the Norwegian Intensive Care Registry and intensive care units, other participants in Norwegian influenza surveillance, as well as the WHO Collaborating Centre for Influenza Reference and Research at the Francis Crick Institute, London, UK and other partners in the WHO Global Influenza Surveillance and Response System GISRS and the European Influenza Surveillance Network. Data on influenza-like illness is provided by the Department of Infectious Disease Epidemiology and Modelling, NIPH, which again receives data from the Norwegian Directorate of Health. The Directorate also provides data from the Norwegian Patient Registry (NPR) and the Norwegian Information System for the Nursing and Care Sector (IPLOS), which is of great value in the epidemiological surveillance of influenza disease and vaccination coverage carried out in The Emergency preparedness register for COVID-19 (Beredt C19) at NIPH. We would also like to thank our colleagues at NIPH working with the MSIS Laboratory Database for providing valuable data on laboratory results for influenza and the National Immunisation Registry (SYSVAK) for data about influenza vaccination uptake. We would also like to thank the Norwegian Veterinary Institute and the Norwegian Food Safety Authority for sharing information on influenza in animals.

We furthermore gratefully acknowledge the excellent technical work performed by Marie Paulsen Madsen, Anne Maria Lund, Elisabeth Vikse, Rasmus Riis Kopperud, Malene Strøm Dieseth, Johanna Tonstad, Magnhild Sekse Erdal, Maria Juul Diekmann, Maja Fjellstad Knutsen and Marianne Morken.

With best regards,

Olav Hungnes, Trine Hessevik Paulsen, Andreas Rohringer, Elina Seppälä, Håkon Bøås, Jesper Dahl, Even Fossum, Jeanette Stålcrantz, Birgitte Klüwer, Kjersti Rydland, Torstein Aune, and Karoline Bragstad

National Influenza Centre/Section of Influenza and other respiratory viruses

Section for Respiratory, Blood-borne and Sexually transmitted infections

Division for Infection Control

Norwegian Institute of Public Health,

Oslo, Norway

11 September 2023

Appendices

Description of the surveillance and monitoring components

Influenza-like illness

Norwegian ILI surveillance data is provided by NorSyss (The Norwegian Syndromic Surveillance System, which receives data from the KUHR-system hosted by the Norwegian Directorate of Health, which daily provides anonymised data on influenza diagnosed in primary health care consultations. The information is admitted to KUHR through doctors' reimbursement claims to the health authorities. NorSyss has been receiving KUHR data since 2014 and is supported by retrospective data from the 2006-07 season and onwards.

Virological surveillance.

Sentinel virological surveillance: Historically, a network of volunteer sentinel physicians throughout the country has been collecting specimens from patients with ILI for analysis at the National Influenza Centre. It was not possible to continue this sentinel surveillance during the first two years of the COVID-19 pandemic, because community respiratory illness testing was redirected away from primary care practices to dedicated SARS-CoV-2 testing infrastructures. However, with the return of patients to general practices the sentinel system was reactivated and strengthened by including more GPs and engaging sentinel laboratories for some of the primary testing. At the same time, the scope of the surveillance was expanded to comprise several non-influenza respiratory viruses and the testing case definition expanded from ILI to ARI. For sentinel specimens first tested in another laboratory, all data and all influenza/SARS-CoV-2 positive specimens are sent to the NIC.

Comprehensive virus surveillance: In addition, medical microbiology laboratories that perform influenza diagnostics report testing data. Since 2020, all testing outcomes are reported in real-time to the national MSIS laboratory database. Surveillance statistics for laboratory confirmed influenza have been harvested from this database. These laboratories also contribute influenza positive specimens to the NIC for further characterisation. Even though most of these laboratories are affiliated to hospitals, a large proportion of specimens tested for influenza virus are from outpatients visiting general practitioners, and, during the COVID-19 pandemic, SARS-CoV-2 testing stations.

Virus characterisation: As many as possible of influenza virus positive sentinel specimens, and a selection of positive specimens from the comprehensive surveillance are subjected to whole genome sequencing (WGS). Viruses are then selected for shipment to a WHO Collaborating Centre and/or isolated in the NIC, in order to ensure that all significant genetic variants are characterised antigenically. Viruses are also analysed with respect to antiviral resistance and other characteristics.

All the virological surveillance data are shared internationally with ECDC and WHO Global Influenza Surveillance and Response System (GISRS).

Registry-based surveillance of influenza hospitalisations

In 2020-2021, a temporary registry-based system for surveillance of influenza hospitalisations was established in order to strengthen the influenza surveillance during the COVID-19 pandemic. In the beginning, individual-level data originating from the Norwegian Patient

Registry (NPR) was used. Influenza hospitalisations were defined as inpatient hospital admissions combined with ICD-10 codes for influenza (J09-J11). To enhance the specificity of the registry-based surveillance, the data on hospital discharge codes from NPR is now linked to data on PCR tests positive for influenza, which is obtained from the Norwegian Surveillance System for Communicable Diseases (MSIS) laboratory database. Case-based data on PCR-positive influenza tests is available from season 2020-2021 onward. A hospital admission with influenza is defined as an overnight stay where the patient tested positive for influenza with a PCR test within 14 days before or up to 2 days after hospital admission, and where an ICD-10 code for influenza was registered, or where the patient hasn't received any diagnosis code yet. The inclusion of influenza-positive patients without any diagnosis codes yet increases the timeliness of the data, but it means also that the numbers presented in this report may change as data become more complete.

Influenza patients in intensive care units

In the 2016-17 and 2017-18 seasons, the Norwegian Intensive Care Registry (NICR) and NIPH carried out a pilot study to see whether national surveillance of influenza patients in intensive care units is feasible. As part of the pilot, NICR asked all ICUs from week 46/2017 to report weekly numbers of patients in ICUs with laboratory-confirmed influenza, the number of patients in ICUs with clinically suspected influenza and the number of deaths among patients with confirmed or suspected influenza admitted to ICUs. Almost all ICUs in Norway reported data to NICR. Since the 2018-19 season, an electronic form has been used. Up to the 2020-2021 season, only anonymised data were reported from NICR to the NIPH. In the season 2021-2022 the NIPH has begun to receive case-based data on a weekly basis.

Influenza-associated deaths

Influenza-associated deaths were based on data from the Norwegian Cause of Death Registry, and were defined as deaths where J09, J10 or J11 (ICD-10) were recorded as an underlying or contributing cause of death on the death certificate.

Influenza seroepidemiology

The National Influenza Seroepidemiology Programme annually in August solicits about 2000 serum samples collected during the weeks 31-35 from clinical/microbiological laboratories covering the 19 counties of Norway. These anonymised convenience sera are aimed to be representative of the Norwegian population geographically and by age composition. In normal times these sera are tested by the haemagglutination-inhibition (HI) test to determine the antibody immunity to relevant circulating influenza viruses. However, due to capacity limitations imposed by the response to COVID-19 and subsequent austerity measures, the sera collected in 2020 were only tested for antibody against SARS-CoV-2 and not against influenza, and only a subset of the 2021 and 2022 collections was tested against influenza.

Vaccine distribution and coverage

Distribution data are reported by Department of Infection Control and Vaccine at NIPH and by IQVIA Solutions (distribution from other wholesalers). Vaccination coverage data are from the Norwegian immunisation registry SYSVAK. This electronic immunisation registry supplies national coverage estimates based on every individual's vaccination status. It is mandatory to register all influenza vaccinations. However, in recent years the rate of registration has been

around 75-80 % of the doses distributed (adjusted for the number of discarded doses). Coverage estimates from SYSVAK are therefore considered minimum estimates.

For individuals under 65 years of age, information on vaccination status is cross-referenced with information on medical risk for severe influenza from the emergency preparedness register for COVID-19 (Beredt C19) in order to produce coverage estimates for younger individuals in the risk groups. Coverage estimates for HCWs are also captured from Beredt C19. Beredt C19 includes information that has already been collected in the healthcare services, national health registries and medical quality registers, as well as other administrative registers with information about the Norwegian population.

Published by the Norwegian Institute of Public Health
September 2023
P.O.Box 222- Skøyen
NO-0213 Oslo
Norway
Tel: + 47-21 07 70 00
The report can be downloaded as pdf
at www.fhi.no/en/publ/