REPORT

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Norway:
Influenza Virological and Epidemiological 2023-2024 season report

October 2024

NIPH
Norwegian Institute of Public Health

Norwegian Institute of Public Health

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Olav Hungnes

Trine Hessevik Paulsen

Andreas Rohringer

Elina Seppälä

Håkon Bøås

Even Fossum

Jeanette Stålcrantz

Birgitte Klüwer

Kjersti Rydland

Torstein Aune

Karoline Bragstad

NIPH

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Authors:
Olav Hungnes
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Karoline Bragstad

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Per Kristian Svendsen

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Table of Contents

Key message

The 2023-24 influenza season in Norway

Overall, the 2023-2024 influenza season was of low-to-moderate magnitude, had a protracted course, with influenza A(H1N1) dominating also this season, but cocirculating with A(H3N2) viruses and with much less influenza B/Victoria-lineage viruses.

- **The population immunity towards influenza** prior to the 2023-24 season was assessed in a panel of residual sera collected in August 2023. Following the A(H1N1) dominated 2022-23 season, there was an increase in seroprevalence against A/Victoria/2570/2019(H1N1) of the pdm09 5a.2 clade, but with less immunity against the subclade 5a.2a.1. The increased seroprevalence was particularly prominent in the 0-4 years age group, where we in 2022 had observed an immunity gap following the absence of influenza during the COVID-19 pandemic. Seroprevalence against A(H3N2) also increased or remained stable, and there was no sign of immune evasion with the new A/Thailand/8/2022 strain. Seroprevalence against B/Victoria-lineage virus increased from very low levels in 2022, likely reflecting the spread of influenza B during the latter part of the 2022-2023 season.

- **The incidence of laboratory confirmed influenza** rose rapidly, like in the preceding season, toward an early peak during the Christmas/New Year period, albeit at lower intensity than the 2022-23 season. Detections declined only slightly after the New Year peak and sustained at moderate level until falling under 10 % positivity rate in week 10/2024. By week 20 the rate had declined to 2 % and it has stayed below this through summer. The proportion of **influenza-like illness (ILI)** consultations in primary health care began to increase gradually from week 44/2023 and the epidemic threshold was crossed in week 49. Influenza activity peaked in week 52 when 1,4 % of the consultations were due to ILI, at low intensity level. The activity declined after week 52 and was stable on a low intensity level until it crossed below the epidemic threshold in week 9/2024.

- Out of the **circulating viruses**, type A viruses predominated during the main outbreak period, but declined faster than type B during late winter and spring, leaving type B as the majority virus during weeks 17-22. Influenza A(H1N1) and A(H3N2) cocirculated, with H1N1 in majority overall and main driver of the winter outbreak with a peak in percent positives at 16 % in week 52. Low compared to many previous seasons. The activity stayed elevated for the following 9 weeks before it rapidly declined after week 10. A large proportion (43 %) of the less commonly detected type B viruses was lineage typed in the National Influenza Centre, FHI, with 1021 Victoria-lineage and zero Yamagata-lineage detections. Influenza A were again in majority among the sporadic detections, with predominance of subtype H3N2 through July and August 2024.

- **Severe outcomes:** between week 40/2023 and week 20/2024, a total of 4403 hospital admissions and 179 ICU admissions were reported, which is less than in the same period in the preceding season 2022-2023. Eleven influenza outbreaks were reported, of which ten from health care institutions and one from an immigration detention center.

- **Genetic characterization** with whole genome sequencing of 17% of all influenza positive samples received for surveillance revealed that A(H1N1) viruses

A/Norway/25089/2022 6B.1A.5a.2a.1 clade dominated in early season, but by mid-season viruses in the A/Sydney/5/2021 6B.1A.5a.2 clade were in slight majority. The circulating H3N2 viruses are categorized as belonging to the A/Thailand/8/2022 3C.2a1b.2a.2a.3a.1 group. The main subclade detected were J.2 with several genetically distinct clusters emerging late in the season, one with clear antigenic drift properties. All influenza B viruses sequenced were B/Victoria lineage, belonging to the V1A.3a.2 clade. The viruses circulating were in well accordance with the composition of the influenza vaccine this season.

- **Antiviral resistance** mutations and reduced susceptibility towards oseltamivir was observed for one influenza B virus this season. A new globally emerging double mutant H1N1 inducing resistance towards oseltamivir was also detected in one single case in Norway.
- **Vaccination coverage** among risk groups 18-64 years decreased compared to the 2022-2023 season and has decreased by 5 percentage points from the 2021-2022 season. The coverage rate for individuals above 65 years was 65 %, which is an increase of over 2 percentage points compared to last season. The total number of distributed doses decreased by 5 % compared to the 2022-2023 season. 1.13 million doses intended for use in risk groups and health care workers were distributed.
- **Highly pathogenic avian influenza** viruses (HPAIVs) H5N1 and H5N5 belonging to HA clade 2.3.4.4b continued to be detected in wild birds in Norway, albeit in far lower numbers compared to the 2023 summer and with fewer outbreaks. During autumn 2023 there was one outbreak of H5N1 in a poultry backyard flock and there was one outbreak in a commercial poultry flock in February 2024. In the same month H5N5 was detected in two red foxes. No human cases have been detected, and the risk of human infection has been assessed as very low.

Hovedbudskap (in Norwegian)

2023-24 influensasesongen i Norge

Generelt var influensasesongen 2023-2024 av lav til moderat styrke, med et langvarig forløp, der influensa A(H1N1) dominerte også denne sesongen, men sirkulerte sammen med A(H3N2)-virus og langt færre influensa B/Victoria-linjevirus.

- **Befolkningsimmuniteten** mot influensa før sesongen 2023-24 ble undersøkt i et panel av restsera samlet inn i august 2023. Etter den A(H1N1)-dominerte sesongen 2022-23, var det en økning i seroprevalens mot A/Victoria/2570/2019(H1N1) av pdm09 5a.2-kladen, men med mindre immunitet mot undergruppen 5a.2a.1. Den økte seroprevalensen var spesielt fremtredende i aldersgruppen 0-4 år, hvor vi i 2022 hadde observert et immunitetsgap etter fraværet av influensa under COVID-19-pandemien. Seroprevalens mot A(H3N2) økte også eller forble stabil, og det var ingen tegn til immunescape med den nye A/Thailand/8/2022-stammen. Seroprevalens mot

B/Victoria-linje virus økte fra svært lave nivåer i 2022, sannsynligvis som en konsekvens av spredningen av influensa B i den siste delen av sesongen 2022-2023.

- Forekomsten av **laboratoriebekreftet influensa** økte raskt, som i den foregående sesongen, mot en tidlig topp i jule-/nyttårsperioden, om enn med lavere intensitet enn sesongen 2022-23. Påvisningene avtok bare litt etter nyttårstoppen og holdt seg på et moderat nivå til de falt under 10 % positivitet i uke 10/2024. Innen uke 20 hadde frekvensen falt til 2 % og har holdt seg under dette gjennom sommeren. Andelen influensalignende sykdom (ILI)-konsultasjoner i primærhelsetjenesten begynte å øke gradvis fra uke 44/2023 og epidemiterskelen ble krysset i uke 49. Influensaaktiviteten nådde toppen i uke 52 da 1,4 % av konsultasjonene skyldtes ILI, på et lavt intensitetsnivå. Aktiviteten avtok etter uke 52 og var stabil på et lavt intensitetsnivå til den krysset under epidemiterskelen i uke 9/2024.

- Av de **sirkulerende virusene** dominerte type A-virus under hovedutbruddsperioden, men avtok raskere enn type B i slutten av vinteren og våren, og etterlot type B som det dominerende viruset i ukene 17-22. Influensa A(H1N1) og A(H3N2) sirkulerte samtidig, med H1N1 i flertall totalt sett og var hovedpådriveren av vinterutbruddet med en topp i prosent positive på 16 % i uke 52. Lavt sammenlignet med mange tidligere sesonger. Aktiviteten holdt seg forhøyet de påfølgende 9 ukene før den raskt avtok etter uke 10. En stor andel (43 %) av de mindre vanlige type B-virusene ble linjetypet, kun med påvisninger av B-Victoria linjen og ingen ingen B-Yamagata. Influensa A var igjen i flertall blant de sporadiske påvisningene, med overvekt av subtype H3N2, gjennom juli og august 2024.

- **Alvorlige utfall**: mellom uke 40/2023 og uke 20/2024 ble totalt 4403 sykehusinnleggelser og 179 intensivinnleggelser rapportert, noe som er mindre enn i samme periode i den foregående sesongen 2022-2023. Elleve influensautbrudd ble rapportert, hvorav ti fra helseinstitusjoner og ett fra et utledningsinternat**.**

- **Genetisk karakterisering** med helgenomsekvensering av 17 % av alle influensapositive prøver mottatt for overvåking viste at A(H1N1)-virusene A/Norway/25089/2022 6B.1A.5a.2a.1-kladen dominerte tidlig i sesongen, men midt i sesongen utgjorde virusene i A/Sydney/5/2021 6B.1A.5a.2-kladen et lite flertall. De sirkulerende H3N2-virusene er kategorisert som tilhørende A/Thailand/8/2022 3C.2a1b.2a.2a.3a.1-gruppen. Hovedandelen av H3 som ble påvist var av J.2 undergruppen med flere genetisk distinkte klynger som dukket opp sent i sesongen, en med klare antigen drift egenskaper. Alle influensa B-virusene som ble sekvensert tilhørte B/Victoria-linjen, V1A.3a.2-kladen. De sirkulerende virusene var i god overensstemmelse med sammensetningen av influensavaksinen denne sesongen.

- **Antiviral resistens** mutasjoner og redusert senitivitet for oseltamivir ble påvist i ett influensa B virus denne sesongen. En ny dobbelmutert H1N1 stamme som også gir redusert sensitivitet mot oseltamivir ble også oppdaget i ett enkelt tilfelle fra Norge.

- **Vaksinasjonsdekningen** blant risikogrupper 18-64 år gikk ned sammenlignet med sesongen 2022-2023 og har gått ned med 5 prosentpoeng fra sesongen 2021-2022. Dekningsgraden for personer over 65 år var 65 %, noe som er en økning på over 2 prosentpoeng sammenlignet med forrige sesong. Totalt antall distribuerte doser gikk ned med 5 % sammenlignet med sesongen 2022-2023. 1,13 millioner doser beregnet for bruk i risikogrupper og helsepersonell ble distribuert.

- **Høypatogene aviære influensavirus** (HPAIV) H5N1 og H5N5 tilhørende HA-klade 2.3.4.4b fortsatte å bli påvist i ville fugler i Norge, om enn i langt lavere antall sammenlignet med sommeren 2023 og med færre utbrudd. I løpet av høsten 2023 var det ett utbrudd av H5N1 i en fjørfehage og ett utbrudd i en kommersiell fjørfebesetning i februar 2024. I samme måned ble H5N5 påvist i to rødrever. Ingen menneskelige tilfeller er påvist, og risikoen for menneskelig infeksjon er vurdert som svært lav.

A look back at the preceding 2022-23 season in Norway

The influenza activity developed rapidly in late autumn 2022 and reached a sharp peak around Christmas/New Year. Influenza A(H1N1) viruses predominated in the early peak and then declined.

The 2022-2023 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. There were two smaller subsequent peaks in weeks 6 and 12, respectively.

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. After midsummer, influenza A viruses were again in majority among the few detections, with a large proportion being H1N1. All circulating influenza B viruses that have been tested for lineage belonged to the B/Victoria/2/1987 lineage.

The proportion of influenza-like illness (ILI) consultations in primary health care crossed the epidemic threshold in week 49/2022 and peaked in week 52/2022, several weeks earlier than normal. There were two minor subsequent 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.
The numbers of hospitalisations and ICU admissions with influenza also peaked in week 52-2022. The number of hospital admissions and clearly exceeded 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.

Both the H1N1 A/Sydney/5/2021 6B.1A.5a.2 clade and its A/Norway/25089/2022 6B.1A.5a.2a.1 subclade were 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. 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 (1). 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.

The 2023-24 influenza season in Norway

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

Influenza like illness (ILI) in primary health care

The proportion of ILI consultations began to rise gradually from week 44/2023 and the present-season epidemic threshold, defined by the Moving Epidemic Method (MEM), was crossed in week 49 (Figure 1,Figure 2) Weekly proportion of consultations for ILI, Norway 2023-2024 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 six previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH. Influenza activity peaked in week 52 at low intensity level at which 1,4 % of consultations were due to influenza-like illness. The outbreak reached its top 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 proportion ILI peaked in week 52/2023 (Figure 3). In the same week, the ILI proportion peaked in all the regions in Norway, except the Southern region which peaked in week 8/2024 (Figure 4).
The influenza activity declined after week 52 and was stable on a low intensity level until it crossed below the epidemic threshold in week 9/2024. The influenza outbreak lasted for 11 weeks according to ILI and the MEM-thresholds. Comparing proportion ILI to proportion positive laboratory tests for influenza virus, ILI seems to reflect the trend of the outbreak.

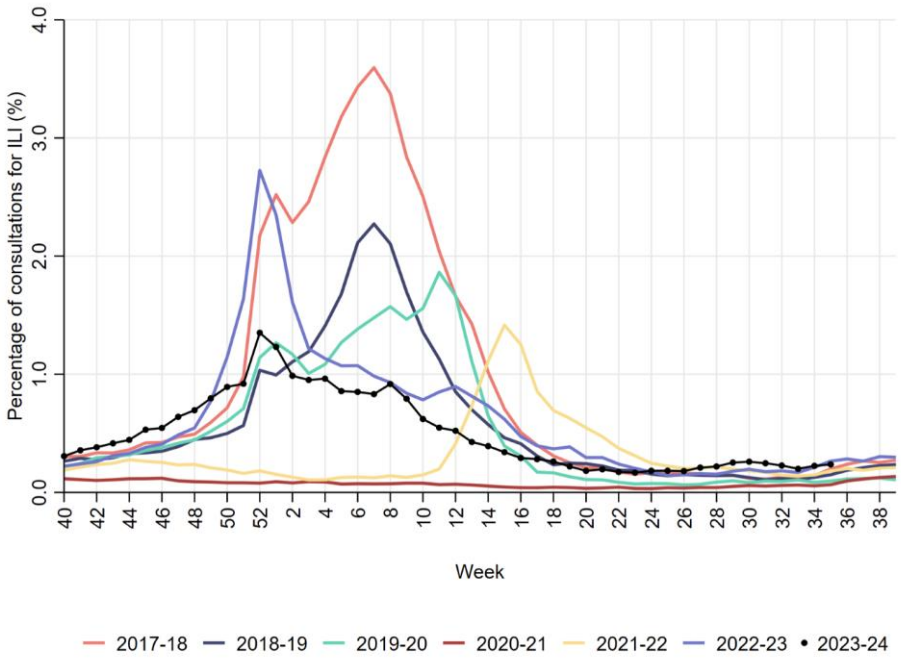


Figure 1: Weekly proportion of consultations for ILI, Norway 2023-2024 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the six previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH

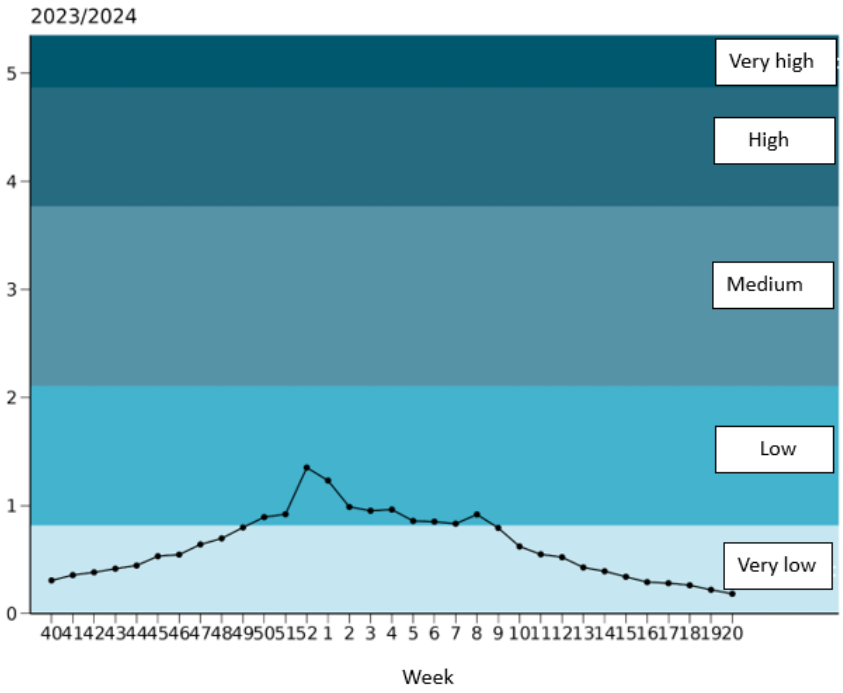


Figure 2: MEM intensity levels, Norway 2023-2024 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSyss with data from KUHR, NIPH

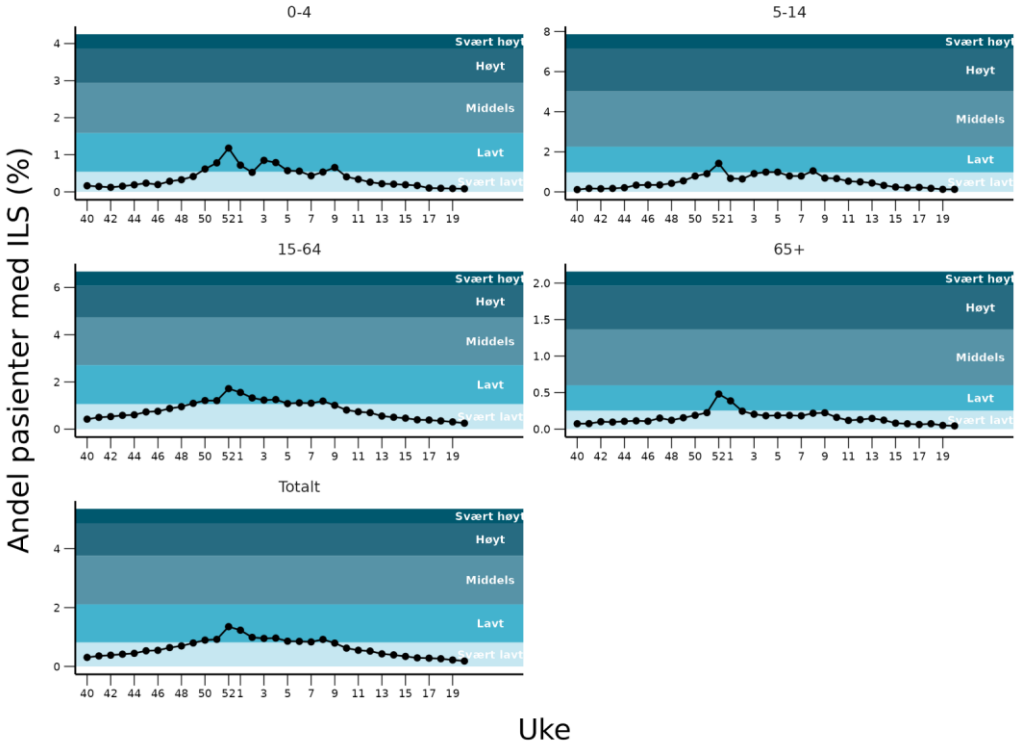


Figure 3: Weekly proportion of consultations for influenza-like illness (ILI) in general practice and emergency clinics by age group and season, and level of influenza activity based on the moving epidemic method (MEM) thresholds, Norway. Svært lavt = very low; lavt = low; middels = medium; høyt = high, svært høyt = very high. Source: NorSyss with data from KUHR, NIPH.

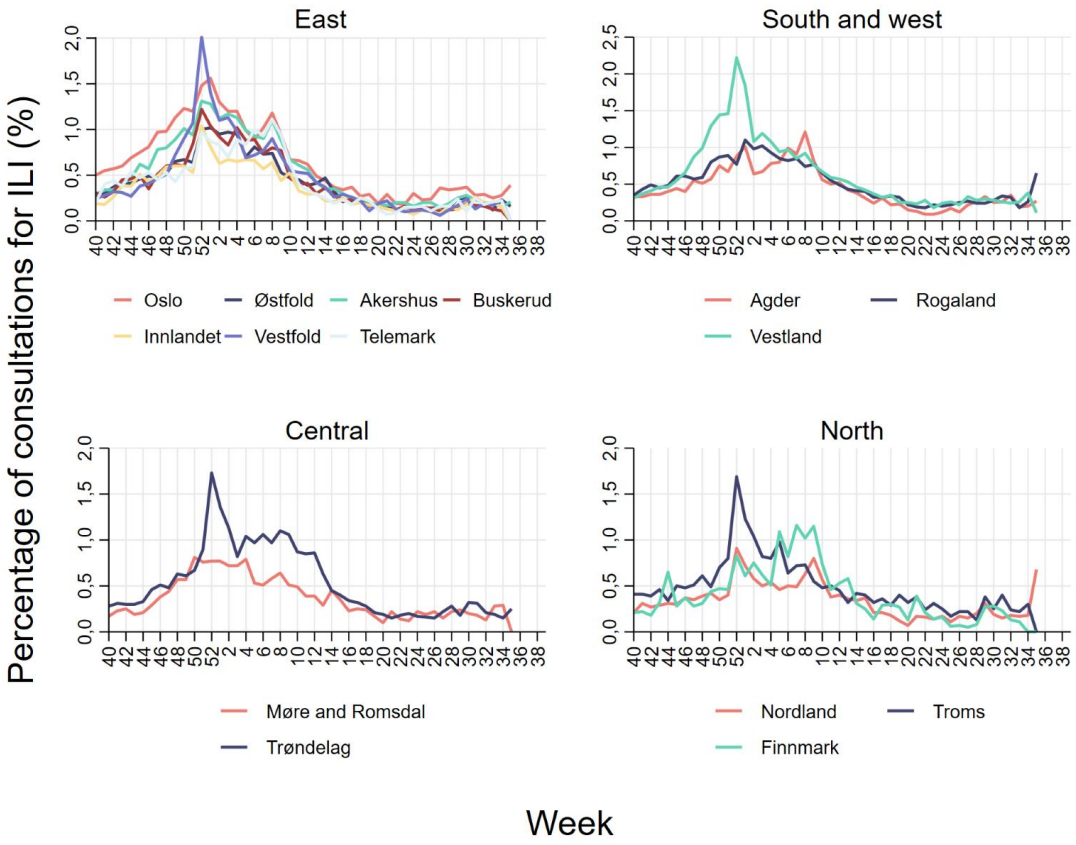


Figure 4: Weekly proportion of consultations for influenza-like illness (ILI) in general practice and emergency clinics by county and geographical region, Norway 2023-2024 season. Source: NorSyss with data from KUHR, NIPH.

Outbreaks in health care institutions

A total of 11 outbreaks were reported to NIPH, of which ten between week 50/2023 to 11/2024 and one in week 26 2024. Seven of the outbreaks were reported from nursing homes, two from hospitals, one from another category health care institution, in addition to one from an immigration detention centre. In ten of the outbreaks, influenza A was reported as causative virus, and in one of these, subtype H1N1 was reported.

Influenza hospitalisations based on registry data

In the registry-based surveillance system, a patient hospitalised with influenza is defined as a person hospitalised overnight, with an ICD-10 code for acute respiratory infection registered upon discharge and a positive influenza PCR test within 14 days before hospital admission or up to 2 days after discharge.

The beginning of the 2023-2024 influenza epidemic was less intense compared to the previous season. Both seasons had a main peak in week 52, with 402 new admissions in week 52 this

season compared to 911 in week 52 the 2022-2023 season. This season, there was another prominent peak in week 8 2024 with 284 new admissions (Figure 5).

Between week 40 2023 to week 20 2024, 4403 (79.3 per 100 000 inhabitants) new hospital admissions with influenza were reported, compared to 5739 (104.6 per 100000 inhabitants) between week 40 2022 to week 20 2023.

Vestfold county had the highest incidence of hospital admissions (111.5 per 100000 inhabitants), followed by Trøndelag (104.8) and Innlandet (101.8) (Table 1). Most admissions were with influenza A. The admission rates were highest in the age groups 65-79 and 80+ years, followed by children aged 0-4 years (Table 1, Table 2, Figure 6).

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 six seasons for which data are available, the 2023-2024 season started earlier and had a higher total number of admissions before the end of the year, than for five out of the six previous seasons (figure 4). However, the total number of admissions between weeks 40 and 20 was lower than during the 2017-2018, 2018-2019 and 2022-2023 seasons (Figure 5).

The median length of stay was 3 days (lower – upper quartile 1-5 days), with variation between age groups (Table 3). Seven percent of the patients received ventilatory support. A total of 174 patients (4 %) hospitalised with influenza died in hospital or within 14 days after discharge, with the majority of the deaths registered among patients aged 65 or older (Table 2).

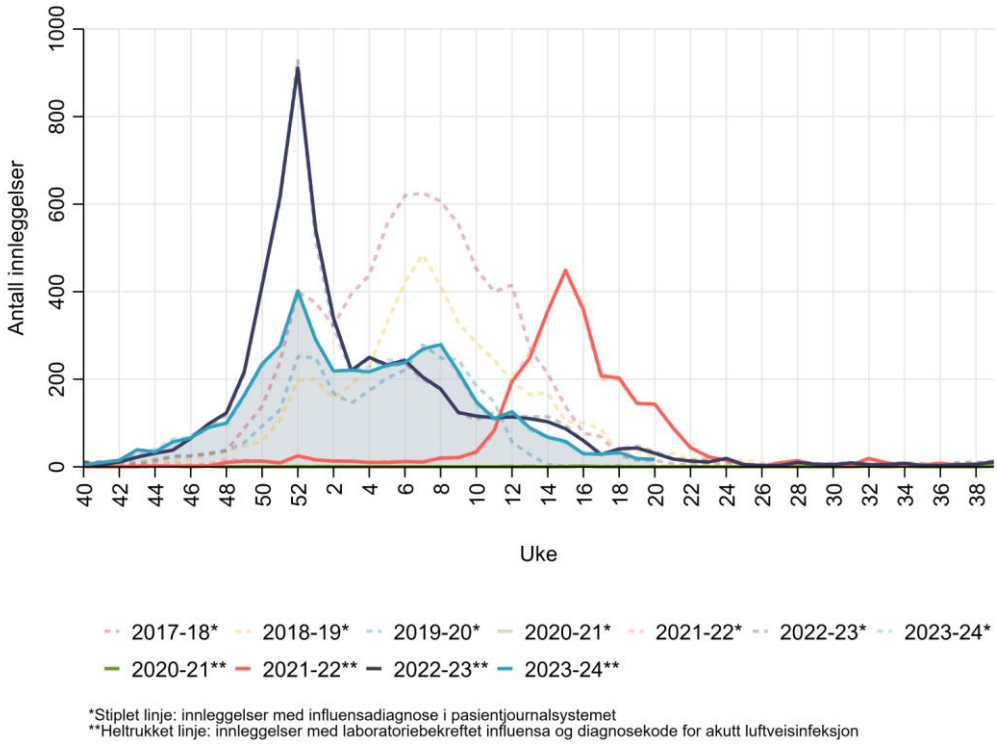


Figure 5: Weekly number of hospital admissions with influenza, Norway, 2 October 2017 – 19 May 2024. Source: The Norwegian Emergency Preparedness Register (Beredt C19) with data from the Norwegian Patient Registry and the Norwegian Surveillance System for Communicable Diseases (MSIS) laboratory database. The solid lines show numbers of admissions with laboratory confirmed influenza and diagnostic code for acute respiratory infection in the patient journal. Dashed lines show numbers of admissions with diagnostic code for acute respiratory infection in the patient journal.

Table 1: Number of patients hospitalised with influenza by county of residence, Norway, 2 October 2023 – 19 May 2024. Source: The Norwegian Emergency Preparedness Register (Beredt C19) with data from the Norwegian Patient Registry and the Norwegian Surveillance System for Communicable Diseases (MSIS) laboratory database.

	Weeks 40/2023 – 20/2024	
County	**Number**	**Incidence per 100000**
Agder	65	20,3
Akershus	382	52,4
Buskerud	271	100,4
Finnmark	53	70,6
Innlandet	383	101,8
Møre and Romsdal	204	75,4
Nordland	235	96,7
Oslo	441	61,4
Rogaland	357	71,5
Telemark	160	90,3
Troms	172	101,4
Trøndelag	506	104,8
Vestfold	286	111,5

Vestland	565	86,7
Østfold	233	74,6
Unknown	90	-
Total	4403	79,3

Table 2: Number of new hospital admissions with influenza by virus type and age group, Norway, 2 October 2023 – 19 May 2024. 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.

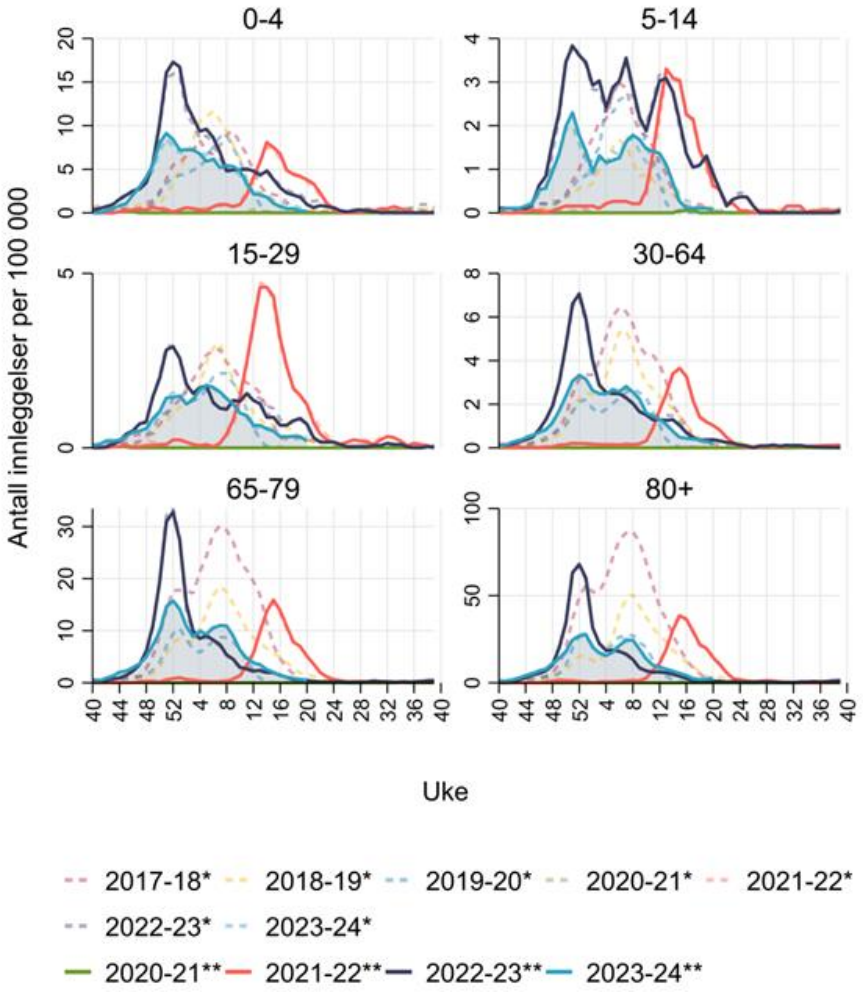
	Weeks 40/2023 – 20/2024			
	Influenza A		Influenza B	
Age group (years)	Admissions	Admissions per 100000	Admissions	Admissions per 100000
0-4	286	103.0	36	13.0
5-14	149	23.3	37	5.8
15-29	228	22.2	43	4.2
30-64	1103	43.5	70	2.8
65-79	1417	185.2	15	2.0
80+	933	378.7	17	6.9
Total	4116	75.0	218	4.0

Table 3: Number of patients hospitalised with influenza, length of stay and in-hospital deaths by age group, Norway, 2 October 2023 – 19 May 2024. Source: The Norwegian Emergency Preparedness Register (Beredt C19) with data from the Norwegian Patient Registry, the Norwegian Surveillance System for Communicable Diseases (MSIS) laboratory database and the National Population Registry.

	Weeks 40/2023 - 20/2024							
	Hospitalisations with influenza			Length of stay (days)[1]			Deaths[12]	
Age group (years)	Number	Incidence per 100000	Proportion (%)	Median	Lower quartile	Upper quartile	Number	Proportion (%)
0-4	323	117.0	7.3	1	1	3	<5	-
5-14	187	29.4	4.2	1	1	3	<5	-
15-29	276	26.6	6.3	1	1	3	<5	-
30-64	1199	46.7	27.2	3	1	5	12	1
65-79	1456	186.7	33.1	4	2	6	61	4
80+	962	375.1	21.8	4	2	7	99	10
Total	4403	79.3	100.0	3	1	5	174	4

[1]For the 4382 admissions where the patient had been discharged

[2]Includes in-hospital deaths and deaths that occurred a maximum of 14 days after discharge



Note that the y axes are different for each age group.
*Dashed line: admissions with diagnostic code for influenza in the patient journal
**Solid line: admissions with laboratory-confirmed influenza and diagnostic code for acute respiratory infection in the patient journal

Figure 6: Three-week moving average of weekly number of new hospital admissions with influenza by week and season, Norway, 2 October 2017 – 19 May 2024. 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.

Influenza in intensive care units

Between week 40 2023 and week 20 2024, a total of 179 patients (3.2 per 100 000 inhabitants) were admitted to ICU with confirmed influenza, with a peak of 16 patients admitted in week 7 2024. The incidence was highest in the age groups 80+ and 65-79 years (Table 4). The median length of stay was 3 (lower-upper quartile 2-9) days. Seventy-nine percent of the patients received ventilatory support, and 7% died in ICU.

In comparison, 188 patients were admitted to ICU with influenza in Norway between week 40 2022 and week 20 2023.

Table 4: Number of patients admitted to intensive care unit with confirmed influenza by age group, Norway, 2 October 2023 – 19 May 2024. Source: The Norwegian Emergency Preparedness Register (Beredt C19) with data from the Norwegian Intensive Care Registry

	Weeks 40/2023 – 20/2024	
Age group	Admissions	Admissions per 100000
0-4	16	5.8
5-14	6	0.9
15-29	9	0.9
30-64	65	2.5
65-79	58	7.4
80+	25	9.7
Total	179	3.2

Laboratory confirmed influenza

Influenza A viruses were dominating the season, and the main outbreak was caused by H1N1 viruses. Some regional differences were observed (Figure 8).

Altogether, 313,019 patients in Norway were tested for influenza during weeks 40/2023-34/2024, resulting in 17,248 recorded case detections of influenza A virus (88% of the influenza detections) and 2,360 influenza B virus (12 % of influenza detections) (Figure 7,Table 5). Of these, 2,800 influenza A (16 % of nonsentinel detections) and 1,028 influenza B (44 % of nonsentinel detections) positive specimens have so far been referred to the NIC and tested for further identification and characterisation. Among these 2,759 type A viruses were subtyped (1,486 H1(54 %) and 1,273 H3 (46 %). Two type A virus specimens were confirmed as such but too weak for successful subtyping and 25 (0.9 %) could not be confirmed as influenza A in the NIC. Three specimens contained both A(H1) and A(H3) viruses. All 988 lineage-typed influenza B viruses belonged to the B/Victoria/2/1987 lineage, 5 were confirmed as influenza B but contained too little viral RNA for lineage determination, and 35 (3.4 %) initially influenza B positive specimens could not be verified in the NIC.

Beside this, primary testing laboratories have identified 1,675 type A viruses as H1 and 36 as H3, of which 329 H1 and 4 H3 specimens have so far been forwarded to the NIC. This testing is biased since several laboratories are testing for H1pdm09 but not H3. In order to avoid this bias, subtyped viruses that have not been tested for both circulating HA subtypes, are not reported by subtype internationally or used for subtype proportion calculations.

The number of detections started to rise in mid-October, picking up pace in mid-November until reaching a long-lasting peak in weeks 51/2023 – 9/2024 (Figure 7). This peak was, however, considerably lower than the 2022-2023 New Year peak; with a maximum influenza positive rate of 16 % versus approx. 25 % one year earlier. The positivity rate fell below 10 % in week 10 and declined gradually toward summer, when it from week 22 and onwards has stayed at a baseline level well below 2 %. (Figure 7). As a rule of thumb, we consider intensity to be at medium level when the positivity rate in the overall national testing is between 10 and 20 %, low when under 10 %, very low when under 5 % and baseline beneath 2 %.

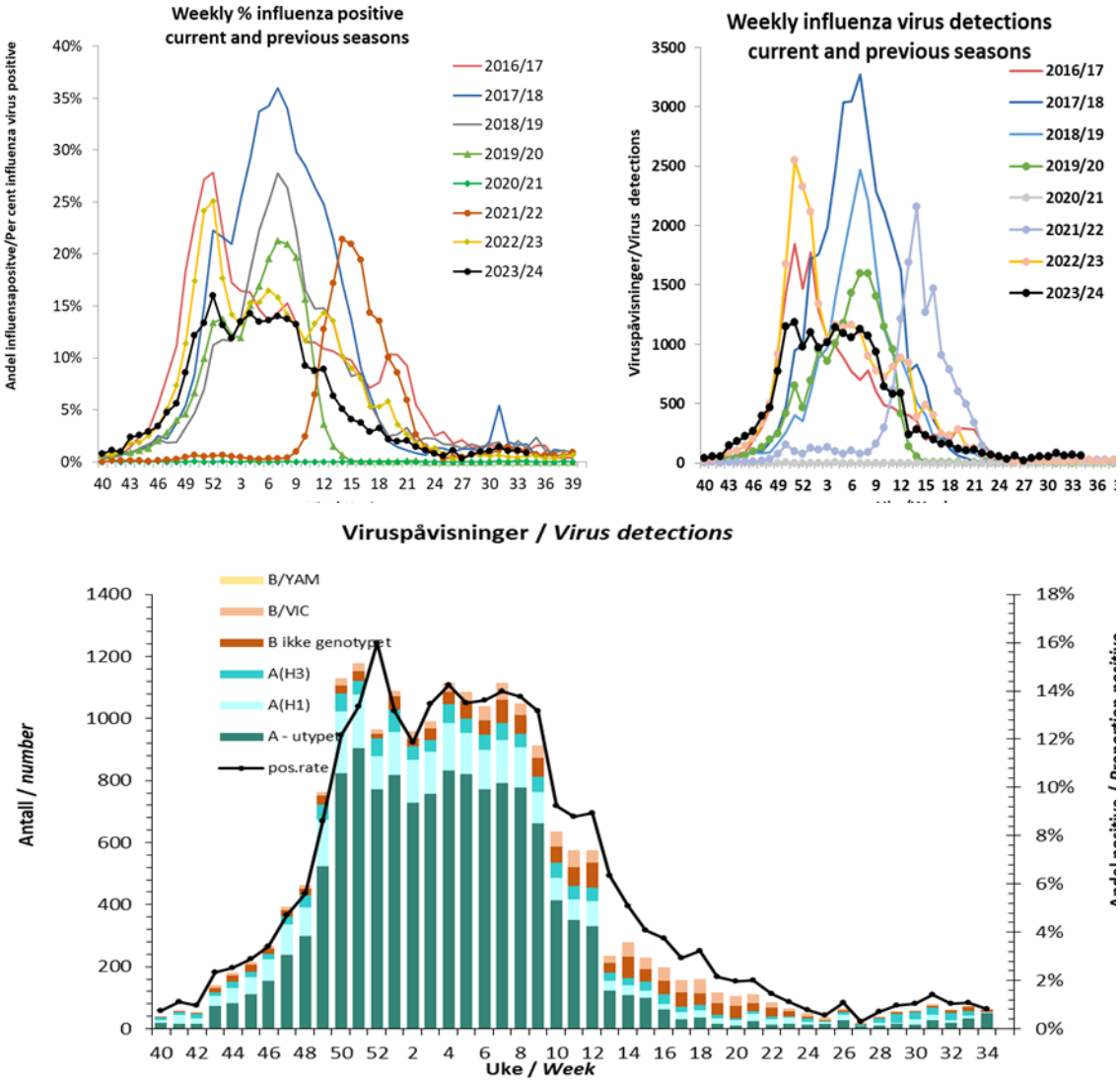


Figure 7: Laboratory detections, Norway 2023-2024. Upper left-hand panel: Weekly proportion of influenza virus positive specimens, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. Seasons impacted by Covid-19 are marked with symbols.
Lower panel: Weekly number of the different influenza viruses, displayed as stacked bars.

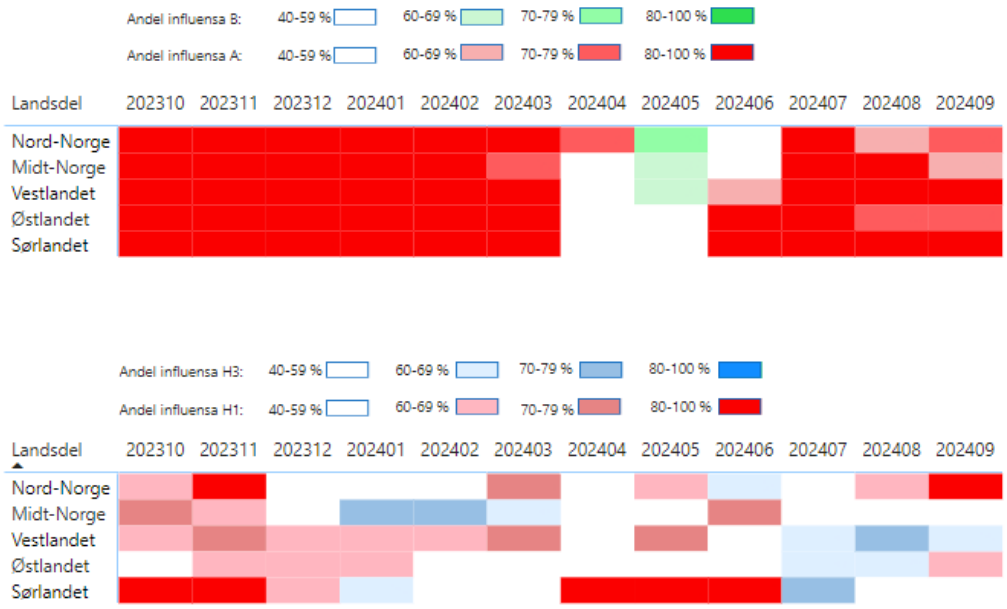


Figure 8: Dominating influenza type by geographical region and month in upper panel, and dominating influenza A subtype by geographical region and month in lower panel.

Type A viruses have been in strong majority over type B throughout the peak period. Among the type A viruses, subtypeH1N1 was in clear majority in the beginning, but the proportions of subtypes H1N1 and H3N2 became more even during the main outbreak weeks, with a slight majority of subtype H1N1 (Figure 8, Figure 9). Through spring H1N1 was again in clearer majority, however, through the summer most have been H3N2 (Figure 9).
Influenza B viruses have been exclusively B/Victoria/2/87-lineage and were equally or more common than type A viruses during the declining phase in the spring.

There has been some regional heterogeneity in the proportions of the different influenza subtypes, e.g., with H3 in majority in mid-Norway. 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.

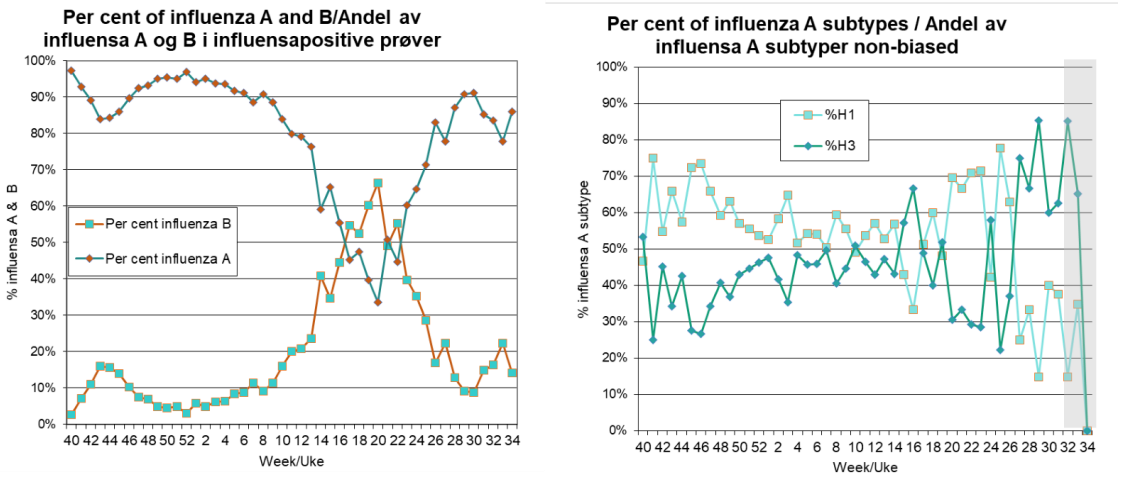


Figure 9: Influenza virus detections since week 40/2023, proportions per type A and B (left panel) and influenza A subtypes H1 and H3 (right panel). Only viruses tested for both subtypes are counted in the subtype analysis

Table 5: 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). Numbers provided here for A(H1) and A(H3) are not comparable since several laboratories test for H1pdm09 but not for H3

UKE/ *week*	Viruspåvisninger/*Virus detections*							
	Prøver/ *Specimens*	% positive	A(utypet) *not subtyped*	A(H1)	A(H3)	B ikke genotypet *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
40	4937	0,7 %	20	8	8	1	0	0
41	5097	1,1 %	17	27	8	3	1	0
42	5616	1,0 %	16	19	14	3	3	0
43	6155	2,3 %	74	33	14	15	8	0
44	7325	2,5 %	81	52	23	23	6	0
45	7664	2,9 %	110	62	19	22	9	0
46	7974	3,4 %	154	72	17	17	11	0
47	8418	4,7 %	237	102	28	18	12	0
48	8348	5,6 %	299	95	42	20	12	0
49	8980	8,6 %	525	158	52	27	11	0
50	9463	12,2 %	823	210	64	27	25	0
51	8901	13,3 %	903	181	45	33	25	0
52	6112	16,0 %	773	112	62	14	15	0
1	8351	13,2 %	818	142	76	44	20	0
2	8215	11,9 %	727	149	50	24	24	0
3	7523	13,5 %	756	152	43	36	27	0
4	8013	14,2 %	832	164	72	40	33	0
5	8112	13,5 %	822	134	48	58	33	0
6	7773	13,6 %	772	134	57	47	46	0
7	8072	14,0 %	793	146	61	75	54	0
8	7779	13,8 %	778	145	49	61	37	0
9	7109	13,2 %	661	116	53	61	46	0
10	6964	9,2 %	415	72	53	50	53	0
11	6638	8,8 %	351	70	45	62	55	0
12	6546	8,9 %	329	87	46	80	42	0
13	3752	6,3 %	123	34	25	31	25	0
14	5544	5,1 %	107	35	25	68	47	0
15	5661	4,1 %	100	22	28	42	38	0
16	5362	3,7 %	61	18	32	43	46	0

17	5447	2,9 %	30	22	20	45	42	0
18	4992	3,2 %	35	26	16	39	46	0
19	5389	2,2 %	16	16	14	36	34	0
20	5409	2,0 %	11	18	7	40	31	0
21	5666	2,0 %	24	23	11	24	32	0
22	5866	1,4 %	13	18	7	30	17	0
23	6204	1,1 %	16	19	6	15	12	0
24	6649	0,8 %	12	10	11	6	12	0
25	6361	0,6 %	15	8	2	3	7	0
26	6072	1,1 %	26	18	10	6	5	0
27	5851	0,3 %	6	2	6	1	3	0
28	5574	0,7 %	11	9	14	3	2	0
29	5674	1,0 %	15	6	29	3	2	0
30	5439	1,0 %	14	17	21	3	2	0
31	5712	1,4 %	26	18	25	6	6	0
32	5902	1,0 %	20	8	23	8	2	0
33	6596	1,1 %	33	8	15	14	2	0
34	7812	0,8 %	52	3	0	9	0	0
Total	313019		12852	3000	1396	1336	1021	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: 17248			Type B: 2357			

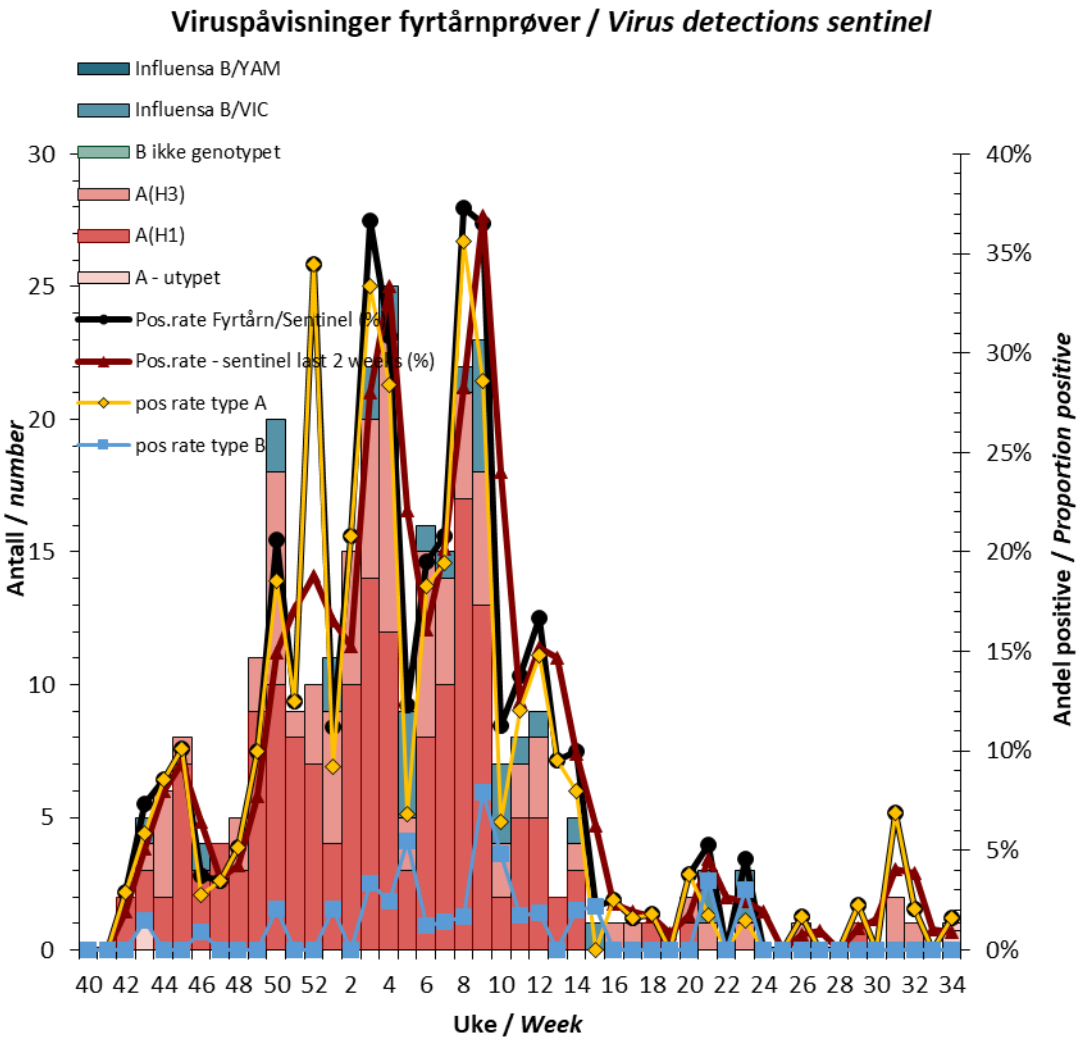
False positives due to vaccine contaminating sampling workstations?

Like in earlier seasons, in a few instances in the autumn trace amounts of virus RNA representing three or four different subtypes/lineages, including B/Yamagata-lineage, 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 pediatric case in December, there was sufficient virus to obtain partial sequence, and the genetic profile was indicating the genetic backbone of live attenuated vaccine strains thus suggesting detection of LAIV in a vaccinated individual. 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

Sentinel-based surveillance, primary care (Fyrtårnsystemet)

From week 40/2023 through week 34/2024, 2,965 geographically representative sentinel specimens have been tested, with 259 detections of influenza virus A (168 subtype H1, 88 subtype H3, and 2 not subtyped due to low viral load), and 33 influenza virus B, all these were Victoria-lineage. In addition, 305 SARS-CoV-2, 81 RSV (63 type A, 26 type B, 1 not yet typed), 394 rhinovirus, 86 human metapneumovirus (hMPV), 118 parainfluenza virus and 81 other human coronaviruses were detected (Figure 10,Table 6).

Approximately half of all sentinel surveillance samples were from the age group 25-59 years old. The second largest age group, constituting 21 %, was the group aged 60 years and above, followed by the 15-24 year olds (17 %). The two least represented age groups were the youngest, with 5-14 year olds making up 8 % and 0-4 year olds 4 %, respectively.


Viruspåvisninger fyrtårnprøver / Virus detections sentinel
Influensa B/YAM
Influensa B/VIC
B ikke genotypet
A(H3)
A(H1)
A - utypet
Pos.rate Fyrtårn/Sentinel (%)
Pos.rate - sentinel last 2 weeks (%)
pos rate type A
pos rate type B
Antall / number
Andel positive / Proportion positive
Uke / Week
0
5
10
15
20
25
30
0%
5%
10%
15%
20%
25%
30%
35%
40%
40 42 44 46 48 50 52 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34

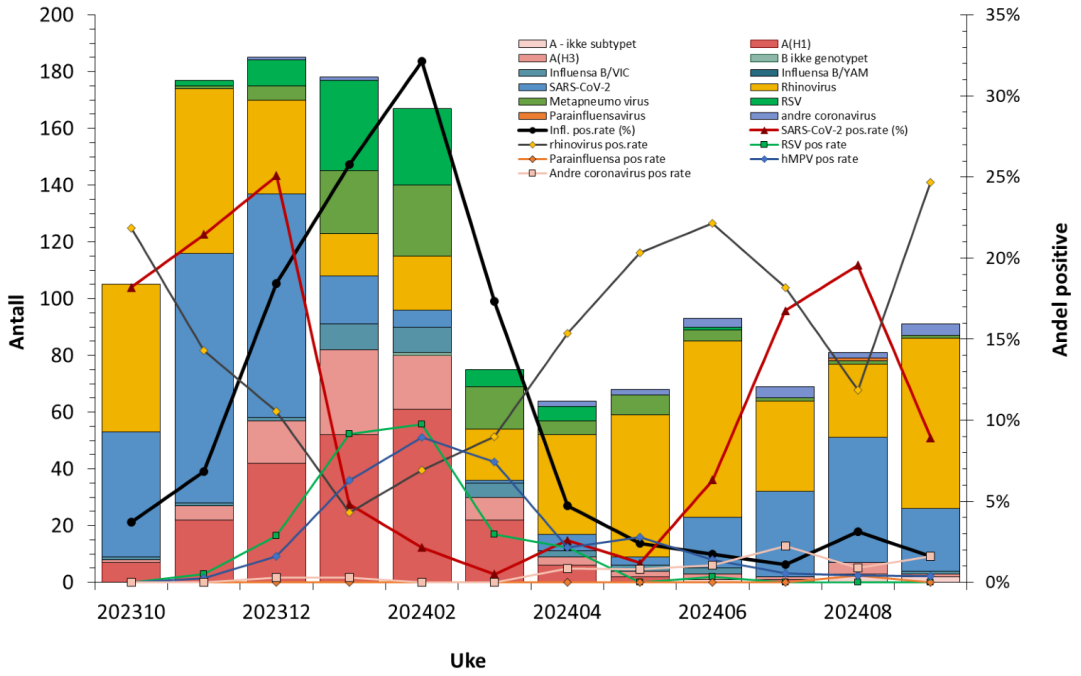


Figure 10: Weekly numbers of detections and per cent positives of influenza viruses (upper panel) and all surveyed respiratory viruses pr. month (lower panel) in the respiratory sentinel surveillance.

Table 6: Weekly virus detections in the virological sentinel system (fyrtårnsystemet)

Week	Specimens tested	Influenza A - untyped	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
40	50	0	0	0	0	0	0	0 %	0 %	0 %	6	12 %	0	0 %	13	26 %	0	2	0	4 %	0	0 %	0	0 %
41	33	0	0	0	0	0	0	0 %	0 %	0 %	5	15 %	0	0 %	8	24 %	0	0	0	0 %	0	0 %	0	0 %
42	69	0	2	0	0	0	0	3 %	3 %	0 %	12	17 %	0	0 %	13	20 %	0	1	0	1 %	0	0 %	1	1 %
43	68	1	2	1	0	1	0	7 %	6 %	1 %	13	19 %	0	0 %	13	20 %	0	2	0	3 %	0	0 %	1	1 %
44	70	0	2	4	0	0	0	9 %	9 %	0 %	11	16 %	0	0 %	11	17 %	0	2	0	3 %	0	0 %	0	0 %
45	79	0	7	1	0	0	0	10 %	10 %	0 %	15	19 %	1	1 %	17	23 %	0	1	1	3 %	0	0 %	0	0 %
46	107	0	3	0	0	1	0	4 %	3 %	1 %	29	27 %	0	0 %	10	10 %	0	1	0	1 %	0	0 %	2	2 %
47	114	0	4	0	0	0	0	4 %	4 %	0 %	22	19 %	1	1 %	16	15 %	0	2	2	4 %	1	1 %	2	2 %
48	97	0	3	2	0	0	0	5 %	5 %	0 %	25	26 %	0	0 %	10	11 %	0	3	2	5 %	0	0 %	3	3 %
49	110	0	9	2	0	0	0	10 %	10 %	0 %	30	27 %	2	2 %	20	19 %	0	3	1	4 %	1	1 %	4	4 %
50	97	0	10	8	0	2	0	21 %	19 %	2 %	30	31 %	1	1 %	8	9 %	0	0	3	3 %	0	0 %	2	2 %
51	72	0	8	1	0	0	0	13 %	13 %	0 %	13	18 %	6	9 %	5	7 %	0	2	0	3 %	4	6 %	4	6 %
52	29	0	7	3	0	0	0	34 %	34 %	0 %	6	21 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	0	0 %
1	98	0	4	5	0	2	0	11 %	9 %	2 %	9	9 %	6	6 %	3	3 %	0	0	2	2 %	5	5 %	2	2 %
2	72	0	10	5	0	0	0	21 %	21 %	0 %	5	7 %	3	4 %	1	1 %	0	0	0	0 %	4	6 %	1	1 %
3	60	0	14	6	0	2	0	37 %	33 %	3 %	0	0 %	8	14 %	2	3 %	0	1	0	2 %	3	5 %	0	0 %
4	81	0	12	11	0	2	0	31 %	28 %	2 %	1	1 %	9	12 %	6	8 %	0	0	1	1 %	5	7 %	4	5 %
5	73	0	3	2	0	4	0	12 %	7 %	5 %	0	0 %	7	10 %	4	6 %	0	0	1	1 %	6	8 %	2	3 %

6	82	0	8	7	0	1	0	20 %	18 %	1 %	1	1 %	6	8 %	2	3 %	0	1	0	1 %	8	10 %	4	5 %
7	72	0	10	4	0	1	0	21 %	19 %	1 %	2	3 %	8	11 %	9	13 %	0	0	4	6 %	6	8 %	5	7 %
8	59	0	17	4	0	1	0	37 %	36 %	2 %	0	0 %	8	14 %	2	3 %	0	0	0	0 %	5	8 %	2	3 %
9	63	0	13	5	0	5	0	37 %	29 %	8 %	2	3 %	4	7 %	6	10 %	0	3	0	5 %	5	8 %	6	10 %
10	62	0	2	2	0	3	0	11 %	6 %	5 %	1	2 %	2	3 %	3	5 %	0	0	0	0 %	2	3 %	5	8 %
11	58	0	5	2	0	1	0	14 %	12 %	2 %	0	0 %	3	5 %	4	7 %	1	0	1	3 %	4	7 %	5	9 %
12	54	0	5	3	0	1	0	17 %	15 %	2 %	0	0 %	0	0 %	6	12 %	1	1	5	13 %	5	10 %	1	2 %
13	21	0	2	0	0	0	0	10 %	10 %	0 %	0	0 %	0	0 %	4	19 %	0	0	0	0 %	4	19 %	0	0 %
14	50	0	3	1	0	1	0	10 %	8 %	2 %	0	0 %	2	4 %	9	18 %	0	1	0	2 %	1	2 %	1	2 %
15	46	0	0	0	0	1	0	2 %	0 %	2 %	1	2 %	0	0 %	8	18 %	0	1	3	9 %	1	2 %	2	4 %
16	40	0	0	1	0	0	0	3 %	3 %	0 %	0	0 %	1	3 %	1	3 %	0	0	1	3 %	1	3 %	2	5 %
17	62	0	0	1	0	0	0	2 %	2 %	0 %	3	5 %	2	3 %	10	16 %	0	1	4	8 %	2	3 %	2	3 %
18	56	0	1	0	0	0	0	2 %	2 %	0 %	1	2 %	0	0 %	13	24 %	1	2	4	13 %	3	5 %	3	5 %
19	62	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	11	18 %	0	0	5	8 %	2	3 %	2	3 %
20	53	0	1	1	0	0	0	4 %	4 %	0 %	0	0 %	0	0 %	10	19 %	0	1	3	8 %	2	4 %	4	8 %
21	57	0	0	1	0	2	0	5 %	2 %	4 %	2	4 %	0	0 %	16	29 %	0	0	1	2 %	0	0 %	1	2 %
22	57	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	7	13 %	0	1	8	16 %	0	0 %	1	2 %
23	66	0	0	1	0	2	0	5 %	2 %	3 %	0	0 %	0	0 %	9	14 %	1	0	6	10 %	0	0 %	1	2 %
24	87	0	0	0	0	0	0	0 %	0 %	0 %	4	5 %	0	0 %	19	22 %	0	1	5	7 %	2	2 %	1	1 %
25	73	0	0	0	0	0	0	0 %	0 %	0 %	2	3 %	1	1 %	20	28 %	0	1	5	8 %	1	1 %	2	3 %
26	59	0	0	1	0	0	0	2 %	2 %	0 %	6	10 %	0	0 %	14	24 %	1	2	2	8 %	1	2 %	0	0 %
27	46	0	0	0	0	0	0	0 %	0 %	0 %	6	13 %	0	0 %	11	24 %	1	0	0	2 %	0	0 %	0	0 %
28	49	0	0	0	0	0	0	0 %	0 %	0 %	6	12 %	0	0 %	10	21 %	1	0	2	6 %	0	0 %	1	2 %
29	44	0	1	0	0	0	0	2 %	2 %	0 %	8	18 %	0	0 %	9	20 %	0	0	1	2 %	0	0 %	1	2 %
30	20	0	0	0	0	0	0	0 %	0 %	0 %	4	20 %	0	0 %	2	11 %	0	0	0	0 %	0	0 %	0	0 %
31	29	0	0	2	0	0	0	7 %	7 %	0 %	2	7 %	0	0 %	0	0 %	0	0	0	0 %	1	3 %	0	0 %
32	49	0	0	1	0	0	0	2 %	2 %	0 %	6	12 %	0	0 %	7	15 %	0	0	0	0 %	1	2 %	1	2 %
34	49	0	0	0	0	0	0	0 %	0 %	0 %	7	14 %	0	0 %	8	17 %	0	0	1	2 %	0	0 %	0	0 %
34	61	1	0	0	0	0	0	2 %	2 %	0 %	9	15 %	0	0 %	4	7 %	1	0	0	2 %	0	0 %	0	0 %
Sum	2965	2	168	88	0	33	0				305		81		394		8	36	74		86		81	

Genetic characterisation of the influenza viruses in circulation

This season NIPH has received 4120 influenza virus positive specimens for analysis and 17 % (720) of these have been characterized further with whole genome sequencing (Table 7). Furthermore, 78 viruses have been shared with the WHO Collaborating Centre in the UK for further characterisations (Worldwide Influenza Centre, Francis Crick Institute).

This season we have submitted 308 A(H1N1) HA and NA sequences and 236 PA sequences for and 238 A(H3N2) HA, 236 NA and 177 PA sequences, and for B/Victoria we submitted 149 HA and 123 NA sequences to the WHO GISRS genomic surveillance database GISAID.

Table 7: Genetic characterisation of Influenza viruses in Norway in 2023/24 Season

Clade & Genetic category	Subclade	2023 okt	2023 nov	2023 des	2024 jan	2024 feb	2024 mar	2024 apr	2024 mai	2024 jun	2024 jul	2024 Aug	Total
A/H1N1		26	73	30	61	36	25	17	19	12	9	8	308
6B.1A.5a.2a		19	26	12	30	27	15	16	15	4	8	7	172
genAH1/Sydney/5/2021	C.1	12	13	4	4	1	2	0	0	0	0	0	36
genAH1/Sydney/5/2021	C.1.7	1	6	1	1	0	0	0	0	0	0	0	9
genAH1/Sydney/5/2021	C.1.8	1	2	2	7	9	6	3	2	0	0	0	32
genAH1/Sydney/5/2021	C.1.9	5	5	5	18	17	7	13	13	4	8	7	95
6B.1A.5a.2a.1		7	47	18	31	9	10	1	4	8	1	1	136
genAH1/Wisconsin/67/2022	C.1.1	0	0	1	1	1	2	0	1	0	0	0	6
genAH1/Victoria/4897/2022	D	0	0	0	0	1	1	0	1	8	1	1	12
genAH1/Victoria/4897/2022	D.1	2	10	7	4	0	2	1	0	0	0	0	26
genAH1/Victoria/4897/2022	D.2	3	35	9	24	7	5	0	2	0	0	0	85
genAH1/Victoria/4897/2022	D.3	2	2	1	2	0	0	0	0	0	0	0	7
A/H3N2		17	35	12	57	23	25	25	12	13	19	25	238
3C.2a1b.2a.2a.3a		0	1	0	0	0	0	1	0	0	0	0	2
genAH3/Finland/402/2023	G.1.3.1	0	1	0	0	0	0	1	0	0	0	0	2
3C.2a1b.2a.2a.3a.1		17	34	12	57	23	25	24	12	13	19	25	236
genAH3/Thailand/8/2022	J	0	2	0	0	0	0	0	0	0	0	0	2
genAH3/Thailand/8/2022	J.1	11	16	3	14	1	3	2	0	0	0	0	50
genAH3/Thailand/8/2022	J.2	3	14	9	40	21	22	22	12	13	19	25	175
genAH3/Thailand/8/2022	J.3	0	0	0	0	1	0	0	0	0	0	0	1
genAH3/Thailand/8/2022	J.4	3	2	0	3	0	0	0	0	0	0	0	8
B/Victoria		30	5	5	11	20	32	35	24	8	4	3	174
V1A.3a.2		30	5	5	11	20	32	35	24	8	4	3	174
genBVicB/Catalonia/2279261NS/2023	C.5	26	5	4	6	9	19	4	7	1	0	0	81
genBVicB/Connecticut/01/2021	C.5	1	0	1	0	0	0	0	0	0	0	0	2
genBVicB/Catalonia/2279261NS/2023	C.5.1	2	0	0	0	4	6	2	3	1	1	1	19
genBVicB/Connecticut/01/2021	C.5.5	0	0	0	1	0	0	0	0	0	0	0	1
genBVicB/Connecticut/01/2021	C.5.6	0	0	0	0	1	5	4	1	1	2	1	14
genBVicB/Catalonia/2279261NS/2023	C.5.7	1	0	0	4	6	2	25	13	5	1	1	57
Total		90	147	59	186	102	107	101	67	46	51	61	720

H1N1 viruses

In the current season, two main genetic groups of A(H1N1) viruses have been predominant in Norway. The **genAH1/Victoria/4897/2022** like viruses belonging to clade 6B.1A.5a.2a.1 and defined by substitutions; *P137S*, *K142R*, *D260E*, *T227A* and *T216A* were the dominant subtype in the beginning of the season until January 2024. The main subclades detected were D.2 and D.1 up until April 2024 then the subclade D was mainly detected (Figure 11, Table 7)

From January 2024 and onwards the **genAH1/Sydney/5/2021** like viruses defined by *K54Q*, *A186T*, *E224A*, *R259K*, and *K308R* substitutions, belonging to clade 6B.1A.5a.2a were dominant. The most common subclades were C.1 in the beginning of the season until December 2023 the mostly C.1.9 and C.1.8 were detected.

Additionally, during the 2023/2024 season, **genAH1/Wisconsin/67/2022-like** viruses were sporadically detected. These viruses share the same defining substitutions as the **genAH1/Victoria/4897/2022-like** viruses, except they lack the *T216A* substitution. However, this genetic group did not contribute significantly to overall detections.

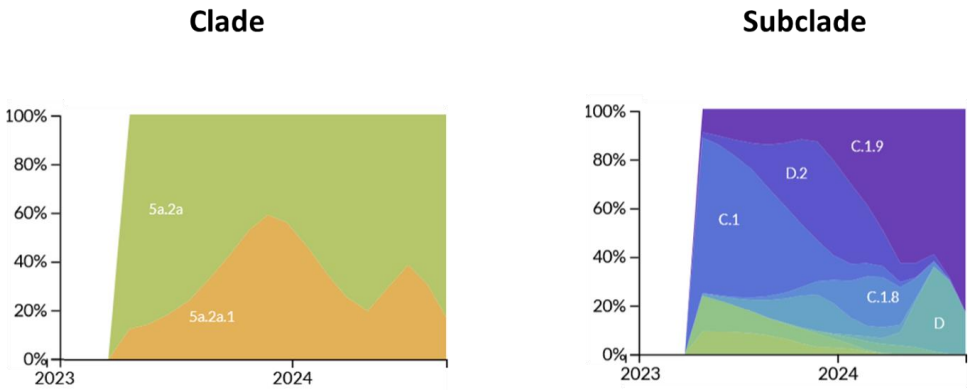


Figure 11: Clade and subclade of H1 influenza frequencies in Norway season 2023-24. Source: https://nextstrain.org/groups/niph

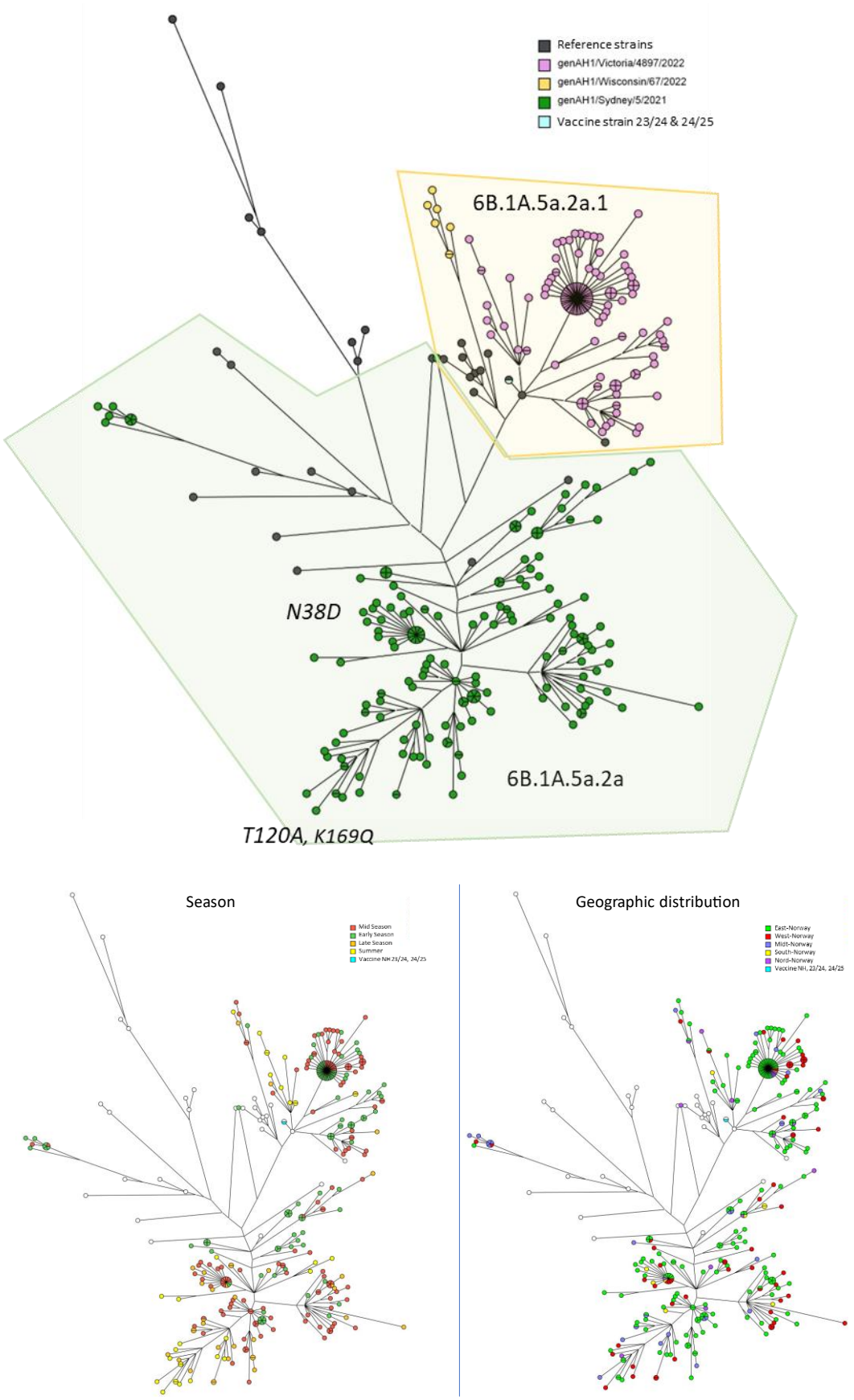


Figure 12: Phylogenetical cluster diagrams of Norwegian H1 influenza color coded by genetic clade, season, and geographical distribution.

Recent detections were clustered in **genAH1/Sydney/5/2021** like viruses within the subclade 5a.2a, C.1.9, one subcluster of which carries an additional *N38D* substitutions which represents an antigenic site and could indicate an immunogenic advantage for the next season. Nonetheless, clade 5a.2a viruses remain well-covered by the more evolved 5a.2a.1 vaccine component (**A/Victoria/4897/2022**) (Figure 12).

We also observed a group of viruses from the **genAH1/Victoria/4897/2022-like** viruses belonging to the 5a.2a.1 subclade D, but they do not carry any additional substitutions compared to the current vaccine component.

Despite thorough investigations across age groups, geographic regions, and vaccination statuses, no discernible patterns have emerged.

H3N2 viruses

A(H3N2) viruses have been circulating all through the 2023-2024 season and were in majority among the few detections during the 2024 summer months. The previous seasons **genH3/Darwin/9/2021** group has further diversified into two distinct groups: **genAH3/Finland/402/2023-like** virus characterized by the substitutions *E50K*, *D53N*, *N96S*, I192F and belonging to clade 3C.2a1b.2a.2a.3a; and **genAH3Thailand/8/2022** defined by *D53N*, *N96S*, *I192F*, and *I140M*, belonging to subclade 3C.2a1b.2a.2a.3a.1. Almost all Norwegian viruses from the 2023/24 season have been in the latter group as seen in Figure 13.

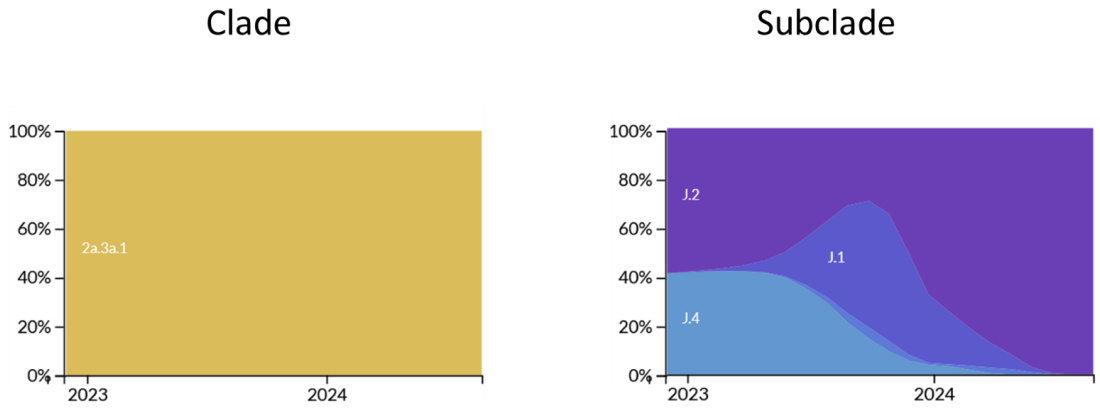


Figure 13: Clade and subclade of H3 influenza frequencies in Norway season 2023-24. Source: https://nextstrain.org/groups/niph

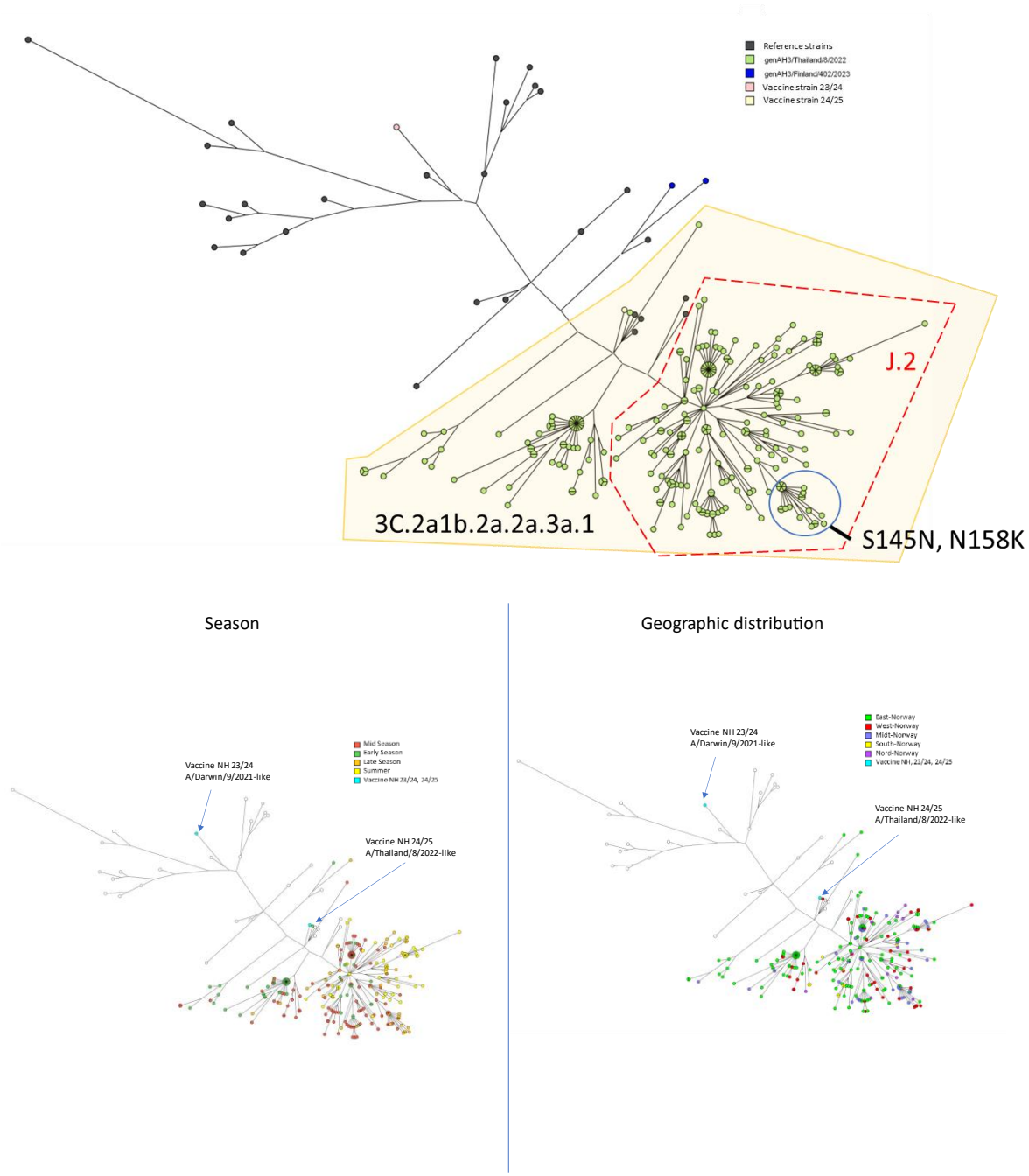


Figure 14: Phylogenetical cluster diagrams of Norwegian H3 influenza color coded by genetic clade, season, and geographical distribution.

This season, the **genAH3/Thailand/8/2022-like** viruses have further evolved into subclades (J-J.4). The majority of Influenza A(H3N2) detections in Norway (175 out of 240) were attributed to the J.2 subclade, although a significant proportion (50 out of 240) was also attributed to J.1 during the early part of the season (October 2023 to January 2024). While J.4 H3N2 viruses are currently circulating in other regions worldwide, detections of J.4 viruses in Norway were limited to late 2023, with no subsequent detections since then (Figure 13).

The A(H3N2) vaccine component for the 2023-24 Northern hemisphere influenza vaccine based on the **A/Darwin/9/2021-like** virus (3C.2a1b.2a.2a), has for the 2024-25 season been **updated** to the **A/Thailand/8/2022-like** of viruses (3C.2a1b.2a.2a.3a.1). As illustrated in

Figure 14, this update aligned the vaccine component more closely with the circulating strains, which was predominantly classified as **A/Thailand/8/2022-like**.
In the latest months of the 2023-24 season an increase in J.2 drifted viruses with especially the *S145N* mutation giving a loss of glycosylation, but also with *N158K* and *K189R* has been observed in Asia, Africa, and South America. WHO has shown that these changes in the J.2 viruses cause antigenic drift and has subsequently in September 2024 updated the H3 component for the Southern hemisphere (https://www.who.int/publications/m/item/recommended-composition-of-influenza-virus-vaccines-for-use-in-the-2025-southern-hemisphere-influenza-season). In Norway, a group of these viruses, J.2 with both *S145N* and *N158K* was circulating in spring, but not detected since.

B-Victoria-lineage viruses

In the previous 2022/23 season, all Influenza B(Victoria) viruses were categorised as **genBVicB/Austria/1359417/2021**-like viruses (Clade V1A.3a.2). This category has since undergone further subdivision, resulting in two distinct genetic clades: **genBVicB/Connecticut/01/2021**-like virus (NextStrain subclades C.5.5 and C.5.6, characterised by the *D197E* substitution), and **genBVicB/Catalonia/2279261NS/2023**-like virus (NextStrain subclade C.5, defined by *D197E* and *E183K* substitutions). Both groups also fall within the V1A.3a.2 clade.

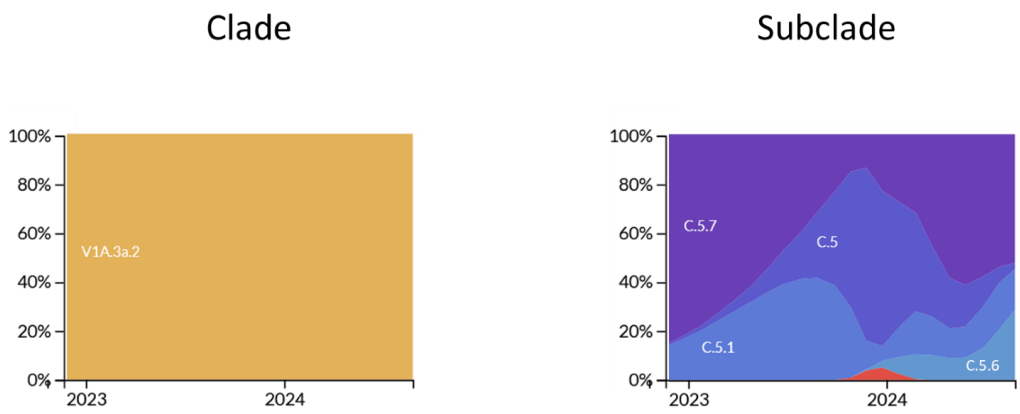


Figure 15: Clade and subclade of B-Victoria influenza frequencies in Norway season 2023-24. Source: https://nextstrain.org/groups/niph

In Norway, there has been a relatively low incidence of Influenza B (Victoria) this season. In the beginning of the 2023/24 season detection of the subclade C.5 were prevalent, until April 2024 where mostly C.5.7 were detected (Figure 15, Figure 16).
The vaccine component for Influenza B (Victoria) for the 23/24 and the 24/25 will stay as a **B/Austria/1359417/2021 -like** virus which is the same genetic clade (V1A.3a.2) as all viruses detected in Norway in the 23/24 season and is therefore expected to confer protection.

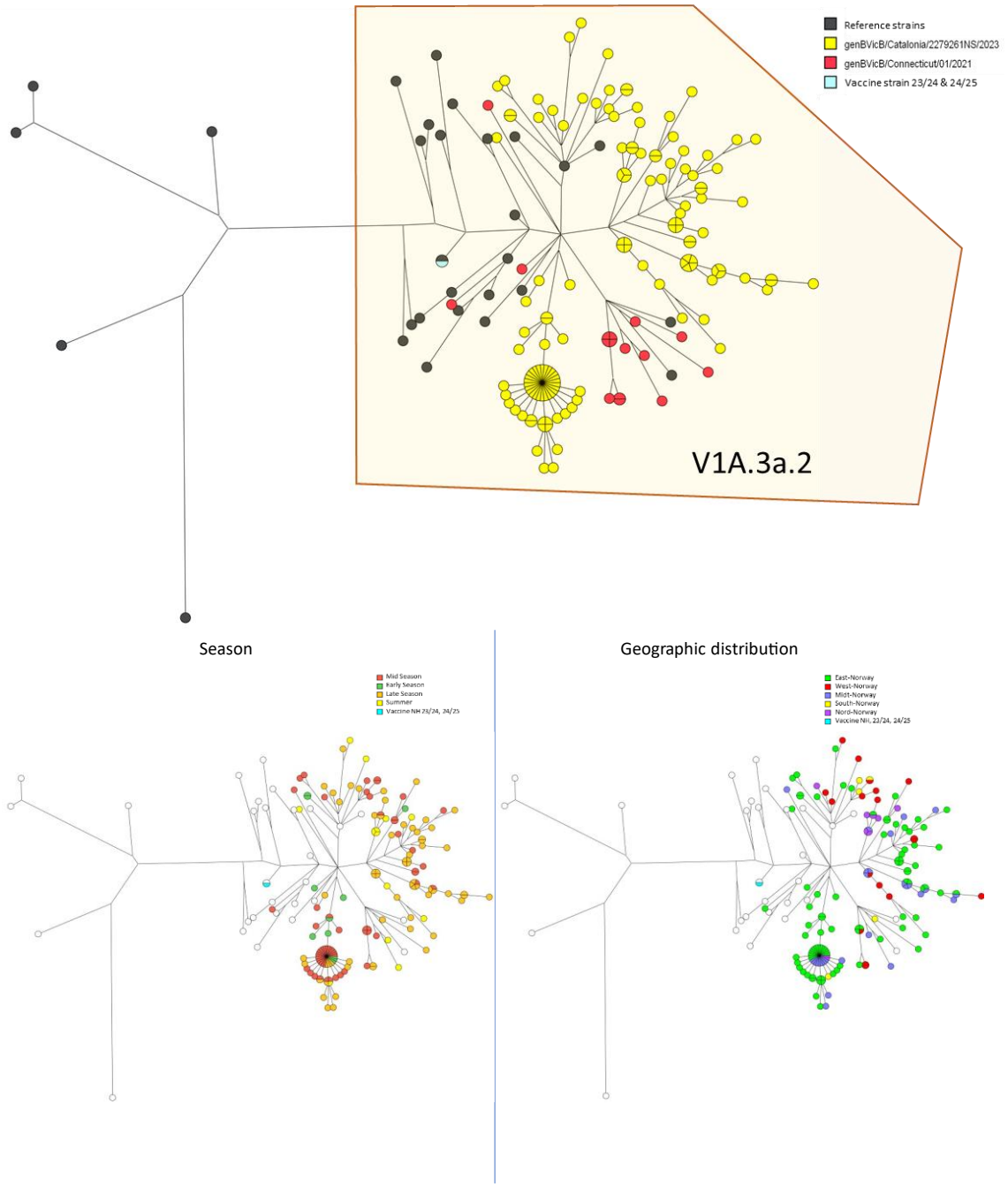


Figure 16: Phylogenetic analysis of Norwegian B-Victoria viruses using the Maximum Parsimony Method. Dot colors indicate the time and location of virus detection, as described in the figure legend. Time periods are categorized as follows: Early Season (week 40–50), Mid-Season (week 51–12), Late-Season (week 12–21), and Summer (week 21–39), or by graphical distribution.

You can read more about in-depth genetic analysis in the VCM rapport https://www.fhi.no/ss/influensa/sesonginfluensa/who-rapporter/ and go to our NEXTstrain build to explore the sequences. (https://nextstrain.org/groups/niph) or explore worldwide seasonal influenza sequences (https://nextstrain.org/seasonal-flu/).

Antiviral susceptibility of influenza viruses

Out of 604 influenza viruses tested for susceptibility to neuraminidase inhibitors this season only one B/Victoria in week 14 showed genetic resistance to oseltamivir due to an A245T substitution in the NA gene (Table 8), the treatment history is unknown. In addition, the H273Y mutation was detected in the same Influenza B case, and in two more cases from the same region. This mutation has been reported both to give normal and reduced inhibition with oseltamivir and reduced to highly reduced inhibition with peramivir. This could indicate some circulation of H273Y mutant viruses in the western part of Norway this season.

During the 2023-24 season a new combination mutation in H1N1 viruses (NA: I223V and S247N) giving reduced sensitivity to neuraminidase inhibitors were discovered by RIVM in the Netherlands. Further investigations have shown a global emergence, and the incidence of strains with I223V or S247N mutations, or both, increased in the fall of 2023, most cases from Europe. The emergence has occurred in different subclades of the N1 viruses and is not believed to be antiviral treatment mediated, but more natural drift of the viruses. Functional assays show that the mutation combination does reduce the sensitivity towards zanamivir slightly, but not above the threshold for zanamivir resistance. However, reduced sensitivity towards oseltamivir (borderline about 10-fold reduction) has been shown.

One single H1N1 case of the double mutant was also detected in Norway from week 43/2023. Phenotypic testing by MUNANA (phenotypic neuraminidase susceptibility assay) at NIPH revealed borderline resistance to oseltamivir at about 10-12 fold reduced susceptibility. Three other isolates possessing the S247N alone did not reach the 10-fold threshold. All other tested or analysed viruses were sensitive to oseltamivir, zanamivir and baloxavir marboxil (Table 8). H1 viruses only possessing one of these mutations was phenotypically investigated and did not show reduced susceptibility to oseltamivir.

All tested circulating influenza A viruses have been resistant to adamantanes, which are not used for treatment in Norway.

Table 8: Norwegian influenza viruses resistant to the neuraminidase inhibitors oseltamivir and zanamivir, during the influenza seasons 2017/18 through 2023/24 (sequences with resistance/total number of analysed sequences).

Season	Oseltamivir resistance			Zanamivir resistance			Baloxavir resistance			Adamantane resistance		
	A(H1N1)	A(H3N2)	B	A(H1N1)	A(H3N2)	B	A(H1N1)	A(H3N2)	B	A(H1N1)	A(H3N2)	B
2017/18	0/120	0/66	1/42	0/28	0/54	0/30	ND	ND	ND	ND	ND	NA
2018/19	0/247	0/108	0/26	0/82	0/107	0/26	ND	ND	ND	ND	ND	NA
2019/20	0/103	0/63	0/42	0/32	0/60	0/42	ND	ND	ND	ND	ND	NA
2020/21	0/2	0/6	0/1	0/2	0/6	0/1	ND	ND	ND	ND	ND	NA
2021/22	0/31	0/634	0/9	0/31	0/634	0/9	0/0	1/442	0/0	19/19	476/47	NA
2022/23	1/494	0/291	0/34	1/494	0/291	0/34	0/74	0/232	0/10	ND	ND	NA
2023/24	1/287	0/206	1/11	0/287	0/206	1/11	0/252	0/190	0/13	287/287	207/207	NA

Pre-season seroprevalence and age distribution of viruses detected

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. Analyses of a subset of 1260 sera collected in August 2023 are presented here.

In Figure 17, the pre-season population immunity within age groups against the different influenza viruses, described in the section on Population immunity, is shown together with the in-season age distribution of detected infections for the corresponding viruses, displayed as normalised incidence of laboratory verified cases.

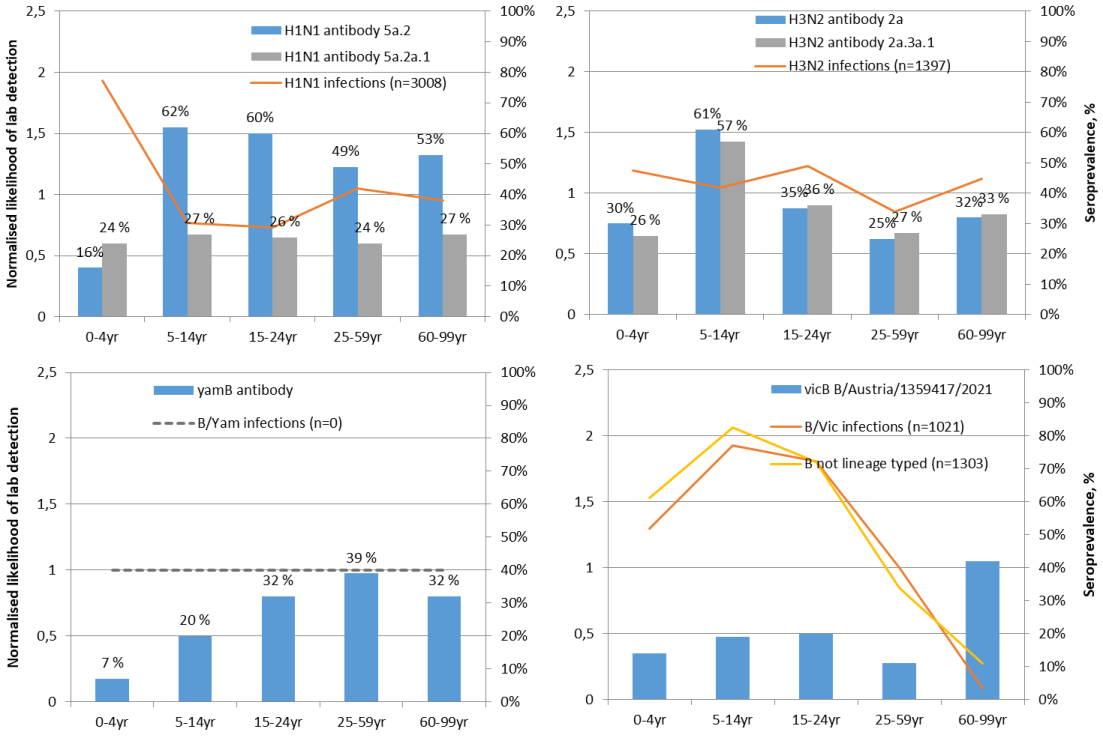


Figure 17: Prevalence of protective antibody to various influenza viruses in August 2023 (% seropositive, bars) and the age distribution of the corresponding influenza viruses in the 2023-2024 influenza season (up to week 34/2024, numbers of subtype/lineage detections per population in age group, normalised against all ages).

The age profiles of immunity, as well as of infection, are very different between the different subtypes/lineages and strains.

For A(H1N1), the youngest children were twice as likely as the general population to get a positive diagnosis, and this group also had the lowest seroprevalence against A/(H1N1)pdm09 clade 5a.2. In the school-age children and young adults, there is some correspondence between high pre-season seroprevalence and slightly suppressed incidence of infection.

The correspondence between recorded incidence of A(H3N2) infections and pre-season seroprevalence is less clear and the incidence of infection did not differ much by age. This differs from earlier seasons when the elderly have been far more likely to have an A(H3N2) detection that other ages.

For influenza B/Victoria-lineage, school-age children and young adults (5-24 year olds) are twice as likely as the general population to get this diagnosis. Of note, there is a strikingly low frequency of recorded infections in the elderly, who also have the highest seroprevalence against the B/Victoria-lineage vaccine strain.

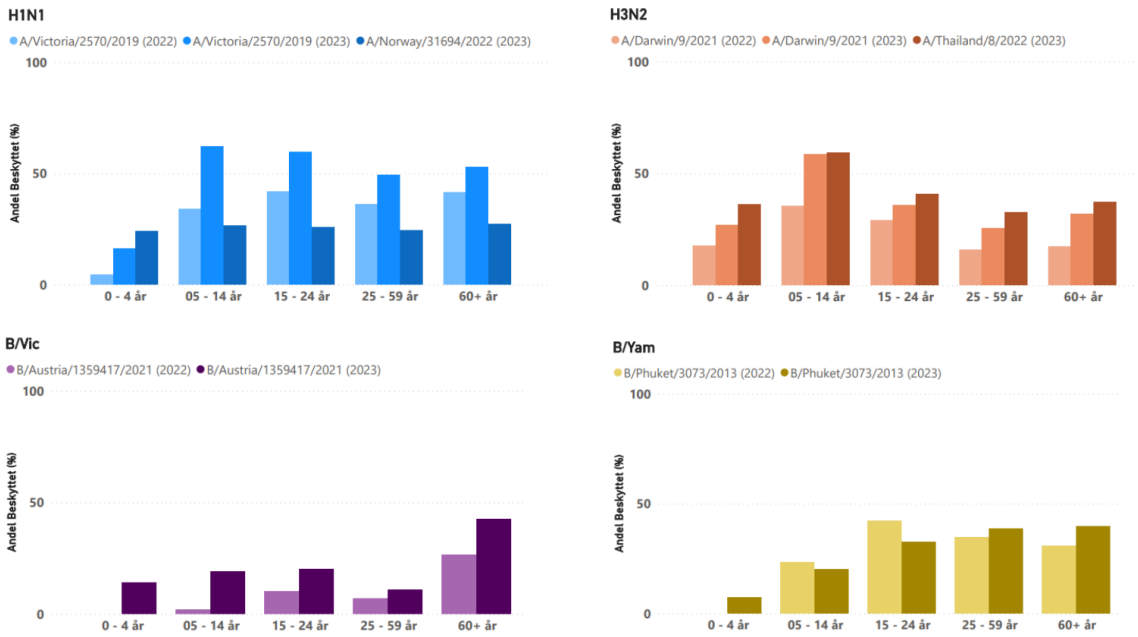


Figure 18: Seroprevalence in August 2022 and 2023 against current influenza A and B strains in various age groups. HAI was performed against A/Victoria/2570/2019 (H1N1, clade 6B.1A.5a.2), A/Norway/31694/2022 (H1N1, clade 6B.1A.5a.2a.1), A/Darwin/9/2021 (H3N2, 3C.2a1b.2a.2), A/Thailand/8/2022 (H3N2, 3C.2a1b.2a.2a.3a.1) B/Austria/1359417/2021 (Victoria lineage, V1A.3a.2) and B/Phuket/3073/2013 (Yamagata lineage). The year the sera was analysed is indicated in parenthesis behind the strain name. Protective HAI titres were defined as ≥40 for influenza A and ≥80 for ether treated influenza B.

From 2022 to 2023 the percentage of sera with protective HAI titres (here referred to as seroprevalence) against A/Victoria/2570/2019 (H1N1) increased from 30-40% to 50-60% in all age groups older than 4 years, likely reflecting the H1N1pdm09 dominated 2022-2023 influenza season(Figure 18). The seroprevalence was, however, ~ 25% against A/Norway/31694/2022 belonging to the drifted 5a.2a.1 clade, indicating higher susceptibility to this clade. The 0-4 years age group only had 4% sera with protective HAI titres in 2022, reflecting an immunity gap that arose during the COVID-19 pandemic due to the absence of influenza. In 2023, the seroprevalence in the youngest age group had increased to 16 % against A/Victoria/2570/2019 and 24 % against A/Norway/31694, suggesting that the immunity gap was at least partially closed and that the antibody response in this age group is more focused on the newer virus than in older groups. The A/Victoria/2570/2019 strain was included in the

seasonal influenza vaccine for the Northern Hemisphere in 2021-2022 and 2022-2023 and may have contributed to the seroprevalence seen in the serum samples collected in August 2022 and 2023.

In 2023, the seroprevalence was 61 % against A/Darwin/9/2021 (H3N2) in the age groups 5-14 years, and between 25 % and 35 % for the remaining age groups (Table 9). The higher seroprevalence seen in the younger age group may reflect the H3N2 outbreak in March/April 2022, in addition to infections during the 2022-2023 season. Seroprevalence remained stable against the newly emerged A/Thailand/8/2022 suggesting limited immune evasion. The A/Darwin/9/2021 strain was included in the vaccine for the 2022-2023 influenza season and may have contributed to increased seroprevalence in the older age groups.

The seroprevalence against contemporary B/Austria/1359417/2021 (Victoria lineage) increased from 0 % to 14 % in the 0 – 4 years age group from 2022 to 2023, likely reflecting the spread of influenza B during the latter half of the 2022-2023 influenza season. Similarly, seroprevalence also increased in the 5 – 14 years and 15 – 24 years age groups in sera from 2023 to 19 % and 20 %, respectively. In the 60+ age group the seroprevalence increased from 26 % to 42 %, which may reflect a combination of infection and introduction of the B/Austria/1359417/2021 strain in the 2022-2023 seasonal influenza vaccine.

For the B/Phuket/3073/2013 strain (Yamagata lineage) which has been included in the tetravalent influenza vaccine since the 2015/16 season, the seroprevalence was 32% in the sera collected in August 2023. The seroprevalence varied from 7% in the 0 – 4 years old, up to 40 % in the 60+ years old.

Table 9: Influenza seroepidemiology results in August 2023 – Seroprevalence* in age groups. For comparison data from studies performed for the preceding years 2018-2022 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 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
H1 Victoria/2570/19 (2023)	***16***	***62***	***60***	***52***	***49***	***53***	***51***
H1 Norway/31694/22 (2023)*	***24***	***27***	***26***	***26***	***24***	***27***	***26***
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
H3 Darwin/9/21 (2023)*	***30***	***61***	***35***	***45***	***25***	***32***	***35***
H3 Thailand/8/22 (2023)	***26***	***57***	***36***	***43***	***27***	***33***	***35***

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/Austria/1359417/21 (Vic-Δ3B) (2023)	***14***	***19***	***20***	***19***	***11***	***42***	***20***
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
B/Yam Phuket/3073/13 (2023)*	***7***	***20***	***32***	***22***	***39***	***40***	***32***
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
Sera analysed (n): 2023 Aug	***108***	***225***	***213***	***546***	***462***	***252***	***1260***

[$]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 2023-2024.

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

Vaccine distribution and coverage

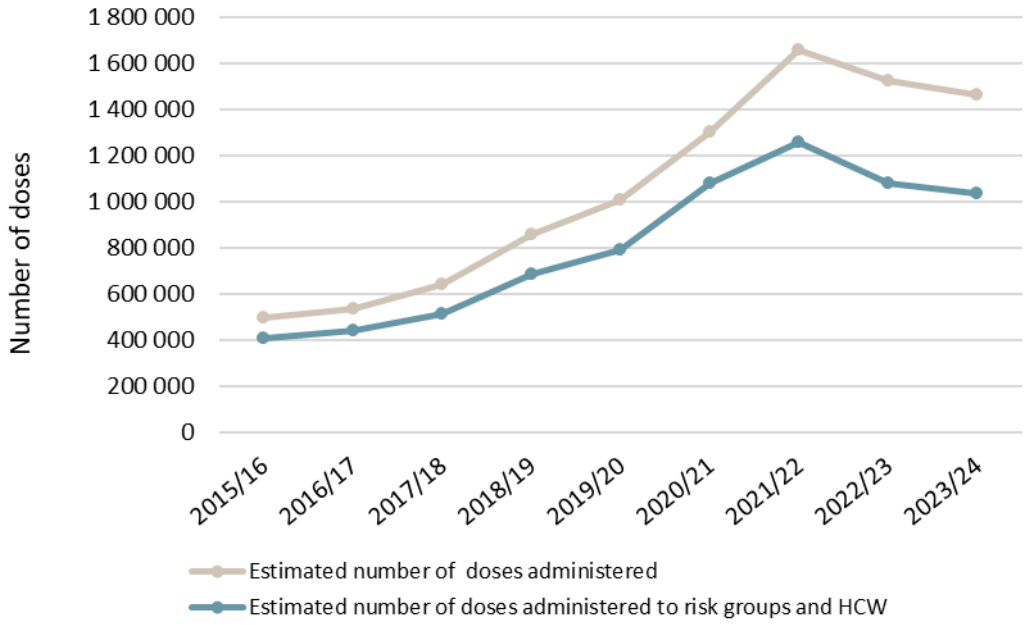


Figure 19: Influenza vaccine doses distributed in Norway, September 2015 through May 2024. HCW = Health Care Workers.

A total of 1.55 million influenza vaccine doses was distributed in the 2023-2024 season both from NIPH and the other wholesalers; 1.13 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. Estimated number of vaccine doses administered to risk groups and HCWs (distributed number minus discarded doses) is 1.04 mill doses. This is slightly lower than in 2022-2023 season (1.08 mill doses) (**Error! Reference source not found.Error! Reference source not found.**).

Vaccine coverage estimates based on registry data

Coverage estimates from National vaccination registry SYSVAK

Coverage data from Norwegian Immunization Registry SYSVAK (SYSVAK) for the population 65 years or older are published yearly in Kommunehelsa statistikkbank[1]. A total of 65% in this age group were registered as vaccinated during the 2023/243-season as of September 2024 (Figure 20). This is 2,2 percentage points higher than the coverage rate for the 2022/23 season as of September 2023.

Approximately 88% of the estimated number of administered doses are registered in SYSVAK, due to underreporting and technical issues. As such, coverage estimates from SYSVAK are considered mimimum estimates.

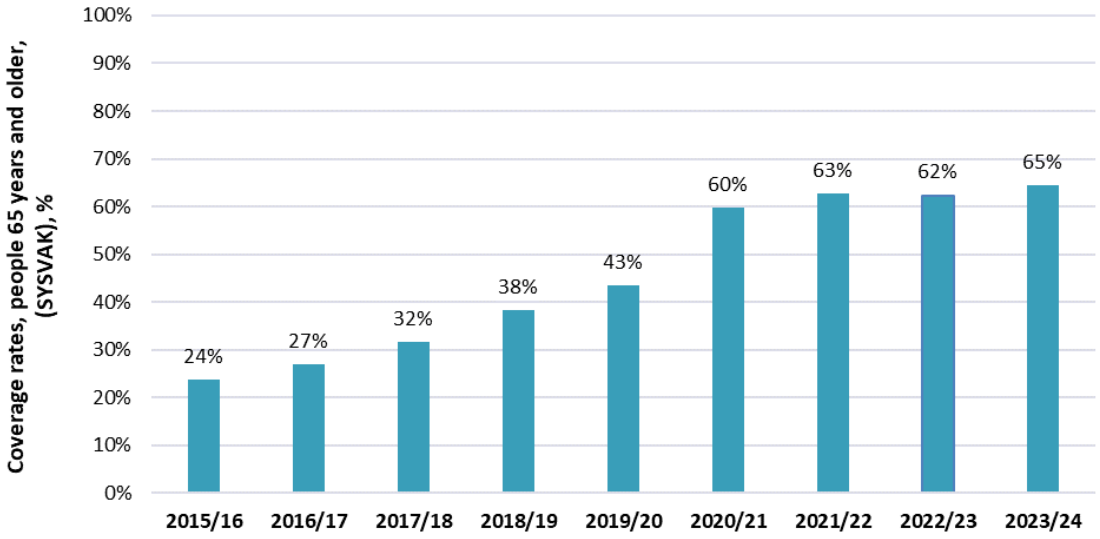


Figure 20: Estimated vaccine coverage among residents 65 years and older in Norway, influenza seasons 2015/16-2023/24. Data from the Norwegian Immunisation Registry (SYSVAK) as of September 2024.

Coverage rate estimates per county from National vaccination registry SYSVAK

The vaccination coverage rate among people 65 years and older differs widely among the counties in Norway. Most counties have a coverage between 63% to 65%. However, some counties have attained a somewhat higher coverage (Rogaland, Vestland and Akershus) of up to 69%, while the three northernmost counties, as in earlier years, have the lowest coverage (Figure 21).

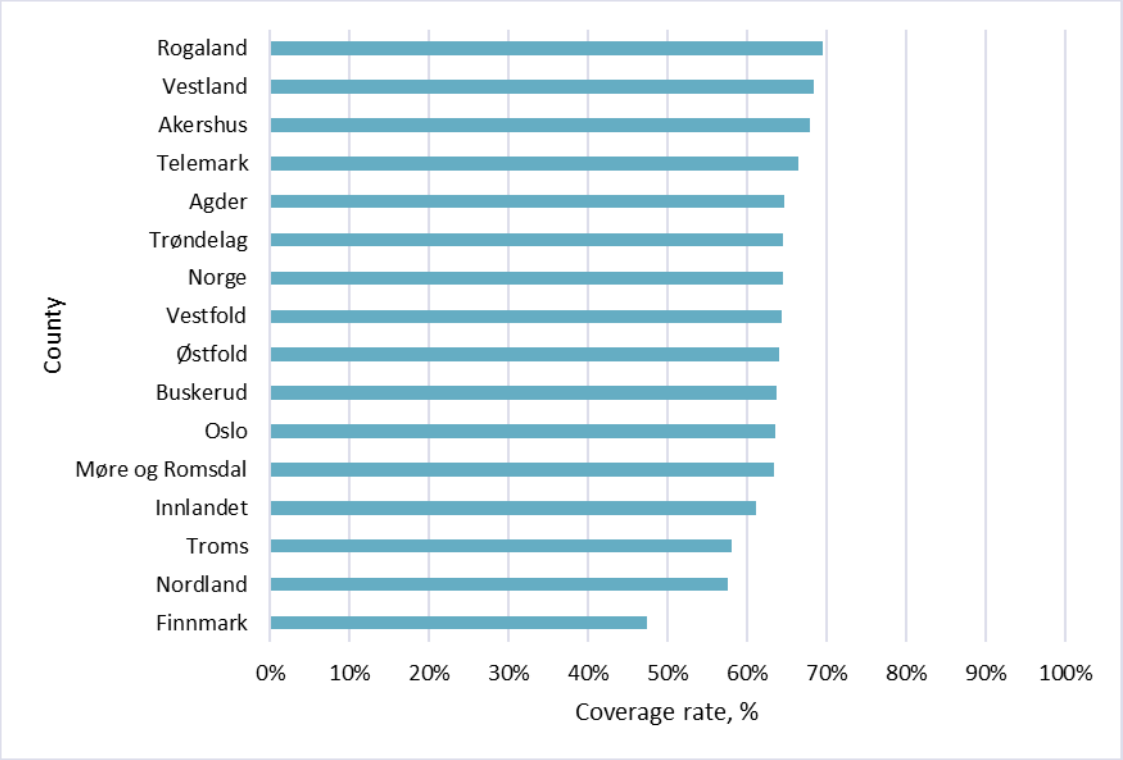


Figure 21: Vaccination coverage among residents above 65 years in Norway by county as of September 2024.

Coverage estimates from the Emergency Preparedness Register (Beredt C19)

Using the Beredt C19 register and the National population registry we have estimated the risk population in Norway to constitute of 1,6 million individuals. According to Beredt C19, vaccine coverage in the risk groups, regardless of age, was 48 % in the 2023/24-season. Coverage increased with age. In risk groups 18-64 years and 0-17 years per 19th of May 2024 the coverage rates were 34% and 7%, respectively. For the adult group this is a 2 percentage points decline compared to the 2022/23 season. The coverage rate in this group has decreased by 5 percentage points since the 2021/22 season.

Among medical risk groups aged 65 years or more, estimated coverage was 67%, while vaccination coverage overall in this age group was 64% as of May 2024.

According to SYSVAK as of May 2024, 23% of the general population received an influenza vaccine this season.

Vaccination timing

Vaccines for the influenza immunisation programme were sent out from week 40-42 to municipalities and hospital trusts. Around the same time, vaccines also became available for the private market in pharmacies. Vaccination increased very rapidly to a peak of over 260,000 vaccinations in week 43 and then gradually declined to a few thousand doses weekly from week 52 (Figure 22). More than 90 % of those vaccinated received their vaccine before week 47, with expected protection by week 49, i.e. before the influenza outbreak started.

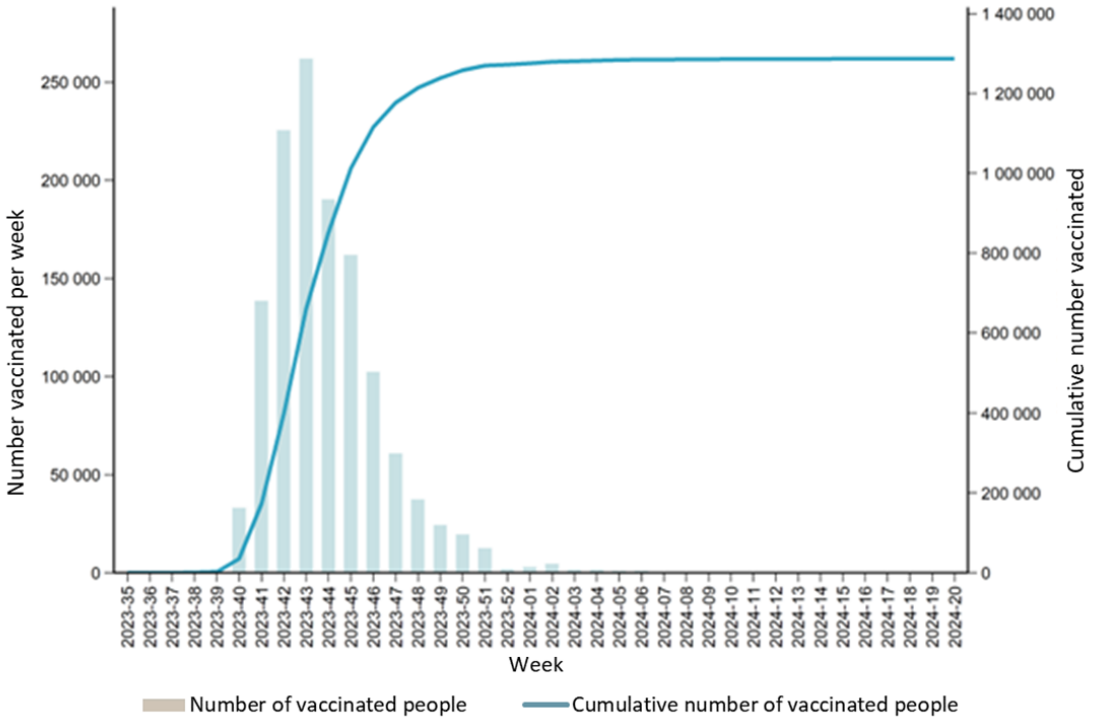


Figure 22: Number of vaccinated people per week and cumulatively in the 2023-24 season, 1. September 2023 – 19. May 2024. Source: National Population Registry and Norwegian Immunization Registry, SYSVAK.

Animal influenza

A historically large epizootic of highly pathogenic avian influenza caused by H5N1 clade 2.3.4.4b virus is ongoing in birds in Europe, Africa, Asia, the Americas and the Antarctic region. Since 2021, in Norway there have been five outbreaks of HPAIV H5N1 in commercial poultry flocks, one of them in February 2024, two in small poultry backyard flocks, and two in municipal parks with captive birds. After a large outbreak among seagulls in North Norway in summer 2023, the Norwegian Veterinary Institute has reported only sporadic infections of HPAIV H5N1 and H5N5 during autumn 2023 and so far in 2024. These have been mainly in gulls and raptors, but also in two few red foxes in February 2024. Detections have been from the mainland Norway.

No cases of avian influenza have been detected in humans in Norway. The Norwegian Institute of Public Health has assessed the risk for human infection as very low for the general population, but increased awareness and precautionary infection control measures are recommended to prevent zoonotic infection.

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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

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Appendices

Description of the surveillance and monitoring systems

Influenza-like illness

Norwegian ILI surveillance data is provided by The Norwegian Syndromic Surveillance System (NorSySS) at NIPH, which receives data from the health finance administration (HELFO), governed by the Norwegian Directorate of Health. The data is based on ICPC-2 consultation codes for influenza on primary care physicians' reimbursement claims. NorSySS has been receiving ILI data since 2014 and is supported by retrospective data from the 2006-07 season and onwards.

Virological surveillance

Sentinel virological surveillance: A geographically representative network of GPs contribute to with clinical data and weekly samples for the integrated surveillance of respiratory viruses in Norway. The sentinel system was reactivated March 2022 after the COVID-19 pandemic and strengthened by including more GPs and engaging sentinel laboratories for most of the primary testing. At the same time, the scope of the surveillance has been expanded to comprise several non-influenza respiratory viruses and the testing case definition expanded from ILI to ARI.

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.

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) by Oxford Nanopore technology. 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. Phenotypic testing for neuraminidase suseptibility is also performed with the MUNANA method.

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 to strengthen the influenza surveillance during the COVID-19 pandemic within The Emergency preparedness register for COVID-19 (Beredt C19). In the beginning, individuallevel 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). From the beginning of the monitoring season 2023-2024, the surveillance of hospital admissions with influenza was more tightly integrated into the surveillance of severe acute respiratory infections (SARI), which also used hospital discharge codes registered in NPR. ICD-10 codes included in the case definition comprise all acute respiratory infections registered with codes J00-J06, J09-J22, J80, U07, A37 and H65-H67. To enhance the specificity and timeliness of the registry-based surveillance, the data on hospital discharge codes were 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 PCRpositive influenza tests were available from season 2020-2021 onward. For seasons where data on PCR tests is not available, ICD-10 codes for influenza from NPR were used. A hospital admission with influenza was 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 SARI was registered, or where the patient hadn't received any diagnosis code yet. Influenza-positive patients without any diagnosis codes yet were included to increase the timeliness of the data, acknowledging that the admissions initially considered as influenza-related may later be excluded. Beredt C19 was terminated in June 2024. Accordingly, all data on hospital admissions was generated before this termination. At the time of preparing this report, this surveillance system is not functioning, as a new digital infrastructure is needed to continue its operation.

Influenza patients in intensive care units

In the 2016-2017 and 2017-2018 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 2018-2019 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 began to receive case-based data daily through Beredt C19. Beredt C19 was terminated in June 2024. Accordingly, all data on ICU admissions was generated before this termination. At the time of preparing this report, this surveillance system is not functioning, as a new digital infrastructure is needed to continue its operation.

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 80-90 % 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 was 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. Beredt C19 included information that had 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. The Beredt C19 registry has been terminated as of June 2024. Accordingly, all data on coverage rates in risk groups was generated before this termination.

Influenza seroepidemiology

The National Influenza Seroepidemiology program annually, in August, solicits about 2000 serum samples collected during the weeks 31-35 from clinical/microbiological laboratories covering the 15 counties of Norway. These anonymised convenience sera are aimed to be representative of the Norwegian population geographically and by age composition. The sera are tested by the haemagglutination-inhibition (HI) test to determine the antibody immunity to relevant circulating influenza viruses. 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 sera in the subsequent collections have been tested against influenza.

NIPH
Norwegian Institute of Public Health

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PO Box 222 Skøyen
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Tel.: (+47) 21 07 70 00

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