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NORWAY:

Influenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2026

September 2025

NIPH
Norwegian Institute of Public Health

folkehelseinstituttet

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Influenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2026, September 2025

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

Spotlight: Within-season A(H1N1) clade replacement

Even though influenza A(H1N1) was in majority throughout the 2024-2025 season the composition of these viruses was far from static. Three subclades dominated in the early-, mid-, and late-season periods, respectively (Figure 1). See also the chapter on genetic characterisations.

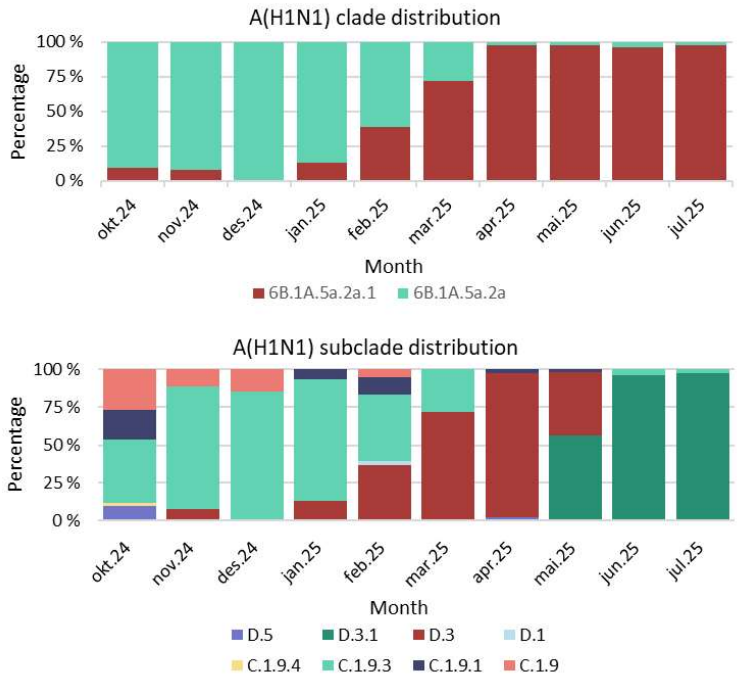

Figure 1 WHO clade (Upper) and NextStrain subclade (Lower) distribution of A(H1N1) viruses in Norway during the Season 2024/2025 surveillance season This graph is part of Figure 8 within this report.

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The 2024-2025 influenza season, Norway

Summary

- Laboratory confirmed influenza started to rise from baseline in late November 2024, crossed the virological outbreak threshold in week 52, and peaked around week 8 with a positivity rate of 35.5 % which is on par with the peak of the 2017-2018 season. Since week 40/2024, 44,930 infections with influenza A and 15,514 with influenza B have been detected by Norwegian laboratories, out of > 520,000 patients tested.
- Based on the weekly total numbers of detected influenza A and B, and the weekly proportions of subtypes and lineages, we estimate that A(H1N1) constituted approximately 46 % of the influenza cases, followed by B/Victoria-lineage with 28 % and A(H3N2) with 27 %.
- In age profile analysis of detected cases, the 0–4-year-olds were more than twice more likely to be diagnosed with A(H1N1) than other ages, similar to profiles in previous seasons. Surprisingly, for A(H3N2) detections, the elderly were not over-represented as they have been in previous years. For influenza B/Victoria, younger age groups, particularly 5–14-year-olds, were much more likely to be diagnosed than those who are older; elderly were particularly under-represented.
- This far, 14,5 % (742/5,115) of all influenza positive samples received for surveillance have been whole genome sequenced. 101 viruses, representing the spectrum of genetic variants we have observed, have been shared with WHO. Among the A(H1N1) viruses, the 5a.2a clade was dominant in early season but was replaced by the 5a.2a.1 viruses from March 2025 onwards. Among the 5a.2a.1 viruses the D.3 subclade was the most common (27%) followed by D.3.1 (26%). A(H3N2) viruses predominantly (99 %) belonged to the 2a.3a.1 clade, of which most (58%) were subclade J.2, followed by J.2.2 (34%). In August, subclade J.2.4 viruses with some additional mutations have appeared. All sequenced influenza B viruses belonged to the B/Victoria V1A.3a.2 clade, with 56% being subclade C.5.1, 20% C.5.7, 15% C.5.6, 7% C.3, and 2% C.5.
- Seroepidemiological analysis of protective antibody responses against relevant strains of all influenza subtypes indicate that immunity was at a relatively high level in late summer 2024. HAI titres against tested influenza strains belonging to clades 5a.2a.1 of A(H1N1), 2a.3a.1 of A(H3N2), and 3A.2 of B/Victoria increased or remained stable for all age groups collected in 2024, compared to sera collected in 2023. The “immunity gap” seen in the youngest age group after the COVID-19 pandemic has now been closed.
- The proportion of influenza-like illness (ILI) began to rise gradually from week 50/2024 and the epidemic threshold was crossed in week 02/2025, two weeks later than crossing the outbreak threshold for per cent test positives. Influenza activity peaked in week 9 when 2,8 % of the consultations were due to influenza-like illness, which indicates a medium intensity level according to the MEM-thresholds. The ILI indicator resided at medium level for four weeks.
- Between week 40/2024 and week 34/2025, 10,657 (190.5 per 100,000 inhabitants) samples positive for influenza virus were reported among hospitalized patients, with the highest incidence among those aged 65-79 and 80+, followed by children under 5 years. Influenza A virus was most common, while influenza B virus to a larger extent affected children. Between week 40/2024 and week 20/2025, 278 (5.0 per 100,000 inhabitants) intensive care admissions with influenza were reported, and 375 influenza associated deaths were registered. The numbers of influenza hospital and intensive care admissions

and influenza associated deaths were greater than the last previous seasons indicating that the 2024-2025 influenza season was more severe than the previous few seasons.

- The vaccine coverage for the age group 65 years and older was 66% per week 20/2025, and the total number of distributed doses in Norway was 1.56 million. This is at the same level as last season. 99 percent of the doses were administered before the epidemic threshold was reached.
- Highly pathogenic avian influenza viruses (HPAIV) belonging to H5 HA clade 2.3.4.4b, during most of the period typically subtype H5N5 but more recently a rise in H5N1, continued to be detected in wild birds in Norway. The detections were fewer and more scattered compared to the summer of 2023. H5N5 was last winter also detected in two euthanized carnivores, a lynx and an otter, and in a red fox carcass. In summer 2025, HPAIV H5N5 was detected in polar foxes on the archipelago of Svalbard. There was one outbreak of HPAIV AH5N5 in a poultry backyard flock in November 2024. No human cases have been detected, and the general risk for human infection is assessed as very low.

Influensasesongen 2024-2025 i Norge (Norwegian summary)

Hovedbudskap

- Laboratoriepåvist influensa begynte å øke fra basalnivå sent i november 2024, overskred utbruddsgrensen i uke 52, og toppet seg rundt uke 8 med en andel influensapositive blant de testede på 35 %. Dette er på høyde med toppnivået i 2017-2018-sesongen. Siden uke 40/2024 har norske laboratorier påvist 44 930 influensa A- og 15 514 influensa B-infeksjoner.
- Basert på de ukentlige antallene influensa A- og B-påvisninger og ukentlige andeler av influensa A-subtyper og B-linjer, estimerer vi at influensa A(H1N1) utgjorde omtrent 46 % av tilfellene, fulgt av B/Victoria-linje med 28 % og A(H3N2) med 27 %.
- Aldersprofilanalyse viser at 0-4-åringer hadde mer enn dobbelt så stor sannsynlighet for påvisning av A(H1N1) i forhold til alle testede. Det er bemerkelsesverdig at personer over 60 denne sesongen ikke er overrepresentert i H3N2-påvisning, slik vi er vant til fra tidligere. For influensa B/Victoria hadde de yngste aldersgruppene, særlig 5-14-åringer, mye større sannsynlighet for å teste positivt enn voksne og eldre. De eldste hadde meget lav påvisningsrate for dette viruset.
- Så langt har 14,5 % (742/5 115) av mottatte influensapositive prøver blitt fullgenomsekvensert, og 101 virus som representerer alle påviste sekvensvarianter har blitt delt med WHO internasjonalt referanselaboratorium.
  Blant A(H1N1)-virus dominerte klade 5a.2a i første del av sesongen, men ble erstattet med virus fra datterkladen 5.a.2.1 fra mars av. Klade 5a.2a.1-virus i subklade D.3 var vanligst (27 %), tett fulgt av D.3.1 (26 %).
  Blant A(H3N2)-virus har nesten alle (99 %) vært i klade 2a.3a.1, 58 % av dem i subklade J.2, fulgt av J.2.2 (34 %). I august 2025 har vi sett framvekst av virus i subklade J.2.4 med ytterligere mutasjoner.
  B/Victoria-virus har alle vært i klade V1A.3a.2, med 56 % i subklade C.5.1, 20 % i C.5.7, 15 % i C.5.6, 7% C.3 og 2% C.5.
- Serologisk analyse av beskyttende antistoffer viser at immuniteten i befolkningen var forholdsvis høy mot alle influensasubtypene sensommeren 2024. HAI titer mot aktuelle

influensastammer fra kladene 5a.2a.1 A(H1N1), 2a.3a.1 A(H3N2) og 3A.2 B/Victoria økte eller holdt seg stabile i sera fra 2024, sammenlignet med sera fra 2023. Den lave immuniteten som ble observert hos de aller yngste etter COVID-19 pandemien har nå tatt seg opp til nivåer som ble observert før pandemien.

- Andelen influensalignende sykdom (ILS) steg gradvis fra uke 50/2024 og utbruddsterskelen ble passert i uke 2/2025 – to uker senere enn for utbruddsterskelen for influensa-positivitetsandelen. Toppen ble nådd i uke 9/2025 da 2,8 % av konsultasjonene i primærhelsetjenesten skyldtes influensalignende sykdom. Dette tilsvarte et middels intensitetsnivå i henhold til ILI MEM-tersklene. ILI-indikatoren holdt seg på middels nivå i fire uker.
- Mellom uke 40/2024 og uke 5/2025 ble det rapportert 10 657 (190,5 per 100 000 innbyggere) prøver positive for influensavirus blant sykehusinnlagte, med høyest forekomst blant dem i aldersgruppene 65-79 og 80+, etterfulgt av barn under 5 år. Influensa A-virus var mest vanlig, mens influensa B-virus i større grad rammet barn. Mellom uke 40/2024 og uke 20/2025 ble det rapportert 278 (5,0 per 100 000 innbyggere) intensivinnleggelser med influensa, og 375 influensa assosierte dødsfall. Det var flere sykehus- og intensivinnleggelser med influensa og influensa-assosierte dødsfall enn de foregående sesongene, noe som indikerer at influensautbruddet i 2024-2025-sesongen var mer alvorlig enn på flere år.
- Vaksinasjonsdekningen blant personer over 65 år var 66 % per uke 20. Det har blitt distribuert 1,56 millioner doser vaksiner totalt. 99 prosent av dosene ble satt før utbruddsterskelen ble passert.
- Høypatogene fugleinfluensavirus (HPAIV) tilhørende H5 HA-klade 2.3.4.4b, har fram til august 2025 blant villfugl hovedsakelig vært av subtype H5N5. Fra august av har det vært en økning i antall påvisninger av subtype H5N1 blant villfugl i Norge. Sammenlignet med sommeren 2023 var påvisningene færre og mer spredte. I fjor vinter ble H5N5 påvist hos to avlivede rovdyr, en gaupe og en oter, og hos et rødrevkadaver. Sommeren 2025 ble det påvist H5N5 hos fjellrev på Svalbard. Det var ett utbrudd av H5N5 i et hobbyfjørfehold i november 2023. Ingen tilfeller av smitte til mennesker har blitt funnet, og risikonivået for mennesker i Norge vurderes som svært lavt.

A look back at the preceding 2023/2024 season

The preceding 2023-24 influenza season in Norway was characterized by a predominance of type A viruses during the main outbreak period, but these declined faster than type B viruses towards the end of winter and spring. Type B viruses were more prevalent in weeks 17-22. A(H1N1) and A(H3N2) circulated simultaneously, with H1N1 being the dominant subtype overall. Among the less common type B viruses, a large proportion (43%) were typed as the Victoria lineage, with no detections of the Yamagata lineage.

The incidence of laboratory-confirmed influenza rose rapidly to an early peak during the Christmas and New Year period, but with lower intensity than the 2022-23 season. After the New Year peak, detections only slightly decreased and remained at a moderate level until they fell below 10% positivity in week 10 of 2024. By week 20, the rate had dropped to 2% and remained below this level through the summer, with influenza A again being predominant among the sporadic detections, with a predominance of the H3N2 subtype through July and August.

The proportion of influenza-like illness (ILI) consultations in primary care began to gradually increase from week 44 of 2023, crossing the epidemic threshold in week 49. Influenza activity peaked in week 52 when 1.4% of consultations were due to ILI, at a low intensity level. Activity declined after week 52 and remained stable at a low intensity level until it fell below the epidemic threshold in week 9 of 2024.

Between week 40 of 2023 and week 20 of 2024, a total of 4403 hospitalizations and 179 intensive care unit admissions were reported, fewer than in the same period in the previous season of 2022-2023.

Vaccination coverage among risk groups under 65 years decreased compared to the 2022-2023 season. The coverage rate for people over 65 was 64%, which is at the same level as the preceding season. The total number of distributed doses decreased by 5% compared to the 2022-23 season. A total of 1.13 million doses intended for use in risk groups and healthcare personnel were distributed.

Highly pathogenic avian influenza viruses (HPAIV) H5N1 and H5N5 belonging to HA clade 2.3.4.4b continued to be detected in wild birds in Norway, but in much lower numbers compared to the summer of 2023 and with fewer outbreaks. During the autumn of 2023, there was one outbreak of H5N1 in a poultry yard and 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 is assessed as very low.

The 2024/2025 season, weeks 40/2024 to 34/2025

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

Virological surveillance data

Laboratory confirmed influenza: Virological surveillance

Altogether, more than 520,000 patients in Norway were tested for influenza during weeks 40/2024-34/2025, resulting in 44,930 recorded detections of influenza A virus (72 % of the influenza detections) and 15,514 influenza B virus (28 % of influenza detections) (Figure 2, Table 1). The number of tests has been unusually large, partly due to high demand for respiratory pathogen testing during a *Mycoplasma pneumoniae* outbreak last autumn.

From these patients, 3,143 influenza A and 1,864 influenza B positive specimens have so far been referred by testing laboratories to the NIC for further identification and characterisation. Among these 3,123 type A viruses have so far been subtyped; 2,047 H1(66 %) and 1,076 H3 (34 %). A few (6) type A virus specimens were too weak for successful subtyping and 39 could not be confirmed as influenza A in the NIC, several of these specimens had also other respiratory viruses detected in the submitting laboratory. Nine influenza A positive specimens were also positive for influenza B. All 1,817 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 22 initially influenza B positive specimens could not be verified in the NIC. Several of these had an additional respiratory virus detected.

In addition to this, primary testing laboratories have identified 6,297 type A viruses as H1 and 107 as H3, of which many have been forwarded to the NIC and also subtyped there. This subtype testing is highly 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 and not used for subtype proportion calculations.

The number of detections started to rise in late November, picked up pace in mid-December reaching a first peak in week 52/2024 when 13,3 % of the patients tested positive for influenza (Figure 2, Table 1). With this, the virological surveillance outbreak threshold at 10 % positivity rate had been surpassed. After a two-week post-New Year stagnation, the rise in detections resumed, climbing rapidly until peaking at 35.5 % in week 8. This level is higher than the peak positivity rates in most recent years, and on par with the peak in the 2017/2018 season but lower than the 39 % peak rate experienced in the 2014/2015 season and the 44% during the 2009 pandemic. We consider intensity to be at high level when the positivity rate in the overall national testing is between 20 and 30 %. Interestingly, this season the detections of influenza A and B, as well as subtypes H1 and H3, peaked almost simultaneously. After passing the peak, detections declined rapidly, fell below 10 % in week 17, and was down at baseline level by week 21. Sporadic detections continued through summer, at a somewhat higher level than in previous summers.

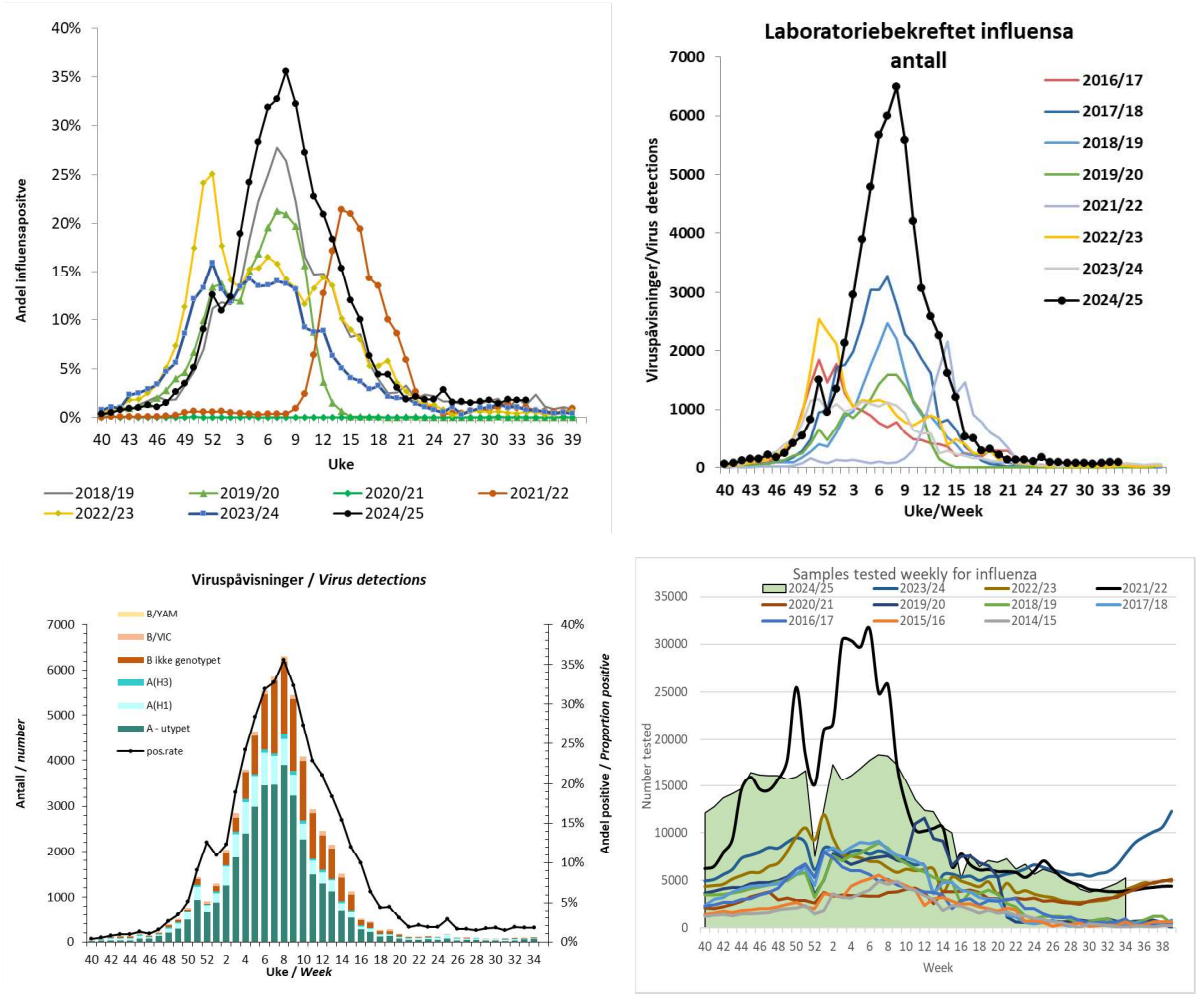

Figure 2. Laboratory detections, Norway 2024-2025. Upper left-hand panel: Weekly proportion of influenza virus positive patients, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. Lower left-hand panel: Weekly number of the different influenza viruses, displayed as stacked bars. Lower right-hand panel: weekly number of patients tested for influenza, compared to other seasons.

Type A viruses have been in clear majority over type B throughout the period with the proportions similar in the different regions of the country. The proportions of A and B were most similar in the months March, April and May (Figure 4). Among the type A viruses influenza A(H1N1) viruses have been in majority, constituting between 60 and 80 % of the subtyped viruses in most weeks and higher during the summer weeks (Figure 3). Influenza B viruses have been exclusively B/Victoria/2/87-lineage. Around 70 % of the influenza A detections in the western and middle part of Norway have been of the H1 subtype whereas the proportion of the H1 subtype has been a little bit less than 65 % in the other regions, with the smallest proportion of H1 in the northernmost region, at 59 % (Figure 4). 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.

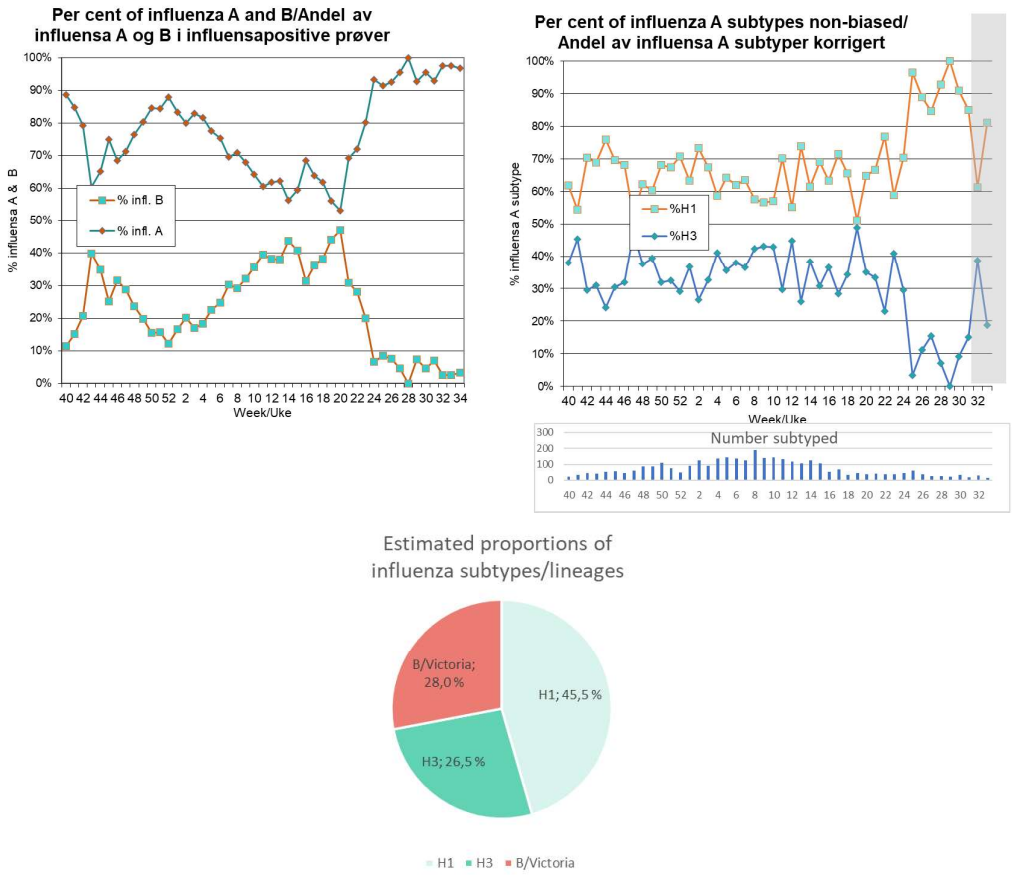

Figure 3. Influenza virus detections since week 40/2024, proportions per type A and B (upper left panel) and influenza A subtypes H1 and H3 (upper right panel). Only viruses tested for both subtypes are counted in the subtype analysis. Bars below show weekly number of subtyped samples.
The lower pie chart displays estimated proportions of the three circulating influenza viruses, produced by projection of the weekly subtype and lineage proportions onto the weekly numbers of influenza A and B detections, respectively.

Figure 4. Monthly proportions of influenza virus detections since week 40/2024, type (top panel) and subtype (bottom panel) proportions per geographic region. Only viruses tested for both subtypes are counted in the subtype analysis.

Age distribution of A(H1N1), A(H3N2), and B/Victoria detections

As in previous seasons, the age profile, in this analysis displayed as normalised incidence of laboratory verified cases, differs between the circulating influenza viruses. In Figure 5, this season's profiles for A(H1N1), A(H3N2) and B/Victoria are plotted together with profiles for some earlier seasons.

For A(H1N1), the youngest children were more than twice as likely as the general population to get a positive diagnosis, with the likelihood in the other age groups being similar to each other. The age pattern is very similar to previous seasons.

For A(H3N2), the youngest age group and the 15–24-year-olds are approximately 50% more likely to test positive than all ages seen together, with the 5-14, 25-59 and 60 years and above groups being about as likely as all ages. This is a surprising pattern that differs from earlier seasons when the elderly have been far more likely to have an A(H3N2) detection than other ages. In the two preceding seasons, the relative frequency in the elderly also has been lower than before, so this may reflect a change that warrants further investigation.

For influenza B/Victoria-lineage, the pattern generally resembles earlier seasons. Children, particularly in school-age, are twice as likely as the general population to get this diagnosis, with declining likelihood with increasing age. Of note, there is a striking lack of recorded infections in the elderly.

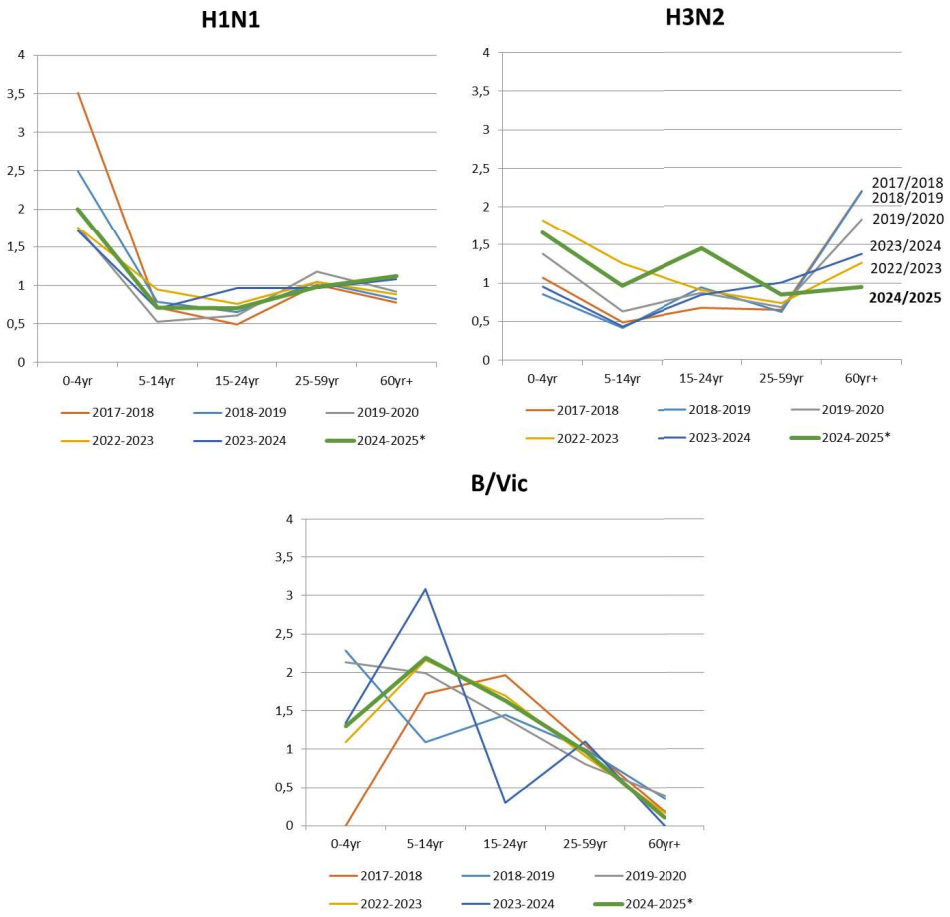

Figure 5. Age profiles of influenza viruses in the 2024/2025 influenza season up to week 34/2025, compared to some previous seasons. The score for each age group is the frequency of detections per age group population size, normalised against the combined frequency for all ages. An age group with a score of 2 means that members of that group are twice as likely to get this diagnosis, compared to all ages.

Table 1 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 40/2024 through week 34/2025 (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.

	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	12124	0,4 %	15	14	10	-2	7	0
41	12750	0,5 %	25	17	14	7	3	0
42	13691	0,8 %	38	38	12	15	4	0
43	14164	1,0 %	32	38	12	34	10	0
44	14666	1,0 %	35	43	15	22	14	0
45	16477	1,3 %	80	58	17	12	20	0
46	16195	1,1 %	68	38	11	18	18	0
47	16111	1,5 %	129	30	12	15	27	0
48	16084	2,6 %	203	86	31	37	31	0
49	15719	3,5 %	295	106	35	39	34	0
50	16012	5,1 %	492	166	35	25	51	0
51	16638	9,0 %	936	287	47	127	54	0
52	7584	12,6 %	677	142	19	12	52	0
1	12342	11,0 %	873	213	43	122	52	0
2	17270	12,4 %	1257	417	35	256	86	0
3	15615	18,9 %	1867	536	52	311	96	0
4	16103	24,2 %	2406	697	80	569	73	0
5	16895	28,4 %	2990	674	50	844	116	0
6	17789	31,9 %	3470	719	78	1223	90	0
7	18335	32,7 %	3479	631	68	1614	104	0
8	18240	35,6 %	3889	595	116	1626	132	0
9	17298	32,3 %	3230	459	96	1598	99	0
10	15437	27,3 %	2273	352	82	1288	108	0
11	13478	22,8 %	1498	312	50	1012	100	0
12	12366	21,0 %	1293	253	57	768	110	0
13	12254	18,4 %	1116	250	34	679	87	0
14	10569	15,4 %	699	166	49	510	100	0
15	9983	12,1 %	533	146	35	336	77	0
16	5229	10,0 %	277	61	21	119	23	0
17	7784	6,4 %	221	75	20	107	36	0
18	6447	4,4 %	121	42	12	56	26	0
19	7106	4,4 %	126	32	19	59	40	0
20	6890	3,0 %	72	28	11	42	28	0
21	7314	1,8 %	48	29	15	11	15	0
22	6197	2,1 %	50	32	13	9	14	0
23	6695	1,9 %	53	31	17	11	7	0
24	5663	1,9 %	44	41	13	1	3	0
25	6226	2,8 %	75	83	3	5	5	0
26	5850	1,6 %	38	42	6	5	1	0
27	5475	1,6 %	44	36	5	2	1	0
28	4878	1,5 %	40	30	2	0	0	0
29	4098	1,7 %	30	33	0	1	2	0
30	3778	1,7 %	25	35	3	1	1	0
31	3978	1,4 %	21	29	3	4	0	0
32	4274	1,8 %	36	29	12	2	0	0
33	4698	1,7 %	54	22	4	2	0	0
34	5255	1,8 %	78	12	0	3	0	0
Total	520024		35351	8205	1374	13557	1957	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: 44930			Type B: 15514			

Sentinel-based virological surveillance, primary care

From week 40/2024 through week 34/2025, 3,180 geographically representative sentinel specimens have been tested, with 295 detections of influenza virus A (175 subtype H1, 103 subtype H3, and 17 not yet subtyped), and 150 influenza virus B (of which 141 are Victoria-lineage, and 9 are not yet lineage identified, with none being Yamagata-lineage). In addition, 147 SARS-CoV-2, 108 RSV, 405 rhinovirus, 88 human metapneumovirus (hMPV), 83 parainfluenza virus and 143 other human coronaviruses were detected (Figure 7, Table 2).

Influenza detections started to rise in early December and peaked with a positivity rate of 40 % in weeks 7 and 8, 2025.

Thus, among the detected influenza viruses, A(H1N1) constituted 39 %, followed by B/Victoria-lineage at 32 % and A(H3N2) at 23 %. Non-subtyped A and B viruses constituted 3 % each and generally were poor specimens with very low viral load (Figure 6). Compared to the frequencies estimated for all laboratory detections (Figure 3), the pattern is similar but the frequency of influenza B/Victoria is larger in the primary care sentinel surveillance than in the comprehensive surveillance that represents a mixture of primary care and hospitalised cases.

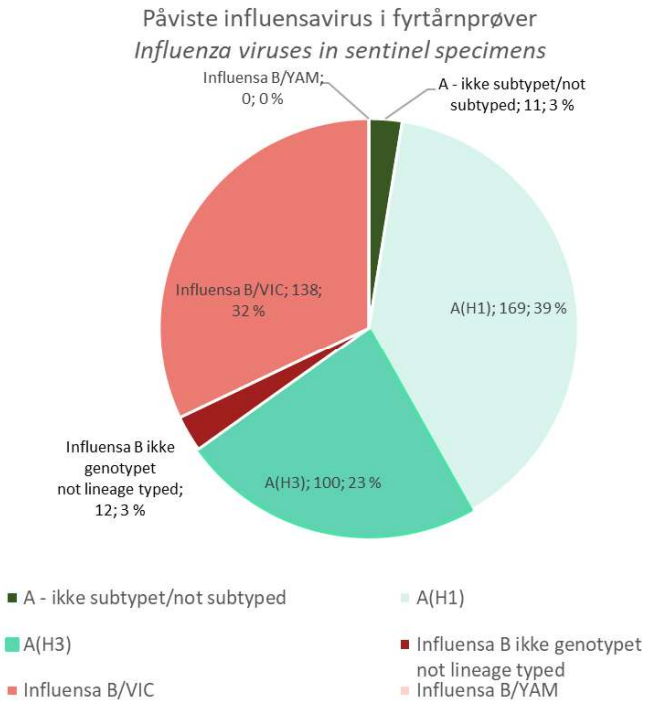

Figure 6. Proportions of influenza virus subtypes and lineages detected in sentinel specimens in the 2024/2025 season, by week 34/2025.

Almost half of all sentinel surveillance samples are taken from the age group 30-64 (45 %). The second-largest group in this dataset is the 15–29-year-olds (23 %), followed by 5–14-year-olds (11 %) and 65–79-year-olds (12 %). The two least represented age groups were the youngest, 0-4 years (5 %), and the oldest, 80 years and older (4 %). Compared to the comprehensive surveillance that captures the testing in all laboratories, the sentinel surveillance has a lower proportion of the youngest and the oldest, and a higher proportion of persons 5-64 years old.

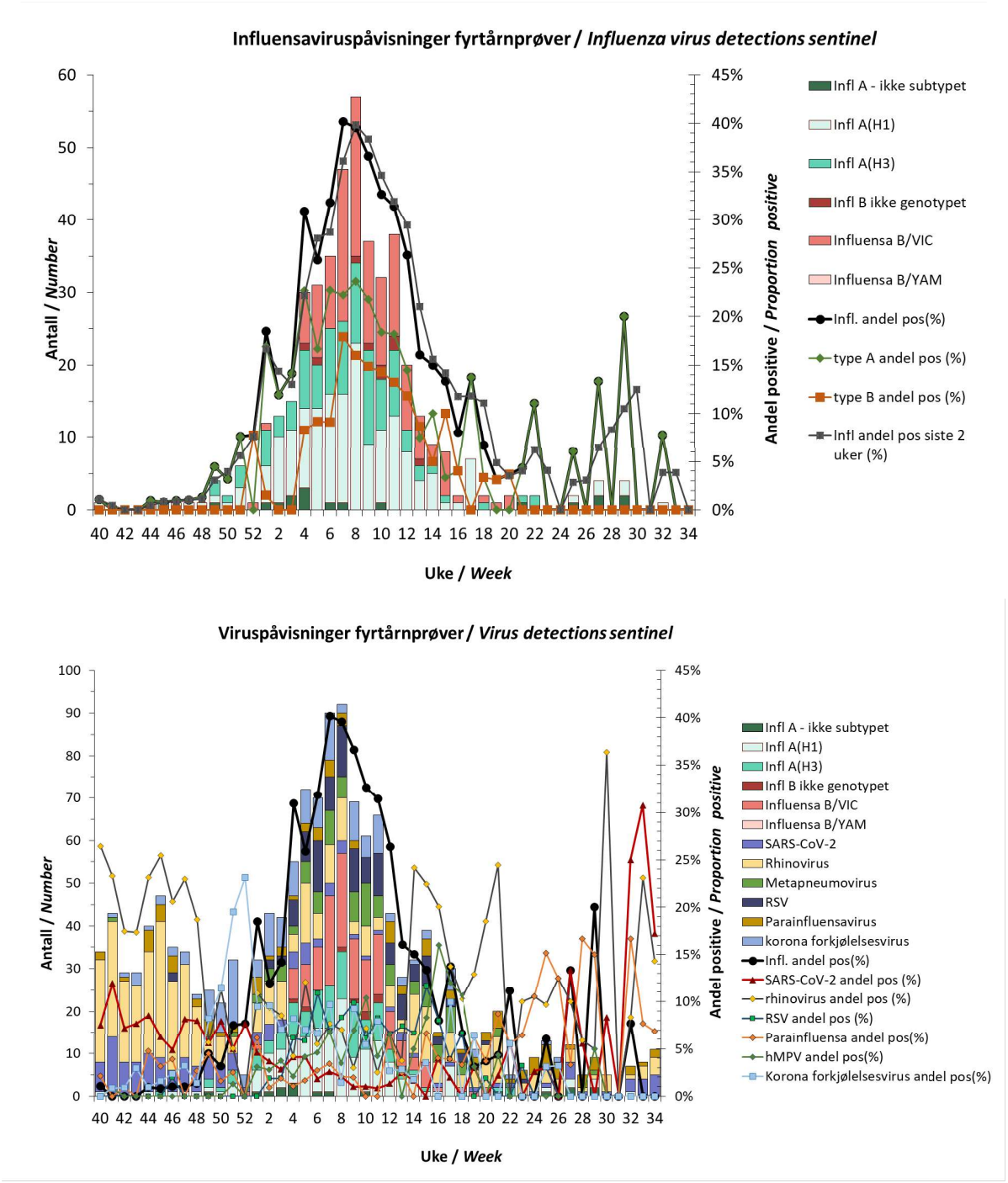

Figure 7. Weekly numbers of detections and per cent positives of influenza viruses (upper panel) and all surveyed respiratory viruses (lower panel) in the respiratory sentinel surveillance.

Table 2. 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
40	93	0	1	0	0	0	0	1 %	1 %	0 %	7	8 %	0	0 %	24	26 %	1	0	1	2 %	0	0 %	0	0 %
41	117	0	0	0	0	0	0	0 %	0 %	0 %	14	12 %	0	0 %	27	23 %	0	0	0	0 %	1	1 %	1	1 %
42	111	0	0	0	0	0	0	0 %	0 %	0 %	8	7 %	0	0 %	19	17 %	1	0	0	1 %	0	0 %	1	1 %
43	104	0	0	0	0	0	0	0 %	0 %	0 %	8	8 %	0	0 %	18	17 %	0	0	0	0 %	0	0 %	3	3 %
44	105	0	1	0	0	0	0	1 %	1 %	0 %	9	9 %	0	0 %	24	23 %	5	0	0	5 %	0	0 %	1	1 %
45	127	0	0	1	0	0	0	1 %	1 %	0 %	8	6 %	0	0 %	32	25 %	3	1	0	3 %	0	0 %	2	2 %
46	102	0	1	0	0	0	0	1 %	1 %	0 %	5	5 %	2	2 %	21	21 %	3	1	0	4 %	0	0 %	2	2 %
47	98	0	1	0	0	0	0	1 %	1 %	0 %	8	8 %	0	0 %	22	23 %	0	0	0	0 %	0	0 %	3	3 %
48	75	0	1	0	0	0	0	1 %	1 %	0 %	6	8 %	0	0 %	14	19 %	2	0	0	3 %	0	0 %	1	1 %
49	89	1	1	2	0	0	0	4 %	4 %	0 %	5	6 %	0	0 %	5	6 %	2	2	0	4 %	0	0 %	7	8 %
50	63	0	1	1	0	0	0	3 %	3 %	0 %	5	8 %	0	0 %	7	11 %	0	1	0	2 %	0	0 %	7	11 %
51	80	0	3	3	0	0	0	8 %	8 %	0 %	4	5 %	0	0 %	4	5 %	0	2	0	3 %	1	1 %	15	19 %
52	13	0	0	0	0	1	0	8 %	0 %	8 %	1	8 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	3	23 %
1	65	1	5	5	0	1	0	18 %	17 %	2 %	3	5 %	0	0 %	7	11 %	3	0	1	6 %	2	3 %	4	6 %
2	109	1	9	3	0	0	0	12 %	12 %	0 %	4	4 %	2	2 %	10	9 %	0	0	1	1 %	3	3 %	10	9 %
3	106	2	9	4	0	0	0	14 %	14 %	0 %	3	3 %	2	2 %	9	9 %	1	1	0	2 %	4	4 %	7	7 %
4	97	3	11	8	1	7	0	31 %	23 %	8 %	4	4 %	6	6 %	4	4 %	1	0	0	1 %	2	2 %	8	8 %
5	120	0	14	6	1	10	0	26 %	17 %	9 %	5	4 %	7	6 %	14	12 %	0	1	1	2 %	5	4 %	8	7 %
6	110	1	15	9	0	10	0	32 %	23 %	9 %	2	2 %	12	11 %	6	6 %	1	0	0	3 %	5	5 %	7	6 %
7	117	1	15	10	0	21	0	40 %	22 %	18 %	3	3 %	8	7 %	9	8 %	2	0	2	3 %	8	7 %	11	9 %
8	144	0	23	11	1	22	0	40 %	24 %	16 %	3	2 %	12	8 %	10	7 %	1	0	1	2 %	5	3 %	2	1 %
9	101	0	9	13	1	14	0	37 %	22 %	15 %	1	1 %	10	10 %	3	3 %	1	0	1	2 %	7	7 %	9	9 %
10	98	1	10	7	2	12	0	33 %	18 %	14 %	1	1 %	6	6 %	7	7 %	0	0	0	0 %	10	10 %	5	5 %
11	121	0	13	9	2	14	0	31 %	18 %	13 %	1	1 %	10	8 %	3	3 %	0	0	0	0 %	5	4 %	9	7 %
12	76	0	8	3	0	9	0	26 %	14 %	12 %	1	1 %	5	7 %	5	7 %	0	0	3	7 %	5	7 %	2	3 %
13	81	0	4	2	1	6	0	16 %	7 %	9 %	2	2 %	6	7 %	3	4 %	0	0	1	2 %	0	0 %	2	2 %
14	60	0	5	1	0	3	0	15 %	10 %	5 %	1	2 %	4	7 %	14	24 %	0	0	0	0 %	3	5 %	1	2 %
15	60	0	1	1	0	6	0	13 %	3 %	10 %	0	0 %	7	12 %	13	22 %	0	0	2	7 %	5	8 %	2	3 %
16	25	0	1	0	0	1	0	8 %	4 %	4 %	1	4 %	2	8 %	5	20 %	0	0	1	4 %	4	16 %	0	0 %
17	51	0	7	0	0	0	0	14 %	14 %	0 %	1	2 %	2	4 %	7	14 %	1	0	1	4 %	6	12 %	5	10 %
18	30	0	0	1	0	1	0	7 %	3 %	3 %	0	0 %	2	7 %	3	10 %	0	0	1	3 %	3	11 %	0	0 %
19	32	0	0	0	0	1	0	3 %	0 %	3 %	1	3 %	0	0 %	4	13 %	0	0	1	6 %	1	3 %	2	6 %
20	54	0	0	0	0	2	0	4 %	0 %	4 %	0	0 %	1	2 %	10	19 %	0	0	1	4 %	0	0 %	0	0 %
21	46	1	0	1	0	0	0	4 %	4 %	0 %	1	2 %	0	0 %	11	24 %	0	0	4	9 %	2	4 %	0	0 %
22	18	0	0	2	0	0	0	11 %	11 %	0 %	1	6 %	0	0 %	0	0 %	0	0	1	6 %	0	0 %	1	6 %
23	31	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	1	3 %	3	10 %	1	0	1	6 %	0	0 %	0	0 %
24	38	0	0	0	0	0	0	0 %	0 %	0 %	1	3 %	0	0 %	4	11 %	0	0	4	11 %	0	0 %	0	0 %
25	33	1	1	0	0	0	0	6 %	6 %	0 %	1	3 %	1	3 %	3	10 %	0	0	5	15 %	0	0 %	1	3 %
26	32	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	4	13 %	1	0	3	13 %	0	0 %	1	3 %
27	30	2	2	0	0	0	0	13 %	13 %	0 %	4	13 %	0	0 %	3	10 %	0	0	0	3 %	0	0 %	0	0 %
28	18	0	0	0	0	0	0	0 %	0 %	0 %	1	6 %	0	0 %	1	6 %	0	0	3	17 %	0	0 %	0	0 %
29	20	2	2	0	0	0	0	20 %	20 %	0 %	0	0 %	0	0 %	1	5 %	0	0	2	15 %	1	5 %	0	0 %
30	12	0	0	0	0	0	0	0 %	0 %	0 %	1	8 %	0	0 %	4	36 %	0	0	0	0 %	0	0 %	0	0 %
31	13	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	0	0 %
32	13	0	1	0	0	0	0	8 %	8 %	0 %	3	25 %	0	0 %	1	8 %	0	0	1	17 %	0	0 %	0	0 %
33	13	0	0	0	0	0	0	0 %	0 %	0 %	4	31 %	0	0 %	3	23 %	0	0	0	8 %	0	0 %	0	0 %
34	29	0	0	0	0	0	0	0 %	0 %	0 %	5	17 %	0	0 %	4	14 %	0	0	1	7 %	0	0 %	0	0 %
Sum	3180	17	175	103	9	141	0				147		108		405		30	9	44		88		143	

Genetic characterization of influenza viruses in Norway

During the current influenza season, the Norwegian Institute of Public Health (NIPH) has received 5,115 influenza virus specimens for analysis. Of these, 14.5 % (742 viruses) have undergone whole-genome sequencing (Table 3). Additionally, 101 viruses have been shared with the WHO Collaborating Centre in the UK (Worldwide Influenza Centre, Francis Crick Institute), according to a sequencing-first selection to ensure phenotypic characterisation of as many genetic variants as possible. All 742 haemagglutinin (HA) gene sequences have been submitted to the GISAID EpiFlu database, along all other genes that meet the quality criteria for submission.

We have here used the term "clade" for the WHO HA clade nomenclature, and "subclade" for the more detailed NextStrain nomenclature.

H1N1 viruses

During the 2024/25 influenza season, Norway observed a shift in the dominant **H1N1** virus clades. Initially, the season was dominated by the 6B.1A.5a.2a clade, with 151 out of 349 (43%) of the classified viruses belonging to this group. However, after February 2025, there was a notable shift in dominance to the 6B.1A.5a.2a.1 clade, which accounts for 195 out of 349 (57%) of the sequenced **H1N1** viruses over this season (Figure 8, Table 3.). The 6B.1A.5a.2a clade

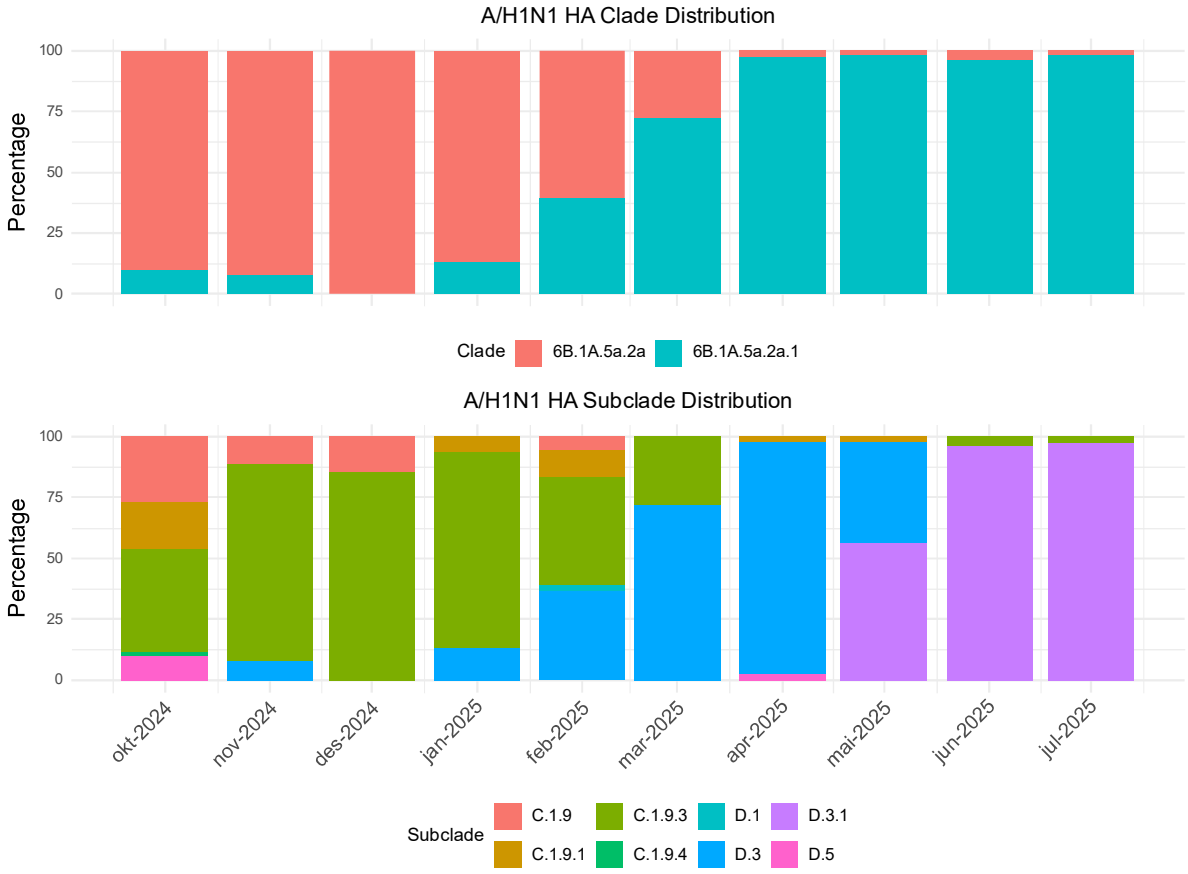

Figure 8. Clade (Upper) and subclade (Lower) distribution of H1N1 viruses in Norway for season 2024/2025

displayed considerable genetic diversity. The most prevalent subclade within this group was C.1.9.3, accounting for 111 detected viruses, all of which were categorized as *genAH1/Hungary/286/2024-like* viruses. These viruses uniformly exhibited the **HA:S83P**

substitution, with a major subcluster further characterized by the **HA:I166V** substitution. Recent strains within this cluster have also developed the **HA: P137S** and **S69P** substitutions. Notably, some of these recent strains with the neuraminidase clade C.1, forming a distinct pattern (Figure 9)

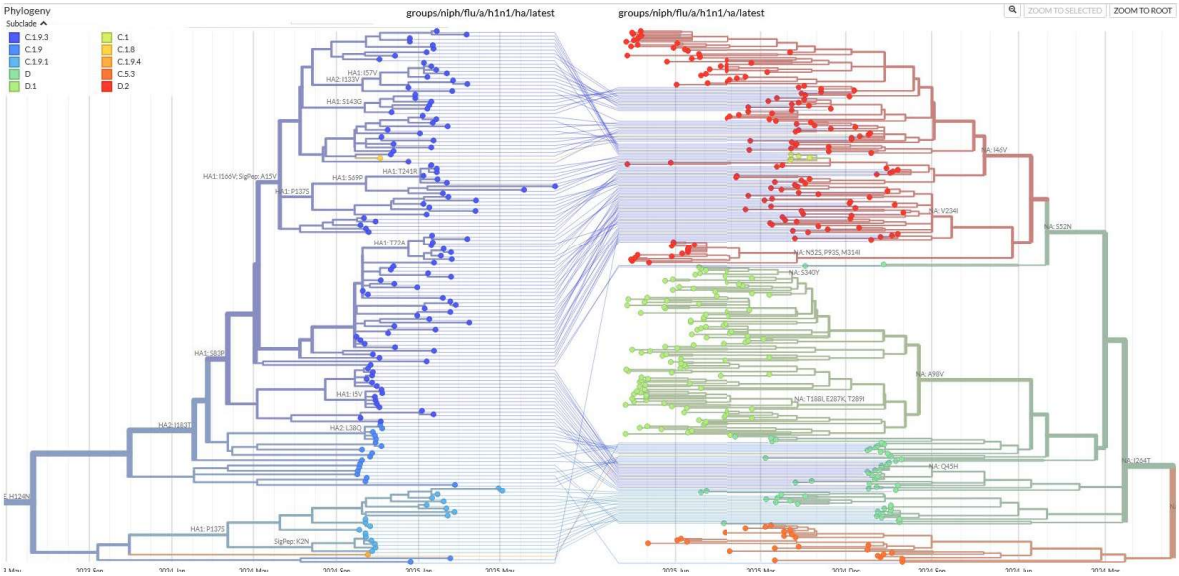

***Figure 9. H1N1** clade **6B.1A.5a.2a** NextStrain phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterisation guidelines on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full Nextclade tree is available here.*

Other H1 viruses within the 6B.1A.5a.2a clade were classified as *genAH1/Lisboa/188/2023-like* and fell into various subclades: C1.9 with 20 cases, C1.9.1 with 19 cases, and one case in subclade C1.9.4. The C.1.9.1 subclade, marked by the **HA: P137S** substitution, is significant as this mutation is one of the founding mutations of the 6B.1A.5a.2a.1 clade. It has arisen multiple times in recent seasons, underscoring the evolutionary importance of this position. Detections of viruses with this substitution continued at low levels until May 2025 across several genetic clusters (Figure 10).

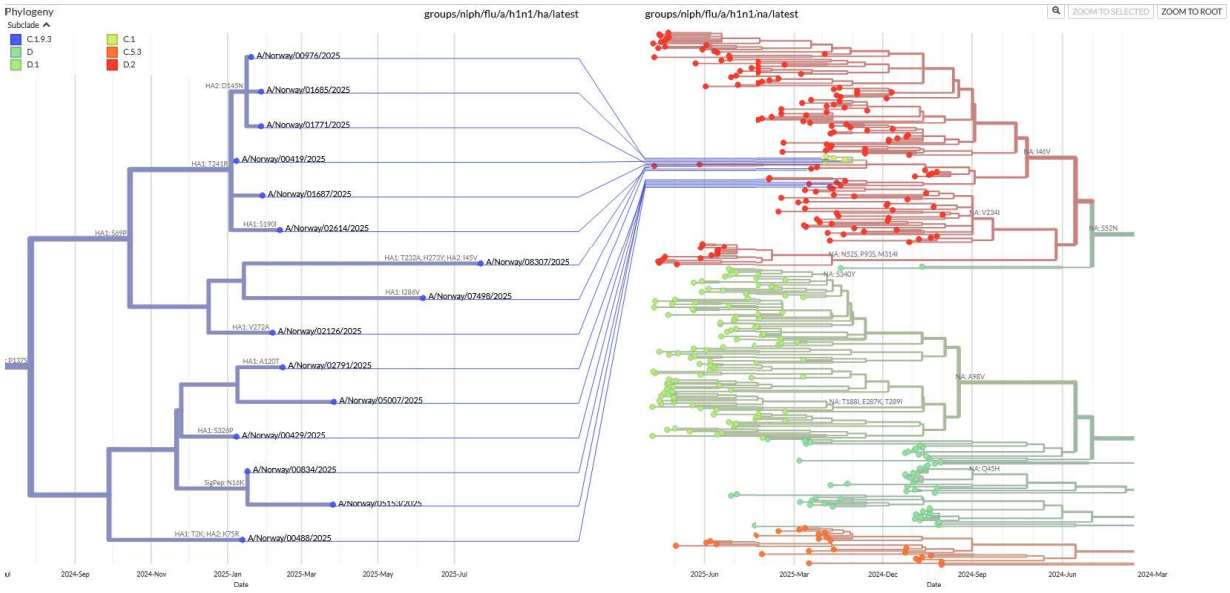

Figure 10. H1N1 *clade* ***6B.1A.5a.2a,*** *subclade* ***C.1.9.3*** *NextStrain phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

The single detected virus from subclade C.1.9.4, from October 2024, carried additional **haemagglutinin** substitutions: **N38D**, **Q54K**, **D86N**, **N125D**, and **I149V**. Both C.1.9.1 and C.1.9.4 subclade viruses clustered with the NA clade D (Figure 11).

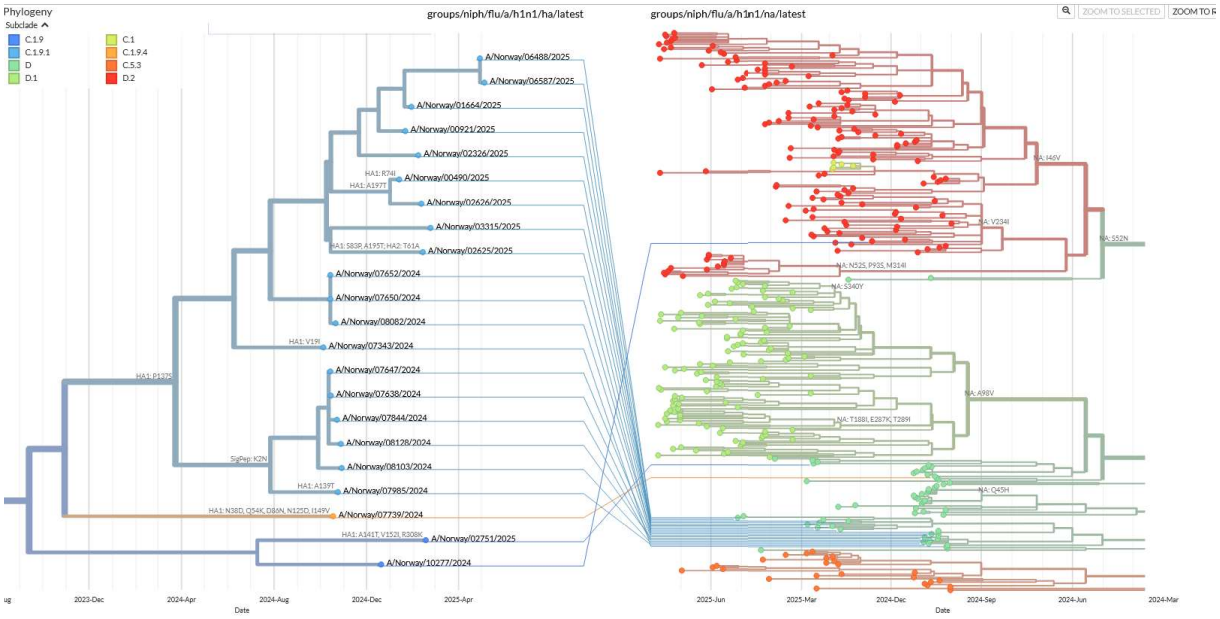

Figure 11. H1N1 *clade 6B.1A.****5a.2a****, subclade* ***C.1.9.1*** *and* ***C.1.9.4*** *NextStrain phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The NextStrain full tree is available here.*

Within the 6B.1A.5a.2a.1 clade, the majority of detections were attributed to subclade D.3, with 97 cases, closely followed by 94 detections in subclade D.3.1. A smaller number of detections were noted in subclade D.5 (6 cases) and D.1 (1 case) (Figure 8,Table 3).

By March 2025, the 6B.1A.5a.2a.1 clade had become dominant, with a variety of genetic clusters identified. The D.3.1 subclade was the largest, defined by **HA2** substitutions: **I45V**, **I133T**, **V193**, and the majority also carrying **HA:R113K**. Viruses from the D.3.1 subclade was observed to circulate across all states in Norway (Figure 12).

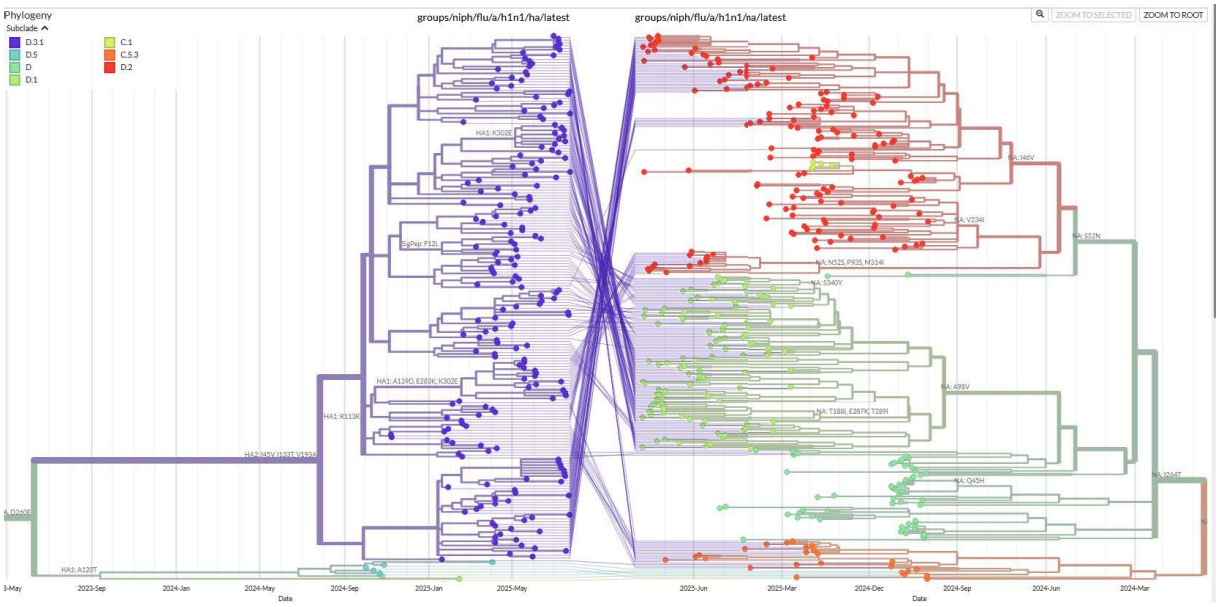

***Figure 12 . H1N1** clade **6B.1A.5a.2a.1,** subclade **D.3.1** NextStrain phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines on a time axis. Colours represent subclades; branches are labelled with Amino Acid substitutions. The full NextStrain tree is available here.*

Recent developments:

Within the D.3.1 subclade two distinct clusters have been developing since July. One with the **HA:K302E** substitution, clustering with D.1 clade viruses on the NA tree with additional **NA** substitutions T188I, E287K and T289I. And another one with the HA substitutions R113K, **A139D, E283K** and **K302E**. Those viruses cluster tightly on the NA tree also with NA clade D.3 and additional **NA:N52S, P93S** and **M314I** substitutions (Figure 13).

Recent detections in both above-described clusters date back from July (latest sequencing run) and show a somewhat higher genetic divergence than other D.3.1 viruses from this season.

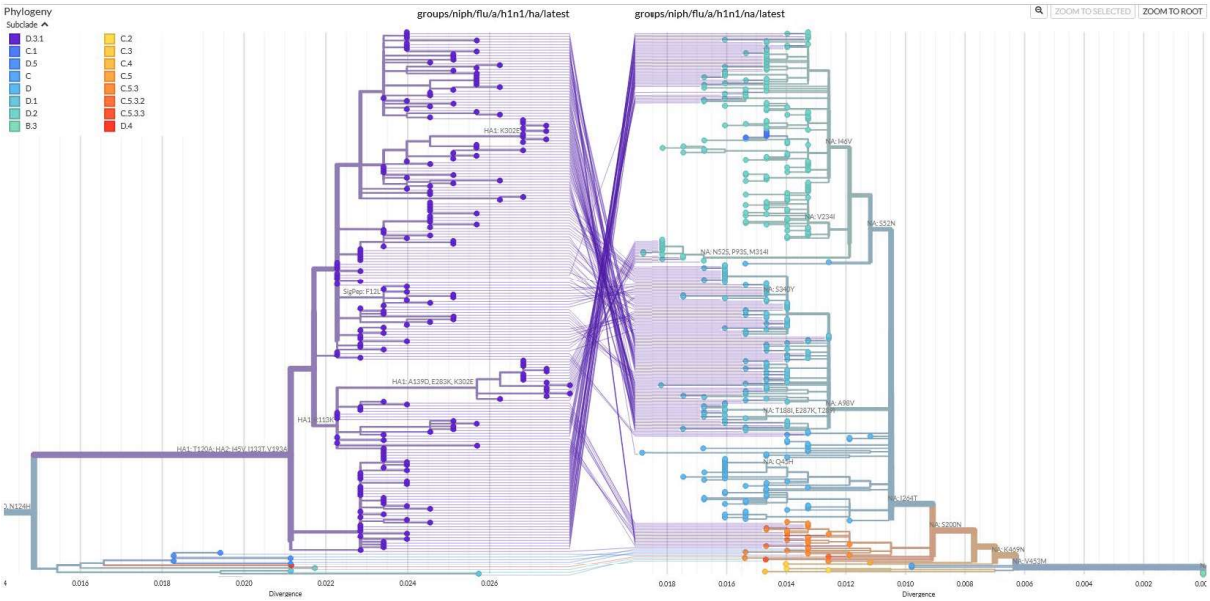

Figure 13. H1N1 *clade* ***6B.1A.5a.2a.1,*** *subclade* ***D.3.1*** *NextStrain phylogenetic* ***divergence*** *tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines. Colours represent subclades; branches are labelled with Amino Acid substitutions. The full NextStrain tree is available here.*

H3N2 viruses

During the 2024/25 influenza season in Norway, the predominant **H3N2** viruses belonged to the 3C.2a1b.2a.2a.3a.1 clade, representing 99% of the strains (222/224). There were only two detections (2/224, 1%) of the 3C.2a1b.2a.2a.3a clade (Figure 14, Table 3).

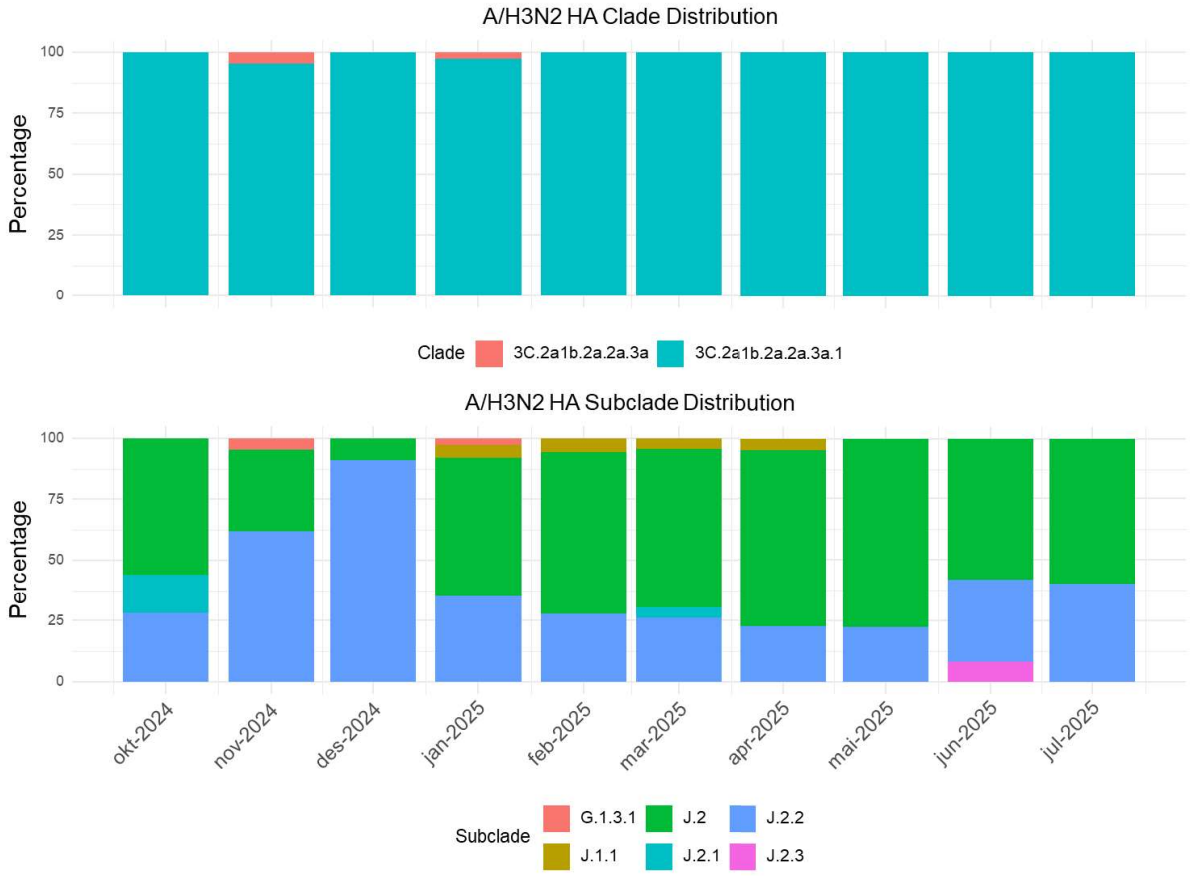

Figure 14 Clade (Upper) and subclade (Lower) distribution of H3N2 viruses in Norway for Season 2024/2025

Within the 3C.2a1b.2a.2a.3a.1 clade, two main groups of viruses were detected. Most notably, the *genAH3/Croatia/1013RV/2023* subclade J2 (130/224) and J.2.3 (1/224) identified by **HA:N122D** and **HA:K276E** substitutions. There was also the *genAH3/Lisboa/216/2023* subclade J.2.2 (11/224) defined by an additional **HA:S124N** which persisted throughout the season. Additionally, a small number (6/224) of *genAH3/Sydney/856/2023-like* viruses (subclade J.1.1) defined by the substitutions **HA:I25V** and **V347M** were detected from January to March 2025. Sporadic detections of *genAH3/West Virginia/51/2024* belonging to subclade J.2 (1/224, 1%) and J.2.1 (5/224, 2%) with an additional **HA:P239S** substitution occurred mostly early in the season (Table 3.).

The two 3C.2a1b.2a.2a.3a clade viruses identified this season were *A/Finland/402/2023-like* viruses from the G.1.3.1 subclade, detected sporadically in the 2023/24 season. However, they have acquired additional substitutions: **HA:I40M** and **HA2:M18K**.

As is normal during an influenza season, these classifications and definitions have drifted. The largest genetic subcgroup detected this season, the J.2. viruses have grouped into 2 large clusters; one with an additional **HA: N8D**, and the other with **HA2: V18M** with a multitude of smaller genetic clusters making up the bulk of **H3N2** detections (Figure 15).

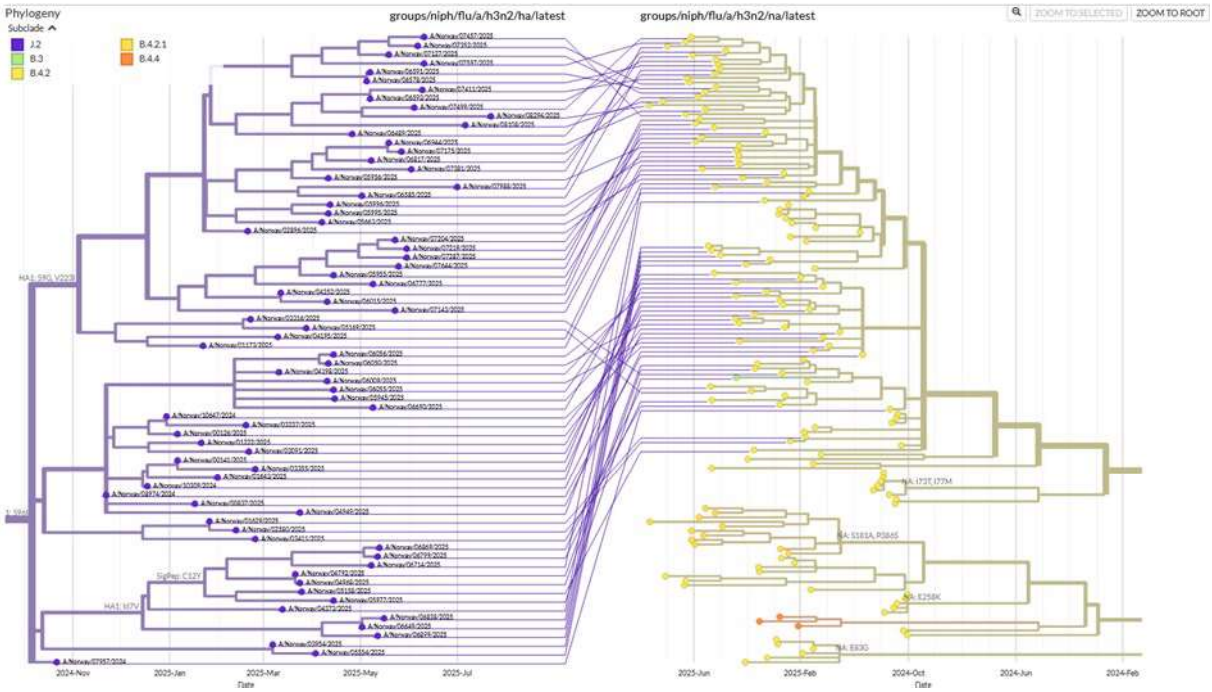

Figure 15 **H3N2** clade **3C.2a1b.2a.2a.3a.1**, subclade **J.2** NextStrain phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO influenza characterization guidelines, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.

The smaller J.2. cluster were *A/Canberra/331/2023* like viruses defined by the **HA S145N** substitution. Those have further subdivided into J.2.3. subclade defined by an additional **HA N158K**, **N145S** and **K189R** only one such virus was detected in Norway so far in May 2025 (Figure 16).

The **J.2.2** were the second most common subclade detected, three distinct clusters were detected in the season, one early in the season with an additional **HA1:P239Q**, and **HA2:V18M** however these have gone extinct in Norway and were not detected in 2025(Figure 17).

The largest cluster had an additional **HA: T65K**, **S145N** and **HA2: S49N**, **L198F**. The most recent and divergent **H3N2**s detected had an additional **HA T65K** and then subdivided into clusters with an additional **HA2:V18M** and **HA D291G** clustering with a B.4.2.1 NA that carries an additional **NA S181A** and **P386S**- This J.2.2s also developed further into the J.3* subclade defined by an additional **HA: N63K**, **S145N**, **K207Q** and **HA2: V176I**. Three viruses were detected in Norway in June/July (Figure 17).

**At the time of writing this report both NextClade web and CLI classified these J.3. viruses as J.2.2. Only NextClade tree builder classified those as J.3, producing uncertainty about their real classification.*

Recent genetic changes in H3N2 viruses:

Additional sequencing of seven H3N2 viruses from various locations in August, which gave anomalous outcomes in our H3 subtyping PCR, reveal that these viruses are **subclade J.2.4**, defined by substitutions T135K, but with **additional substitutions K2N, S144N, N158D, I160K, Q173R, T328A in HA1 plus S49N in HA2**.

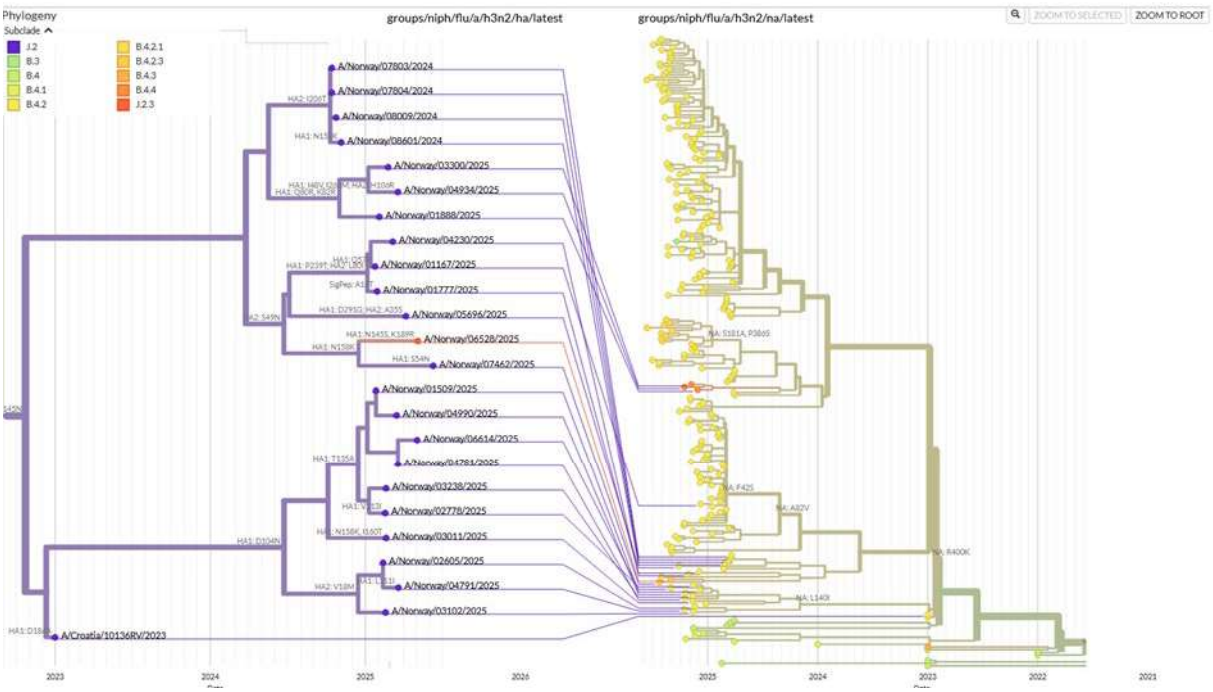

Figure 16 H3N2 *clade* ***3C.2a1b.2a.2a.3a.1*** *subclade* ***J.2*** *NextStrain phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

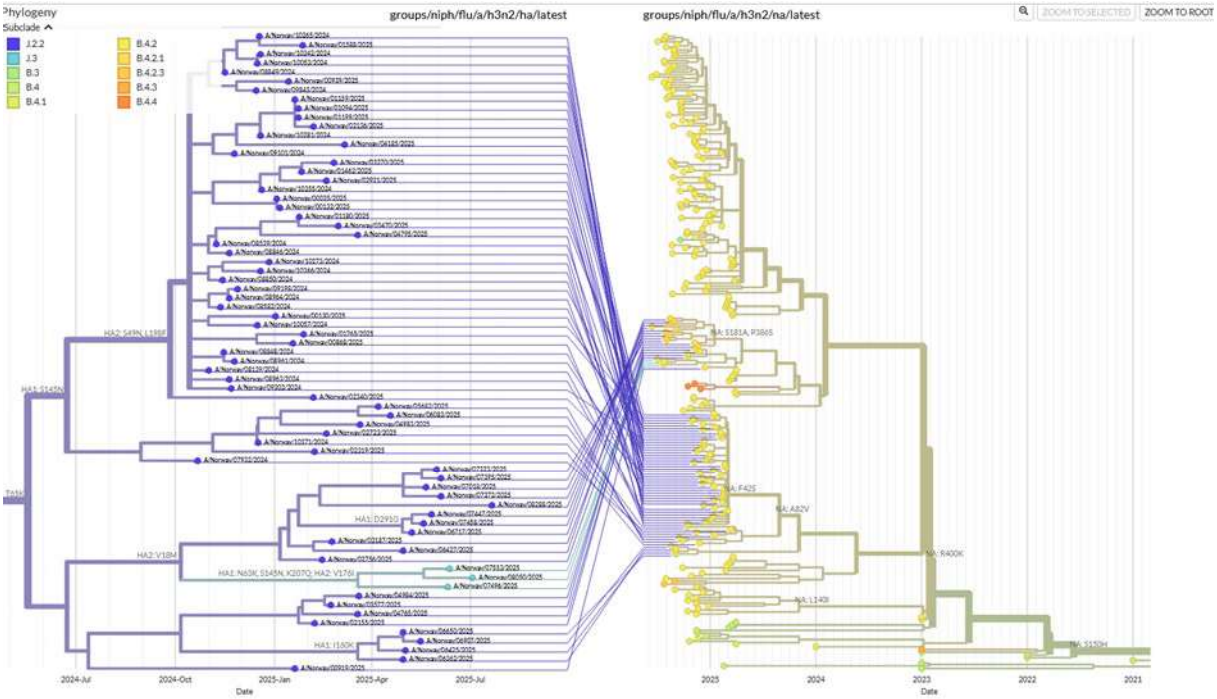

Figure 17 H3N2 *clade* ***3C.2a1b.2a.2a.3a.1*** *subclade* ***J.2.2/J.3*** *NextStrain phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 40 2024 until week 34 2025, compared on a time axis to the reference sequences for season 2024/25 provided by the ECDC/WHO influenza characterization guidelines. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

B/Victoria-lineage viruses

During the 2024/25 influenza season, the sequenced **B/Victoria-lineage** viruses in Norway all belong to the V1A.3a.2 clade (169/169, 100%)(Figure 18,Table 3.).

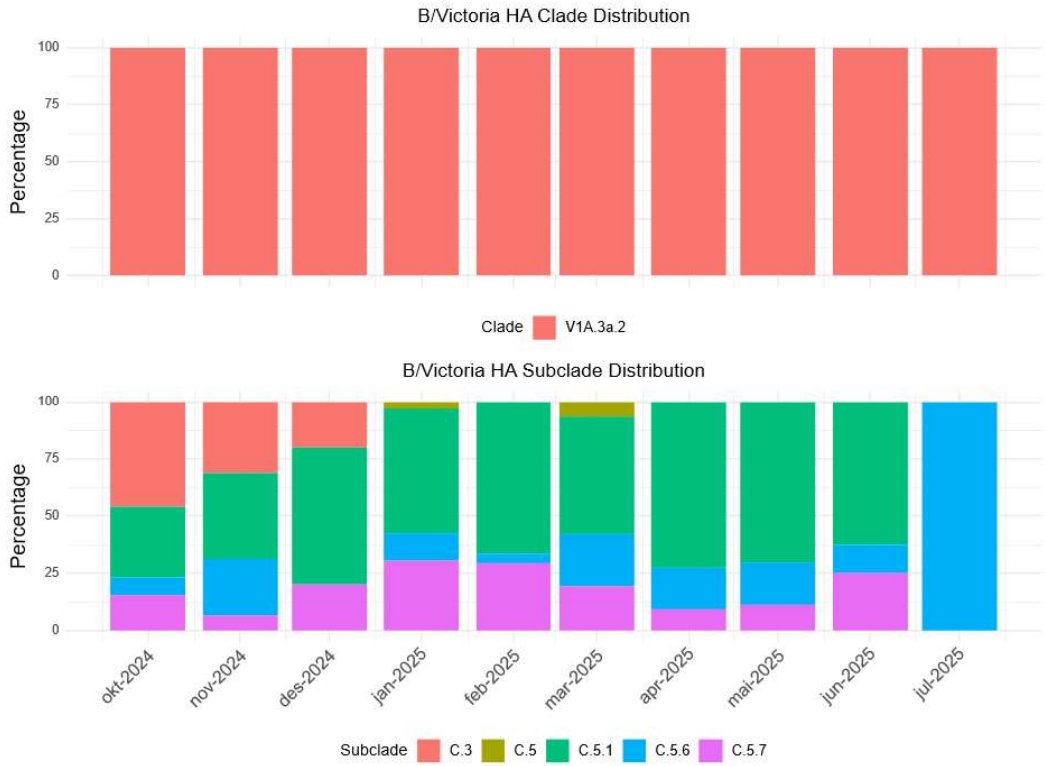

Figure 18 Clade (Upper) and subclade (Lower) distribution of B/Victoria viruses in Norway during season 2024/2025.

Within the V1A.3a.2 clade, 3 main groups of viruses were detected. The largest group is classified as *genBVicB/Catalonia/2279261NS/2023* belonging to the C.5 (3/169) and C.5.1 subclade (95/169, 56%) and defined by **HA: D197E** and **E183K** and **E128K** substitutions. These viruses were detected throughout the season. Over the season a subset of those virsues aquired additonal substitutions **HA: A154T**, **A202V** and **HA2: R151K**. These viruses cluster on the NA gene with the **NA: B.7** clade (Figure 19).

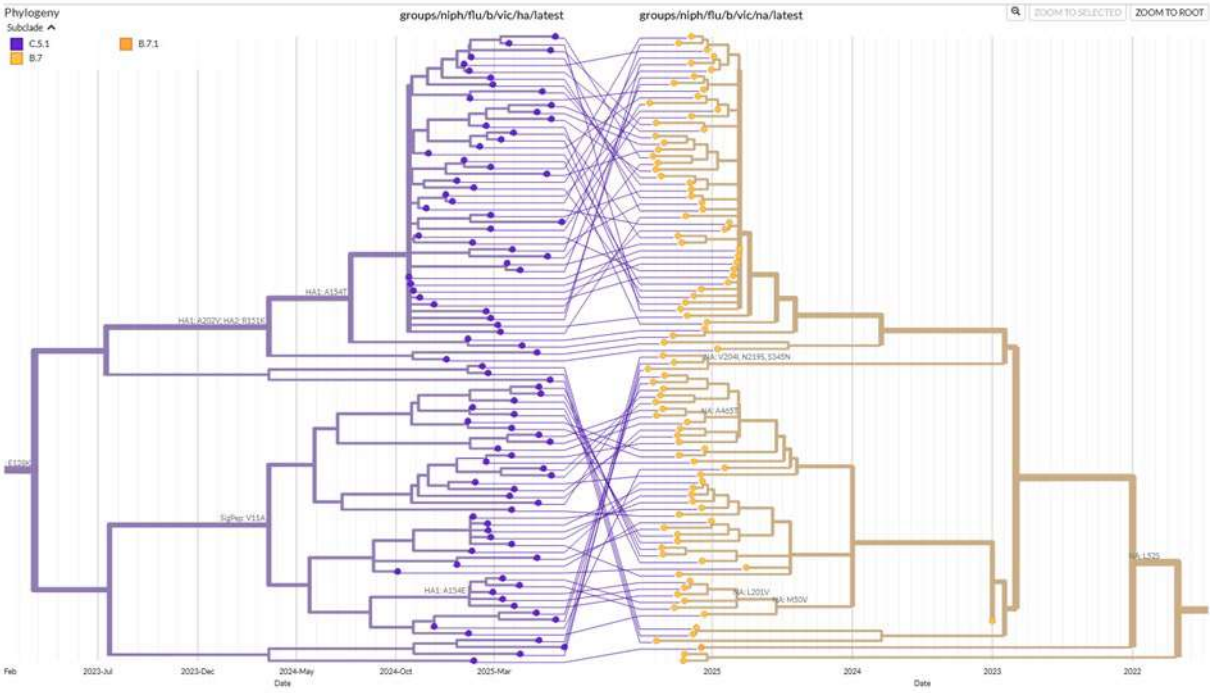

Figure 19 B/Victoria *clade* ***V1A.3a.2,*** *subclade* ***C.5.1*** *NextStrain phylogenetic tree of the haemagglutinin of the B-Victoria viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

The second biggest group of detected V1A.3a.2 clade viruses is classified as the *genBVicB/Guangxi-Beiliu/2298/2023* with five detections (5/38, 13%) belonging to the subclade C.5.7 defined by the **HA: D197E, E183K** and **E128G** substitutions.Recent representatives of this group have aquired additional **HA:V15I** and **E184G** substitiutions. These viruses cluster on the NA gene with NA: B.7.3 clade (Figure 20, Table 3.).

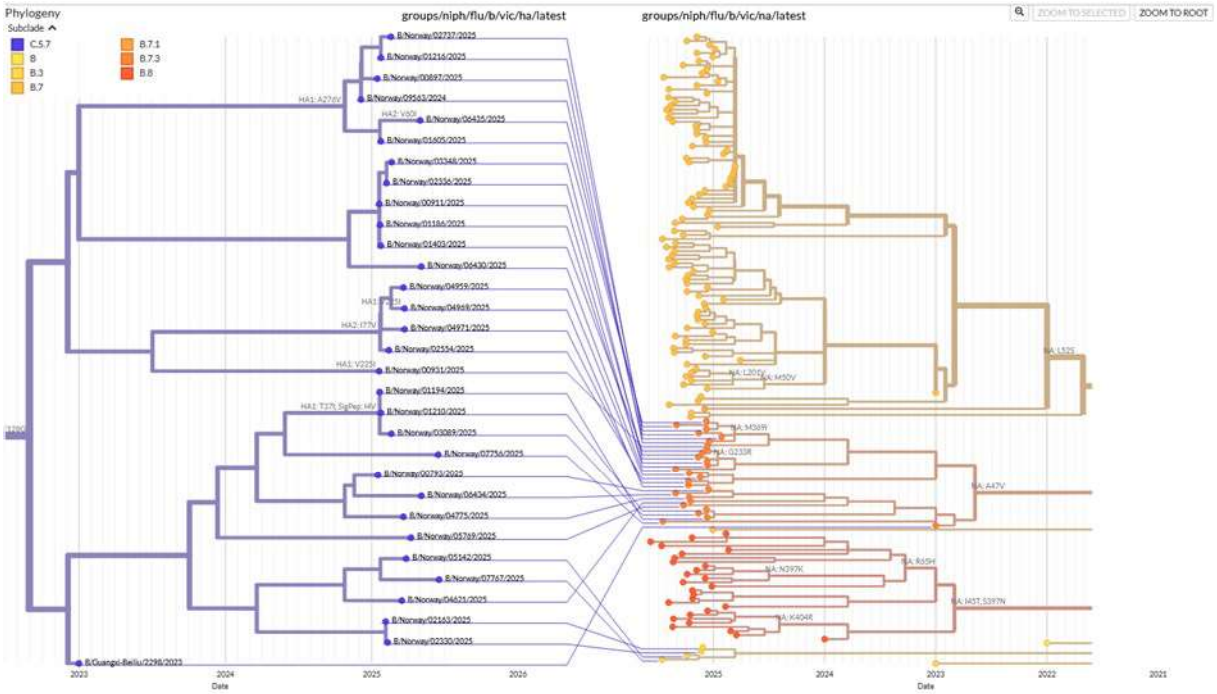

Figure 20. B/Victoria *clade* ***V1A.3a.2,*** *subclade* ***C.5.7*** *NextStrain phylogenetic tree of the haemagglutinin of the B-Victoria viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

The third cluster is categorized as *genBVicB/Switzerland/329/2024* belonging to the C.5.6 (26/169, 15%) and subclade and the third cluster is categorized as *genBVicB/Switzerland/329/2024* belonging to the C.5.6 (26/169, 15%) defined by the **HA: D197E** and **D129N.** Within this cluster a new subclade (C.5.6.1) has been detected with the key mutation **HA: T31I,** four viruses with that sublcade have been detected in Norway from January to May 2025. All these viruses cluster with the NA counterparts in clade B.8 (Figure 21, Table 3.).

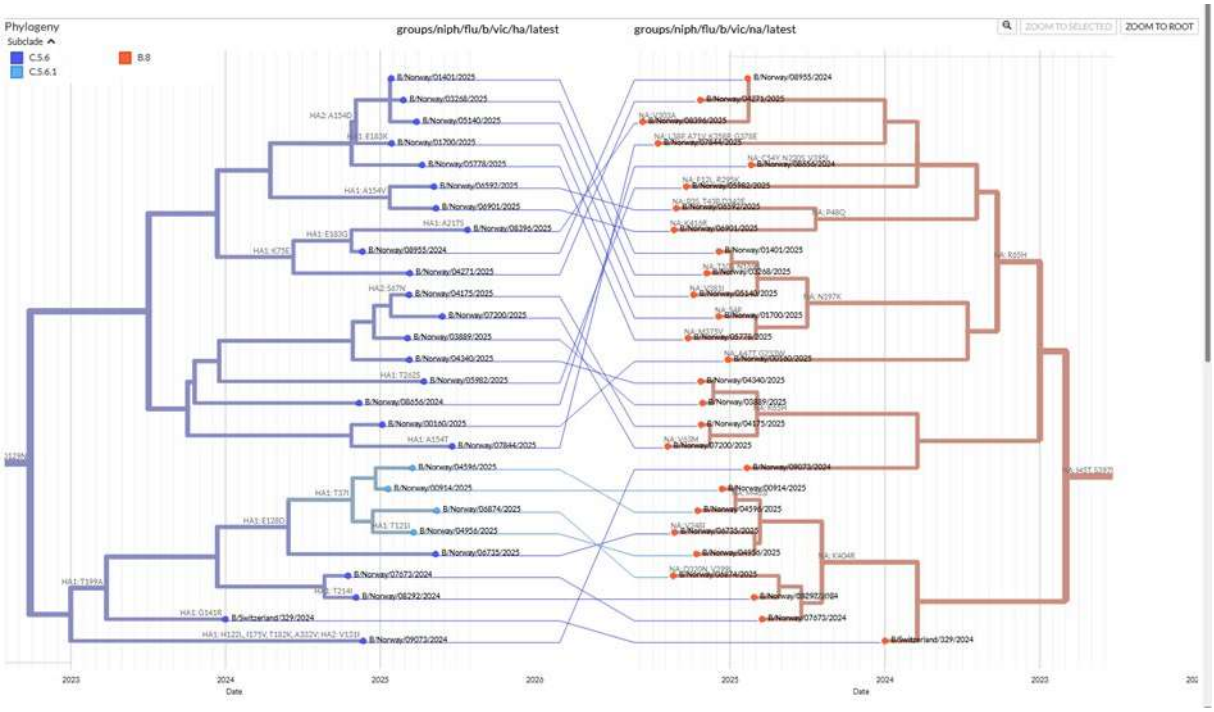

Figure 21 B/Victoria *clade* ***V1A.3a.2,*** *subclade* ***C.5.7*** *NextStrain phylogenetic tree of the haemagglutinin of the B-Victoria viruses from Norway from week 40 2024 until week 34 2025, compared to the reference sequences for season 2024/25 provided by the ECDC/WHO Influenza characterization guidelines on a time axis. Colours represent subclades of each isolate; branches are labelled with amino acid substitutions. The full NextStrain tree is available here.*

Table 3. 3 Genetic classification of Influenza viruses 2024/25 Season in Norway

WHO/ECDC category	HA-Clade	HA-Subclade	okt.24	nov.24	des.24	jan.25	feb.25	mar.25	apr.25	mai.25	jun.25	jul.25	Total
A/H1N1	-	-	52	26	7	46	36	25	40	48	25	44	349
genAH1/Lisboa/188/2023	6B.1A.5a.2a	C.1.9.1	10 (19.2%)	0 (0%)	0 (0%)	3 (6.5%)	4 (11.1%)	0 (0%)	1 (2.5%)	1 (2.1%)	0 (0%)	0 (0%)	19
genAH1/Lisboa/188/2023	6B.1A.5a.2a	C.1.9	14 (26.9%)	3 (11.5%)	1 (14.3%)	0 (0%)	2 (5.6%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	20
genAH1/Lisboa/188/2023	6B.1A.5a.2a	C.1.9.4	1 (1.9%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1
genAH1/Victoria/4897/2022	6B.1A.5a.2a.1	D.5	5 (9.6%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (2.5%)	0 (0%)	0 (0%)	0 (0%)	6
genAH1/Victoria/4897/2022	6B.1A.5a.2a.1	D.1	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (2.8%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1
genAH1/Norway/00926/2025	6B.1A.5a.2a.1	D.3	0 (0%)	2 (7.7%)	0 (0%)	6 (13%)	13 (36.1%)	18 (72%)	38 (95%)	20 (41.7%)	0 (0%)	0 (0%)	97
genAH1/Norway/00926/2025	6B.1A.5a.2a.1	D.3.1	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	27 (56.2%)	24 (96%)	43 (97.7%)	94
genAH1/Hungary/286/2024	6B.1A.5a.2a	C.1.9.3	22 (42.3%)	21 (80.8%)	6 (85.7%)	37 (80.4%)	16 (44.4%)	7 (28%)	0 (0%)	0 (0%)	1 (4%)	1 (2.3%)	111
A/H3N2	-	-	25	21	11	37	36	23	23	31	12	5	224
genAH3/Croatia/10136RV/2023	3C.2a1b.2a.2a.3a.1	J.2	14 (56%)	5 (23.8%)	1 (9.1%)	21 (56.8%)	24 (66.7%)	15 (65.2%)	16 (69.6%)	24 (77.4%)	7 (58.3%)	3 (60%)	130
genAH3/Croatia/10136RV/2023	3C.2a1b.2a.2a.3a.1	J.2.3	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (8.3%)	0 (0%)	1
genAH3/Lisboa/216/2023	3C.2a1b.2a.2a.3a.1	J.2.2	7 (28%)	13 (61.9%)	10 (90.9%)	13 (35.1%)	10 (27.8%)	6 (26.1%)	5 (21.7%)	7 (22.6%)	4 (33.3%)	2 (40%)	77
genAH3/Sydney/856/2023	3C.2a1b.2a.2a.3a.1	J.1.1	0 (0%)	0 (0%)	0 (0%)	2 (5.4%)	2 (5.6%)	1 (4.3%)	1 (4.3%)	0 (0%)	0 (0%)	0 (0%)	6
genAH3/West Virginia/51/2024	3C.2a1b.2a.2a.3a.1	J.2.1	4 (16%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (4.3%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	5
genAH3/West Virginia/51/2024	3C.2a1b.2a.2a.3a.1	J.2	0 (0%)	1 (4.8%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1
genAH3SubgroupNotListed	3C.2a1b.2a.2a.3a	G.1.3.1	0 (0%)	1 (4.8%)	0 (0%)	1 (2.7%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2
B/Victoria	-	-	13	16	5	33	24	31	11	27	8	1	169
genBVicB/Austria/1359417/2021	V1A.3a.2	C.3	6 (38.5%)	5 (31.2%)	1 (20%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	12
genBVicB/Catalonia/2279261NS/2023	V1A.3a.2	C.5.1	4 (30.8%)	6 (37.5%)	3 (60%)	18 (54.5%)	16 (66.7%)	16 (51.6%)	8 (72.7%)	19 (70.4%)	5 (62.5%)	0 (0%)	95
genBVicB/Catalonia/2279261NS/2023	V1A.3a.2	C.5	0 (0%)	0 (0%)	0 (0%)	1 (3%)	0 (0%)	2 (6.5%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3
genBVicB/Guangxi-Beiliu/2298/2023	V1A.3a.2	C.5.7	2 (15.4%)	1 (6.2%)	1 (20%)	10 (30.3%)	7 (29.2%)	6 (19.4%)	1 (9.1%)	3 (11.1%)	2 (25%)	0 (0%)	33
genBVicB/Switzerland/329/2024	V1A.3a.2	C.5.6	1 (7.7%)	4 (25%)	0 (0%)	4 (12.1%)	1 (4.2%)	7 (22.6%)	2 (18.2%)	5 (18.5%)	1 (12.5%)	1 (100%)	26

Surveillance of antiviral resistance in Influenza viruses

Out of 604 influenza viruses tested in the 24/25 season only one A/H1N1 virus sampled in week 40/2024 carried an oseltamivir resistance substitution, H275Y, in its NA gene. Additionally, we found one influenza A/H1N1 from week 41 2025 that had the E23G substitution in the PA gene, which has been shown to lower the susceptibility to baloxavir marboxil. The treatment history of both cases is unknown. All other tested viruses were susceptible to oseltamivir, zanamivir, and baloxavir marboxil.

No case of the newly emerged I223V / S247N NA substitution combination was detected in Norway 2024/25.

All circulating seasonal influenza A viruses have been resistant to adamantanes for many years. and. Furthermore, adamantanes are not inhibiting influenza B viruses, and are thus not a relevant drug for treatment of influenza B. Adamantanes are not used for treatment of influenza in Norway.

Seroepidemiology:
Population immunity against recent influenza viruses, August 2024

This part was also presented in the interim report in February

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 1266 sera collected in August 2024 are presented here. The main findings are shown in Figure 22 in comparison to data from 2022 and 2023, in Table 4 for the last 5 years, and summarised as follows:

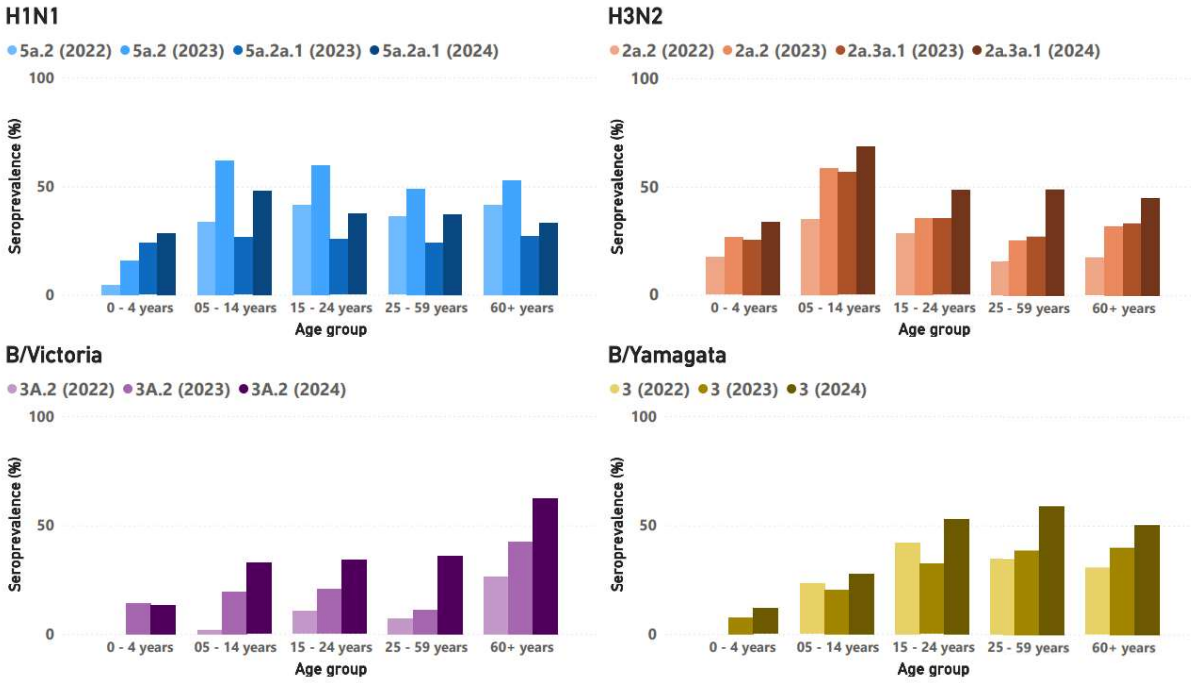

Figure 22. Seroprevalence in August 2022, 2023, and 2024 against current influenza A and B strains in various age groups. HAI was performed against A/Victoria/2570/2019 (H1N1, clade 6B.1A.5a.2), A/Norway/31694/2022 (H1N1, clade 6B.1A.5a.2a.1), A/Darwin/9/2021 (H3N2, 3C.2a1b.2a.2), A/Thailand/8/2022 (H3N2, 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 clade name. Protective HAI titres were defined as ≥40 for influenza A and ≥80 for ether treated influenza B.

In 2023, the percentage of sera with protective HAI titres (here referred to as seroprevalence) against the H1N1 5a.2a clade (A/Victoria/2570/2019) was 50-60% in all age groups older than 4 years. However, there was a marked drop in seroprevalence against the 5a.2a.1 clade (A/Norway/31694/2022). In sera from 2024, following the H1N1 dominated 2023/24 season, there was a clear increase in seroprevalence against the A/Norway/31694/2022 virus in the age groups 5 – 14 years, 15 – 24 years and 25 – 59 years, ranging from 37 – 48%. In the youngest and the oldest age group there was a more modest increase in HAI titres against A/Norway/31694/2022 from 2023 to 2024, to 29% and 33%, respectively. The A/Victoria/4897/2022 strain (clade 5a.2a.1) was a part of the seasonal influenza vaccine for the Northern Hemisphere in 2023/2024 and may have contributed to the increased seroprevalence seen in the serum samples collected in August 2024.

The seroprevalence against clade 2a.3a.1 (A/Thailand/8/2022) increased in sera from most age groups from 2023 to 2024, ranging from 34% in the 0-4 years age group up to 69% in the 5-14 years age group. While the sera from 2024 was not tested against A/Darwin/9/2021 (clade 2a.2), data from 2023 indicate similar seroprevalence between the two strains. The A/Thailand/8/2022 strain was first included in the vaccine for the 2024/2025 influenza season.

The seroprevalence against contemporary B/Austria/1359417/2021 (Victoria lineage, clade 3a.2) increased in all but the youngest age group from 2023 to 2024. In the age groups from 5-14, 15-24 and 25-59, seroprevalence in 2024 was similar at approximately 35%. The oldest age group had a seroprevalence of 62%, while the 0-4 years age group had a seroprevalence of 13%. The seroprevalence likely reflects a combination of infection and that the B/Austria/1359417/2021 strain has been included in the seasonal influenza vaccine since the 2022/2023 season.

For the B/Phuket/3073/2013 strain (Yamagata lineage clade 3), which has been included in the tetravalent influenza vaccine since the 2015/16 season, the August 2024 seroprevalence was 50 – 60% in the age groups 15 – 24, 25 – 59 and 60+ years. This was an increase compared to sera collected in 2022 and 2023. In the youngest age groups, we also observed a slight increase in seroprevalence compared to 2023, i.e. 12% in the 0 – 4 years group and 28% in the 5 – 14 years group.

Table 4. Influenza seroepidemiology results in August 2024 – Seroprevalence* in age groups.

For comparison data from studies performed for the preceding years 2019-2023 are also included. Due to the covid-19 pandemic, no HAI assays were performed in 2020.

Influenza strains (year$)	Age groups						
	0-4	5-14	15-24	0-24	25-59	60+	All ages
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
H1 Norway/31694/22 (2024)*	***29***	***48***	***38***	***40***	***37***	***33***	***38***
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)	27	59	36	45	25	32	35
H3 Thailand/8/22 (2023)**	26	57	36	43	27	33	35
H3 Thailand/8/22 (2024)*	***34***	***69***	***49***	***53***	***49***	***45***	***50***
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/Austria/1359417/21 (Vic-Δ3B) (2024)*	***13***	***33***	***34***	***29***	***36***	***62***	***38***
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
B/Yam Phuket/3073/13 (2024)*	***12***	***28***	***53***	***33***	***59***	***50***	***46***
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
Sera analysed (n): 2024 Aug	***114***	***205***	***189***	***508***	***412***	***226***	***1146***

$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 2025-2025.

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

Selected epidemiological surveillance data

Influenza-like illness (ILI) in primary health care

The proportion of ILI consultations began to rise gradually from week 50/2024, a few weeks later than in the preceding seasons. This season's epidemic threshold, defined by the Moving Epidemic Method (MEM), was crossed in week 02/2025 (Figure 23, Figure 24). Influenza activity peaked in week 9 when 2,8 % of the consultations were due to influenza-like illness, which indicates a medium intensity level according to the MEM-thresholds. The ILI indicator resided at this level for four weeks (Figure 24).

After its peak, there was a gradual decrease in the proportion of ILI until it crossed below the epidemic threshold in week 15/2025. The 2024-25 influenza outbreak lasted for 13 weeks according to ILI and the MEM, which is the usual length of an average influenza outbreak in Norway.

This season's ILI seems to have lagged two weeks behind crossing of the virological outbreak threshold (week 52 when proportion positive tests increase above 10 %). However, as shown in Figure 24, during these two weeks the ILI proportion was very close to the threshold.

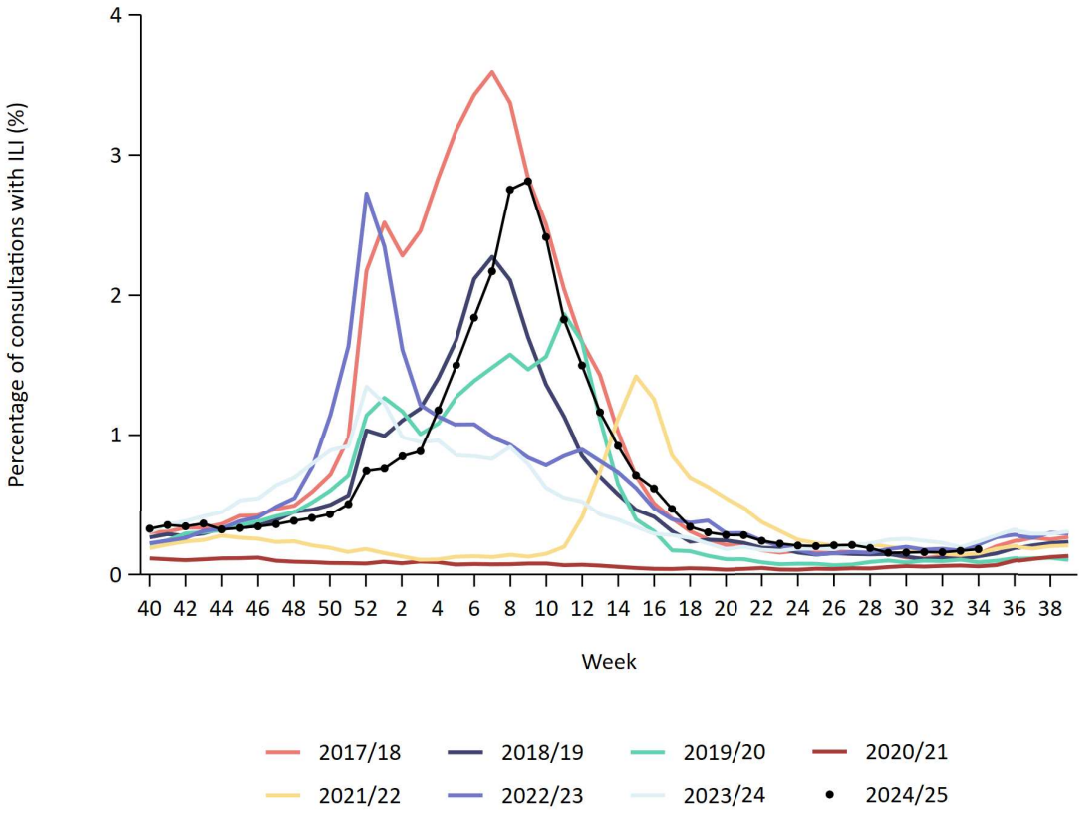

Figure 23. Weekly proportion of consultations for ILI, Norway 2024-2025 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the seven previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH.

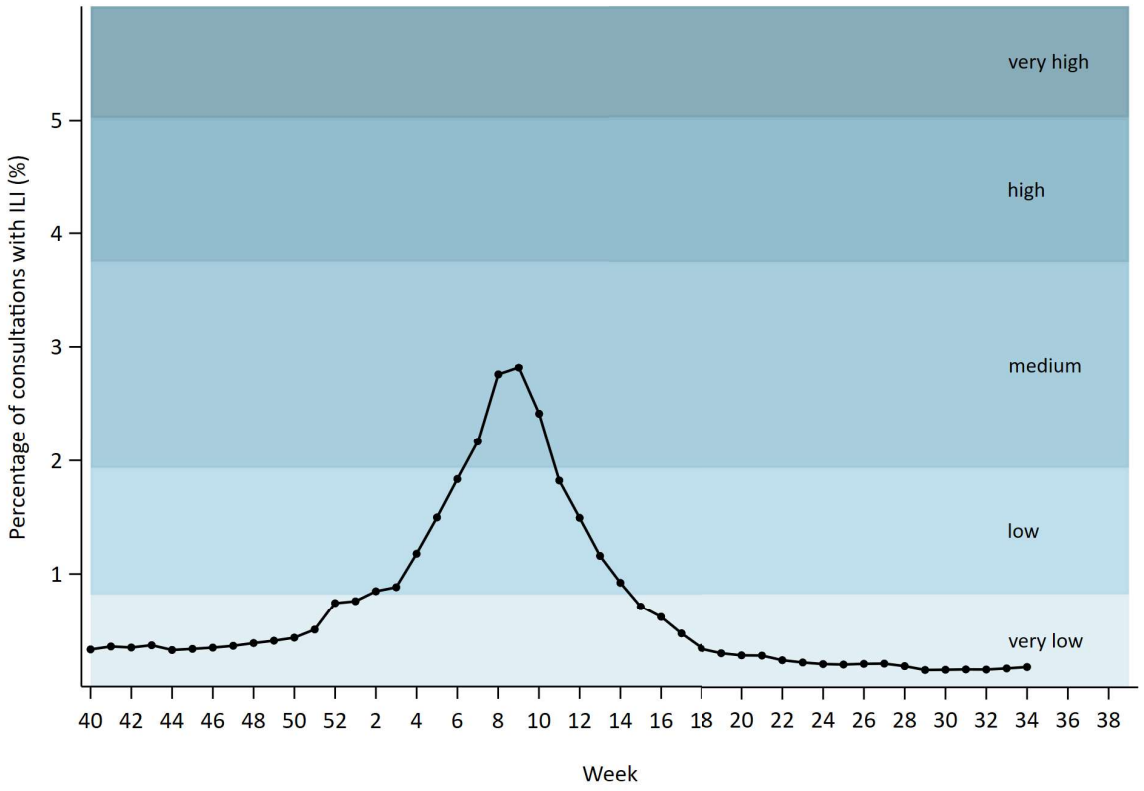

Figure 24. MEM intensity levels, Norway 2024-2025 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSySS with data from KUHR, NIPH.

Influenza hospitalisations based on registry data

Between week 40/2024 and week 34/2025, 10,657 (190.5 per 100,000 inhabitants) samples from hospitalized patients tested positive for influenza by PCR, with a peak of 1,055 positive tests in week 8/2025 (Figure 25). The highest incidence was in the age groups 65-79 and 80+ years, followed by children aged 0-4 years (Table 5). The dominance of influenza A viruses was reflected in the admissions; however, for influenza B the incidence was highest among children, with few elderly patients testing positive for influenza B, reflecting the different age profiles in the virological surveillance (Table 5; see also "Laboratory confirmed influenza: Virological surveillance" for more information). In total, 1.4% of influenza positive samples from hospital admitted patients did not have information on typing in the MSIS laboratory database, of these, none were from children <15 years of age.

In comparison, 6,294, 8,722 and 4,444 samples from hospitalised patients tested positive for influenza by PCR between weeks 40 and 34 in the seasons 2023-24, 2022-23 and 2021-22, respectively. In the 2024-25 season, there were 64% more influenza detections among hospitalized patients than the average for the three previous seasons. This indicates that the 2024-25 influenza outbreak was more severe than the previous three seasons, even if the numbers must be interpreted with caution due to potential changes in e.g. testing and coding practices.

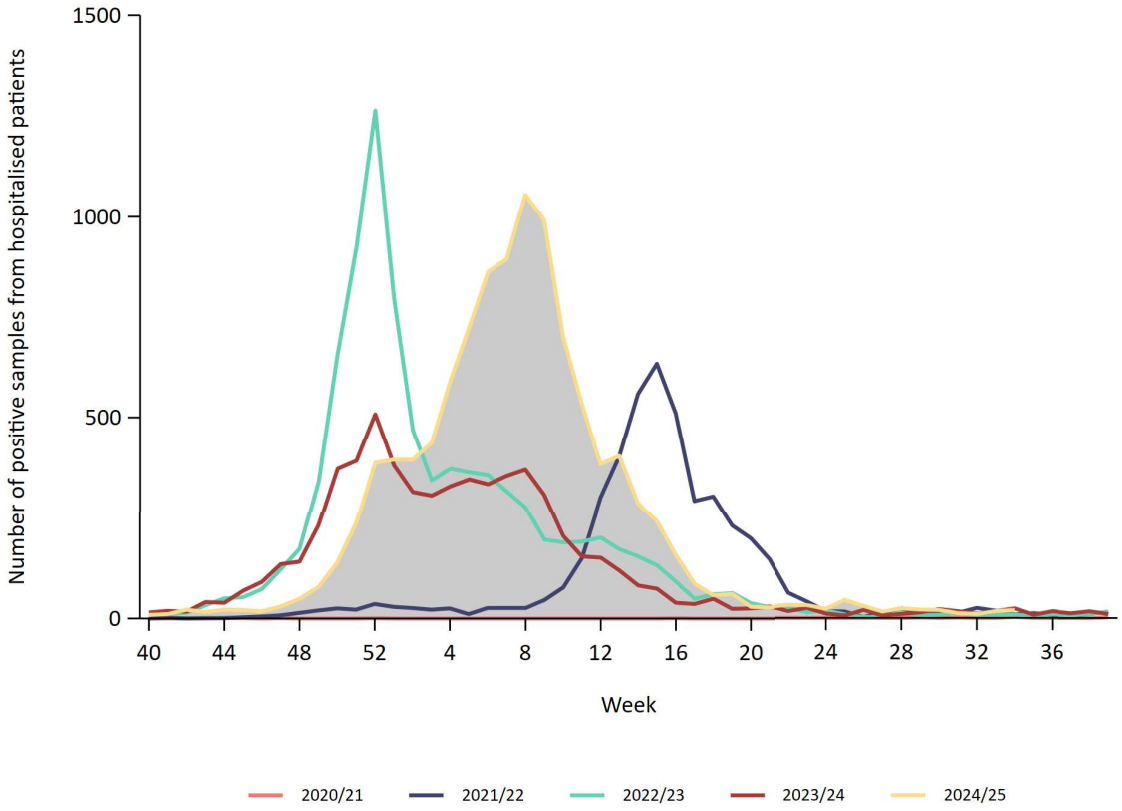

Figure 25. Weekly number of PCR analyses positive for influenza viruses among hospitalised patients by week and season, Norway, 28.09.2020 – 24.08.2025. Source: The Norwegian Surveillance System for Communicable Diseases laboratory database.

Table 5. Number of PCR analyses positive for influenza A and B viruses among hospitalised patients by age group, Norway, 30Table 5.09.2024 – 24.08.2025. Source: The Norwegian Surveillance System form Communicable Diseases laboratory database

	2024-W40 – 2025-W34					
	Total		Influenza A virus		Influenza B virus	
Age group	Number of samples	Samples per 100000	Number of samples	Samples per 100000	Number of samples	Samples per 100000
0-4 years	847	308,0	647	235,2	200	72,7
5-14 years	687	109,5	364	58,0	323	51,5
15-29 years	772	74,0	531	50,9	231	22,1
30-64 years	3193	123,4	2589	100,1	543	21,0
65-79 years	3024	382,9	2895	366,5	83	10,5
80+ years	2130	787,3	2058	760,7	41	15,2
Total	10657	190,5	9088	162,4	1421	25,4

Influenza patients in intensive care units (ICUs)

Between week 40/2024 and week 20/2025, a total of 278 ICU admissions (5.0 per 100,000 inhabitants) with influenza were reported, with a peak of 32 admissions in week 8/2025. The median age of the 269 patients with information on age was 65 (lower – upper quartile 52–73)

years, and 78% of them had underlying medical risk factors for severe influenza. The median length of stay was 2 days (lower – upper quartile 1–5 days). Seventy percent of the patients received ventilatory support, and 9% died.

In comparison, 215, 203, 63, 120 and 231 ICU admissions with influenza were reported in Norway between week 40 and week 20 during the 2023-24, 2022-23, 2021-22, 2019-20 and 2018-19 seasons, respectively. This means that also influenza intensive care admissions were more numerous during the 2024-25 seasons than previously recorded.

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 40-2024 and 34-2025 there were 375 recorded influenza-associated deaths in Norway, compared to 207 (2023-24), 265 (2022-23), 131 (2021-22), <7 (2020-21), 130 (2019-20), 214 (2018-19), 415 (2017-18) and 309 (2016-17) for the same period in the preceding seasons. The total number of deaths caused by influenza is most likely underestimated by these estimates, 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. On the other hand, testing and coding practices might have changed since the COVID-19 pandemic resulting in increasing numbers for the most recent seasons. Nevertheless, the number of influenza associated deaths being greater than most previous seasons is consistent with the findings for influenza hospital and intensive care admissions, together indicating that the 2024-2025 influenza season was quite severe.

Vaccine distribution and coverage

In the 2024/25 season as of 21 May 2025, a total of 1.56 million doses of influenza vaccine have been distributed, both from NIPH and from other wholesalers. 1.1 million of these were distributed by NIPH to the municipalities and hospitals specifically intended for persons in medical risk groups and health care workers (HCW) involved in direct patient care. The number of distributed doses is approximately the same as in the 2023/24 season, and so was the estimated number of administered doses (1 million doses). Approximately 100,000 doses of the doses for the vaccination programme were discarded in the municipalities after the season. (Figure 26).

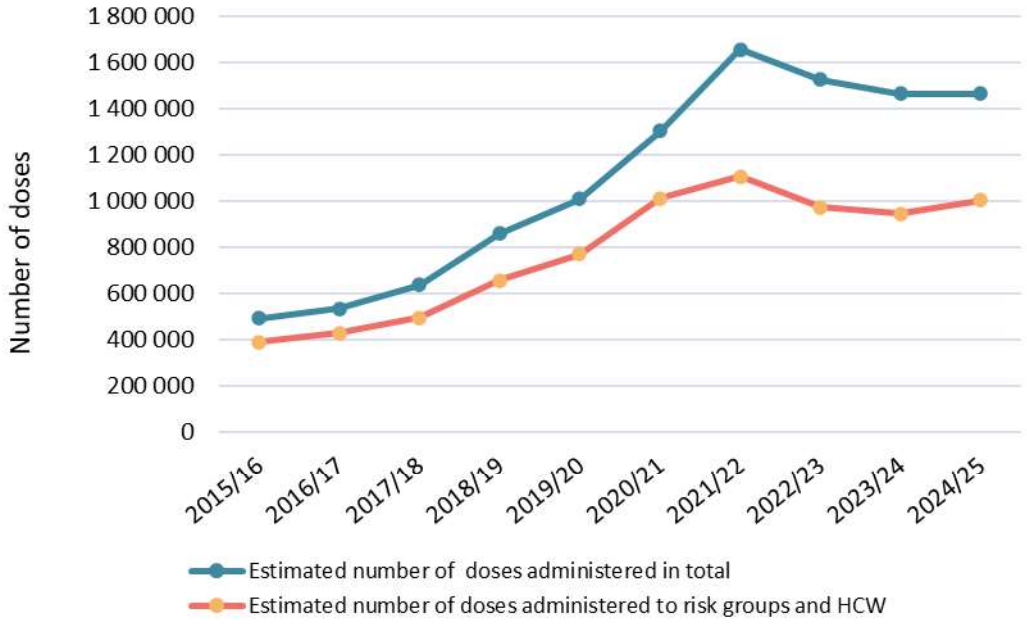

Figure 26. Influenza vaccine doses distributed in Norway, September 2015 through January 2025. HCW = Health Care Workers.

According to the Norwegian Immunization Registry SYSVAK (SYSVAK), at least 66 percent of the population above 65 years of age received an influenza vaccine this season (Figure 27).

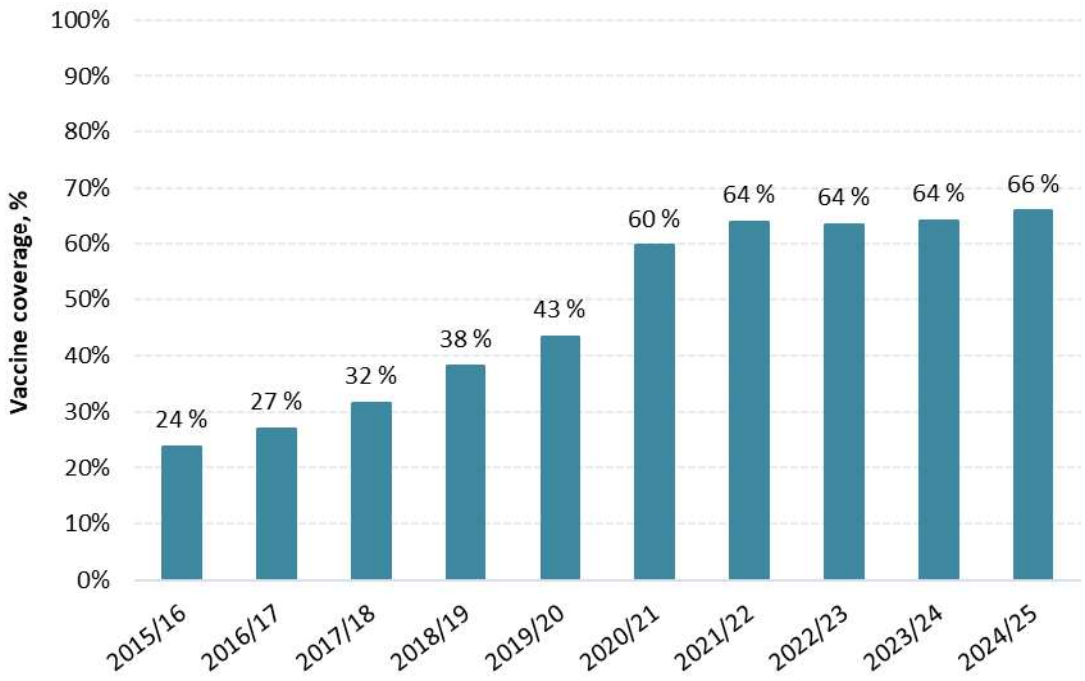

Figure 27. Vaccination coverage among residents above 65 years in Norway, 2015/16 season through to 2024/25 season as of May 2025.

Approximately 91% of the doses accounted for (distributed doses – reported discarded doses) are so far registered in SYSVAK. This is probably due to a combination of underreporting and technical issues. Due to this, the vaccination coverage is also estimated by survey data from Statistics Norway for the various risk groups and HCWs. However, these estimates will not be available until October 2025.

Vaccination timing

Vaccines for the influenza immunisation programme were sent out from week 40 to municipalities and health enterprises. Around the same time, vaccines also became available for the private market in pharmacies. Vaccination increased very rapidly to a peak of 300 000 vaccinations in week 43 and then gradually declined to a few thousand doses weekly from week 52 (Figure 28). 95% of those vaccinated received their vaccine within week 48, with expected protection within week 51, i.e. before the influenza outbreak started. 99% of the doses were administered before the epidemic threshold was passed in week 2.

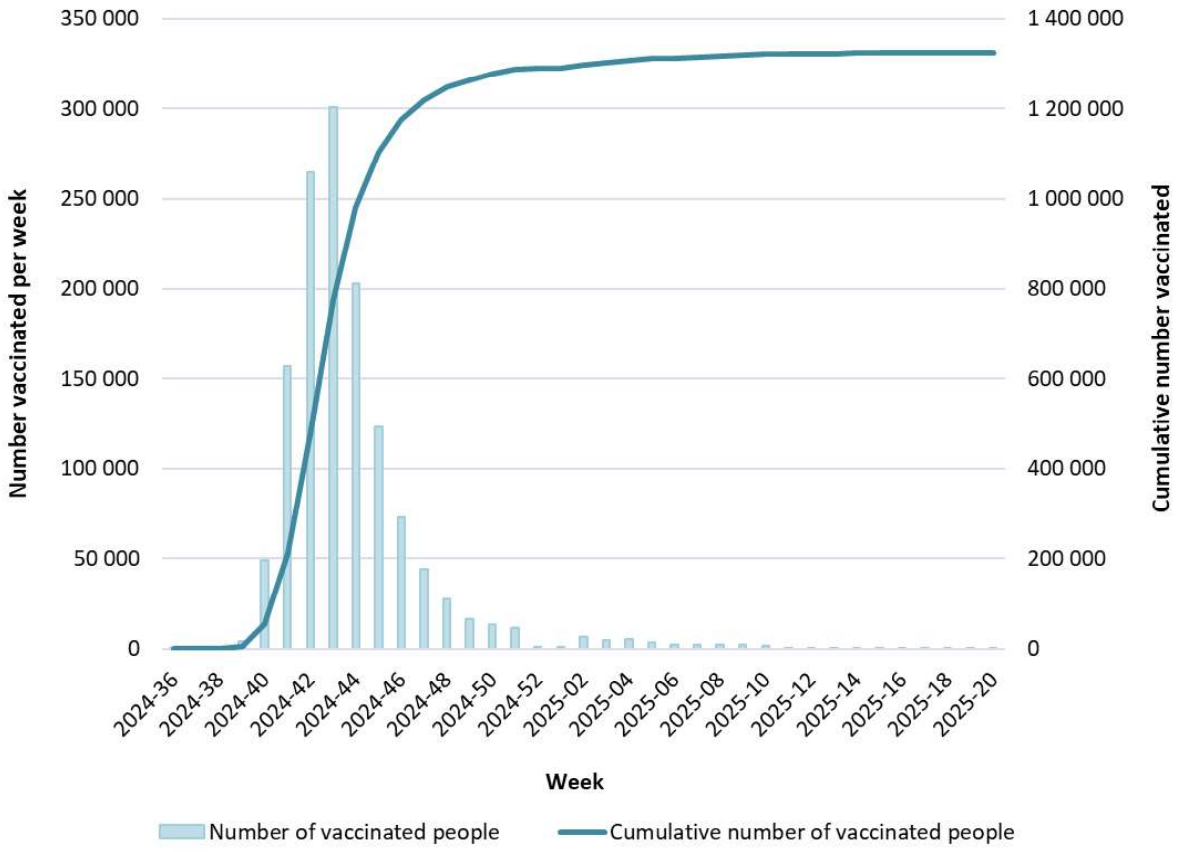

Figure 28. Number of vaccinated people per week and cumulatively in the 2024-25 season, 1. September 2024 – 18. May 2025. Source: National Population Registry and Norwegian Immunization Registry, SYSVAK.

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. In Norway, there have since 2020 been five outbreaks of avian influenza H5 in commercial poultry flocks, three in small poultry backyard flocks, and two in municipal parks with captive birds (1). During autumn 2024 and through 2025 so far, the Norwegian Veterinary Institute has reported scattered detections of HPAIV H5N5 genotype EA-2021-I, mainly in gulls, corvids and raptors and most of them in the northern parts of Norway, particularly in Finnmark county (2, 3). There have in this period been three detections of H5N5 in wild mammals; in a lynx and in an otter euthanized due to illness, and in a red fox carcass. During summer 2025, there has been an increase in detections of HPAIV H5N1 in seagulls in the northern part of Norway, mainly due to an outbreak of the same virus variant (genotype EA-2022-BB) that caused the high mortality of seabirds, primarily seagulls, in summer 2023. This outbreak is still ongoing at the time of reporting. In addition, H5N5 have for the first time been detected in polar foxes on the archipelago of Svalbard (4).

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 (5).

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

Available here: https://www.fhi.no/sv/influensa/influensaovervaking/who-rapporter/

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Division for Infection Control

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Appendices

Description of the surveillance and monitoring components

Influenza-like illness

Norwegian ILI surveillance data is provided by The Norwegian Syndromic Surveillance System (NorSySS), 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 contributes with clinical data and weekly samples for the integrated surveillance of respiratory viruses in Norway. The sentinel system has been reactivated after the COVID-19 pandemic 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.

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) 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. Sequences are shared in the GISAID EpiFlu database.

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

Since July 2024, the surveillance of hospitalisations with influenza has temporarily relied on the MSIS laboratory database (described under "Comprehensive virus surveillance"). Information on the requisitioners of the samples for influenza viruses is used for identifying samples taken from patients who were hospitalised at the time of sampling. Historical data is available from the autumn of 2020 onward. The system is well suited for monitoring trends in weekly numbers of positive tests from admitted patients but cannot be used for assessing the actual number of patients hospitalised due to influenza. No information is available on admission or discharge dates, clinical picture, treatment or status at discharge.

Influenza patients in intensive care units

In the 2016-17 and 2017-18 seasons, the Norwegian Intensive Care Registry (NIR) 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, NIR 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 NIR. Since the 2018-19 season, an electronic form has been used. In the season 2024-25 the NIPH receives anonymized, aggregated data on a weekly basis for surveillance purposes.

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

In August each year the National Influenza Seroepidemiology Programme 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. Sera are tested by the haemagglutination-inhibition (HI) assays 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.

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 84-88 of the doses distributed (adjusted for the number of discarded doses). Coverage estimates from SYSVAK are therefore considered minimum estimates.

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