REPORT

2024

NORWAY:

Interim influenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2024/2025

February 2024

NIPH
Norwegian Institute of Public Health

folkehelseinstituttet

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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

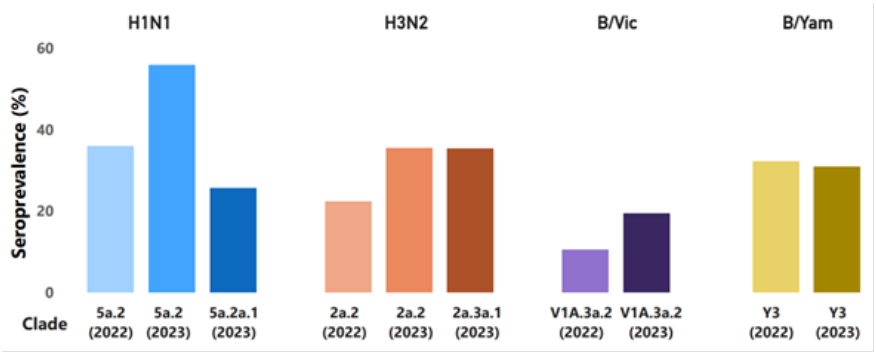

Figure 1. Seroprevalence in Norwegian sera from August 2022 and 2023, against relevant influenza variants.

In the section in this report on Population immunity against recent influenza viruses, we show that the proportion of sera with protective levels of antibodies (seroprevalence) against H1N1 clade 5a.2 increased from 2022 to 2023, but that considerably fewer had antibodies against the newer 5a.2a.1 clade. This also shows that human antibodies discriminate between these groups.

While seroprevalence against H3N2 clade 2a.2 also increased from 2022 to 2023, there was no reduction in seroprevalence against the new 2a.3a.1 clade. Thus, our sera did not discriminate between these H3N2 virus groups.

Finally, seroprevalence against B/Victoria-lineage clade V1A.3a.2 increased from 2022 to 2023, while it remained stable against B/Yamagata-lineage virus over the same period.

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

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The 2023-2024 influenza season, Norway

Summary

- The preceding 2022-2023-influenza outbreak developed early, with a sharp peak during Christmas/New Year. This peak was dominated by influenza A(H1N1) viruses with subclades 5a.2a and 5a.2a.1 cocirculating. There were two smaller subsequent peaks; in week 6 consisting of a mixture of A(H1N1), A(H3N2), and B/Victoria; and in week 12 consisting of B/Victoria-lineage viruses.
- Following the A(H1N1) dominated 2022-2023 season, there was an increase in seroprevalence against A/Victoria/2570/2019 of the 5a.2 clade, although immunity was lower against the 5a.2a.1 clade. The increased seroprevalence was particularly prominent in the 0-4 years age group, where we in 2022 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 current season is also A(H1N1) dominated however the early clear dominance has been challenged in recent weeks by an increase in A(H3N2) prevalence. Influenza B viruses have been much less common, all that have been typed are B/Victoria-lineage. Like the preceding season the timing of the current influenza season also shows an early peak during the Christmas period with a following decline, currently the trend is stable but elevated and we expect either a second peak or a long tail season. The Christmas peak was of clearly lower magnitude than the one of 2022-2023.
- 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 has been stable through weeks 2-4 2024.
- The numbers of hospitalisations and ICU admissions with influenza began to increase around week 44/2023, reaching a peak in week 52/2023. As of week 4/2024, 2414 hospital admissions and 85 ICU admissions have been reported, which is significantly less than in the same time period in the preceding season 2022-2023.
- 15% (234/1523) of all influenza positive samples received for surveillance have been whole genome sequenced. A(H1N1) viruses predominated early in the season with the clade 5a.2a represented by A/Sydney/5/2021 and 5a.2a.1 represented by A/Wisconsin/67/2022 and A/Victoria/4897/2022. The genetic makeup is balanced between genAH1/Sydney/5/2021 and genAH1/Victoria/4897/2022 with no clear dominance to be observed. Within the clade 5a.2s the genAH1/Sydney/5/2021 show a wide genetic variability with several clusters evolving with their unique substitutions which continue to grow in the mid-season. Within the genAH1/Victoria/4897/2022 like viruses 3 defined clusters are observed with the biggest one carrying an S85P and R113K substitutions. A(H3N2) viruses have mostly been in the 2a.3a.1 subclade (A/Thailand/8/2022 group), with a couple of subgroups of which one with additional substitutions N122D and K276E is largest and expanding. B/Victoria strains are rarely

detected in the early and mid-season of 2023/24, with the majority falling in the B/Catalonia/2279261NS/2023 subgroup.

- Vaccination coverage among risk groups younger than 65 years decreased compared to the 2022/2023 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 5 % compared to the 2022/23 season. 1.12 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 clade 2.3.4.4b continued to be detected in wild birds in Norway. During autumn 2023 there was one outbreak of H5N1 in a poultry backyard flock and no outbreaks in commercial poultry flocks. No human cases have been detected, and the risk of human infection has been assessed as very low.

Influensasesongen 2023-2024 i Norge (Norwegian summary)

Hovedbudskap

- Det foregående influensautbruddet vinteren 2022-2023 startet tidlig, med en kraftig topp rundt jul og nyttår. A(H1N1)-viruses i undergruppene 5a.2a og 5a.2a.1 sto for dette utbruddet. Deretter kom to mindre topper, én i uke 6 som var en miks av A(H1N1), A(H3N2) og B/Victoria virus, og til slutt en topp i uke 12 med B/Victoria-virus.
- I kjølvannet av 2022-2023-sesongen, med mye A(H1N1)-virus, var det sommeren 2023 en økning av andelen i befolkningen med beskyttende antistoffnivå (seroprevalens) mot A/Victoria/2570/2019(H1N1), klade 5a.2. Det var imidlertid mindre immunitet mot virus i den nyere kladen 5a.2a.1. Mest markert var økningen i immunitet hos 0-4-åringene, hvor det hadde vært veldig få immune sommeren 2022 som en følge av at det nesten ikke hadde forekommet influensa de to første årene av COVID-19-pandemien. Seroprevalensen mot H3N2-virus hadde også økt eller holdt seg på samme nivå, og det var ikke tegn til at immuniteten var dårligere mot den nyere A/Thailand/8/2022-stammen. Seroprevalens mot B/Victoria-linje virus hadde økt fra svært lave nivå sommeren 2022, trolig reflekterer dette at det var mye influensa B-aktivitet sent i 2022-2023-sesongen.
- Også denne influensasesongen har det vært mest A(H1N1)-virus, men de siste ukene har A(H3N2)-virus økt til å bli omtrent like utbredt. Influensa B-virus har vært langt mindre vanlig og alle undersøkte virus har tilhørt B/Victoria-slektslinjen. Også i denne sesongen har vi hatt en tidlig topp rundt jul og nyttår, men den var klart mindre enn på samme tid forrige sesong. Influensaaktiviteten har nå flatet ut på middels nivå og det vil vise seg om vi heretter går mot en ny topp eller en langsom nedgang.
- Andelen konsultasjoner for influensalignende sykdom i primærhelsetjenesten økte gradvis fra uke 44/2023, og krysset utbruddsterskelen i uke 49. Influensaaktiviteten nådde et toppunkt i uke 52, hvor 1,4 % av konsultasjonene fikk influensadiagnose. Aktiviteten sank deretter, og har vært stabil i uke 2-4/2024.
- Antallet sykehus- og intensivinnleggelser med influensa begynte å øke rundt uke 44/2023, og nådde en topp i uke 52. Per uke 4/2024 er det rapportert 2414 sykehusinnleggelser og 85 intensivinnleggelser, noe som er betydelig færre enn i samme tidsperiode forrige sesong 2022/23.
- 15 % (234/1523) av influensaovervåkingsprøvene mottatt på FHI har blitt helgenomsekvensert. A(H1N1)-virus har vært vanligst i begynnelsen med forekomst av både klade 5a.2 (A/Sydney/5/2021-gruppen) og subkladen 5a.2a.1 (A/Wisconsin/67/2022-gruppen inkludert en undergruppe representert med A/Victoria/4897/2022). De fleste norske virus har vært enten i A/Sydney/5/2021-gruppen eller i A/Victoria/4897/2022-gruppen, uten har én av gruppene har tatt ledelsen. Innenfor A/Sydney/5/2021-gruppen er det ganske mye genetisk variasjon med enkelte undergrupper i framvekst, mens det innenfor A/Victoria/4897/2022-gruppen er sett tre undergrupper der den største bærer aminosyresignaturene S85P og R113K i HA-genet. A(H3N2)-virus har stort sett tilhørt subklade 2a.3a.1 (A/Thailand/8/2022 gruppen), fordelt på noen få undergrupper der én med mutasjonene N122D og K276E er størst og fremvoksende. Det har vært lite B/Victoria-linje virus hittil, flertallet av de sekvenserte virusene har tilhørt B/Catalonia/2279261NS/2023-undergruppen.
- Vaksinasjonsdekningen i risikogrupper under 65 år gikk ned sammenlignet med 2022-2023-sesongen. Dekningen blant personer over 65 år holdt seg på omtrent samme nivå

(64 %) som i fjor. Antallet distribuerte doser gikk ned med 5 prosent fra sesongen før. Det ble distribuert 1,12 millioner doser til bruk for risikogrupper og helsepersonell.

- Høypatogene aviære influensa virus (HPAIV) H5N1 og H5N5 tilhørende klade 2.3.4.4b ble fortsatt påvist hos ville fugler i Norge. Høsten 2023 var det ett utbrudd av HPAI H5N1 i et hobbyfjørfehold. Det var ingen utbrudd i kommersielle fjørfebesetninger. Det har ikke blitt påvist fugleinfluensa hos mennesker i Norge. Risikoen for smitte til mennesker er vurdert som svært lav.

A look back at the preceding 2022/2023 season

Following an unusually late-peaking 2021-2022-influenza season, possibly held back by a combination of viral interference from the very large SARS-CoV-2 Omicron outbreak as well as by distancing measures against COVID-19 that were lifted in February 2022, 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 lineage and its A/Norway/25089/2022 6B.1A.5a.2a.1 sub lineage 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. 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 2023/2024 season so far

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

Influenza-like illness (ILI) in primary health care

The proportion of ILI consultations began to rise gradually from week 44/2023 and the present-season epidemic threshold, defined by the Moving Epidemic Method (MEM), was crossed in week 49 (Figure 2, 3). Influenza activity peaked in week 52 at low intensity level at with 1,4 % of consultations were due to influenza-like illness. The activity declined after week 52 and has been stable through weeks 2-4, still at low intensity level.

Comparing proportion ILI to proportion positive laboratory tests for influenza virus, ILI seems to reflect the trend of the outbreak.

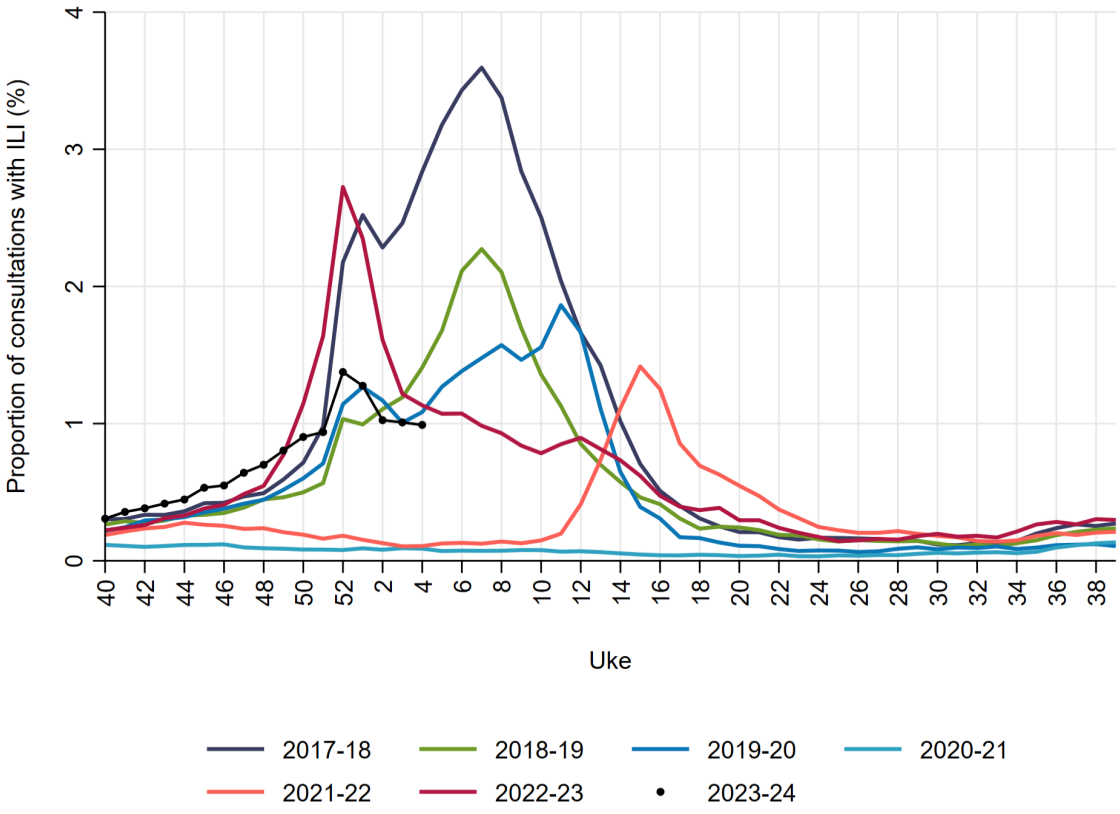


Figure 2. Weekly proportion of consultations for ILI, Norway 2023-2024 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the six previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH.

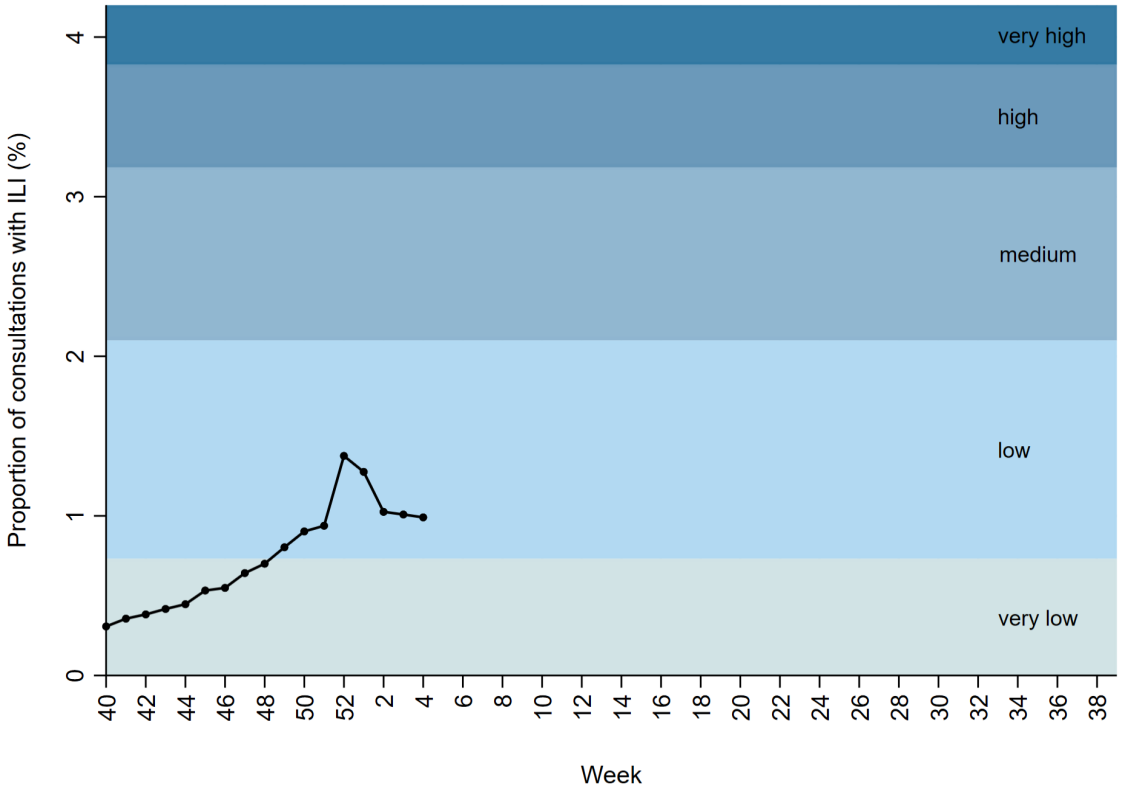


Figure 3. MEM intensity levels, Norway 2023-2024 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSyss with data from KUHR, NIPH.

Influenza hospitalisations based on registry data

Between 2023-w40 and 2024-w04, 2414 (44.0 per 100 000 inhabitants) new hospital admissions with influenza, based on diagnosis code for acute respiratory infection and positive influenza test, were reported, with a peak of 399 new admissions in week 52/2022 (Figure 2). The median age of the patients was 68 years, and 48 % (1161) of the admissions were among females. The admission rates were highest in the age groups 65-79 and 80+ years, followed by children aged 0-4 years (Table 1). The dominance of influenza A viruses was reflected in the admissions; however for the few admissions with influenza B, mostly children and almost no elderly patients were admitted, reflecting the different age profile in the virological surveillance (Table 1; see "Laboratory confirmed influenza: Virological surveillance" for more information). Thirty-seven percent of all patients hospitalised with influenza were vaccinated ≥14 days before testing positive for influenza virus.

In comparison, in season 2022-2023, the beginning of the influenza epidemic was more intense and had several peaks, with the main peak in 2022-w52 (915 new admissions). By week 2023-w04, 3919 admissions had been reported.

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 6 seasons for which data are available, the 2023/24 season started earlier and had a higher total number of

admissions before the end of 2023, than for 5 out of the 6 previous seasons (figure 4). However, the incidence remained on a lower level compared to the 2022/2023 season. For ages above 15 years the incidence more closely resembles that of the pre-pandemic seasons. In comparison to the previous 6 seasons for which data are available, the peak in 2023-w52 was higher than the first peaks seen in the 2018-19 and 2019-20 seasons, and of equal size compared to the first peak of the 2017-18 season (Figure 4). This was, however, not the case for all age groups (Figure 5).

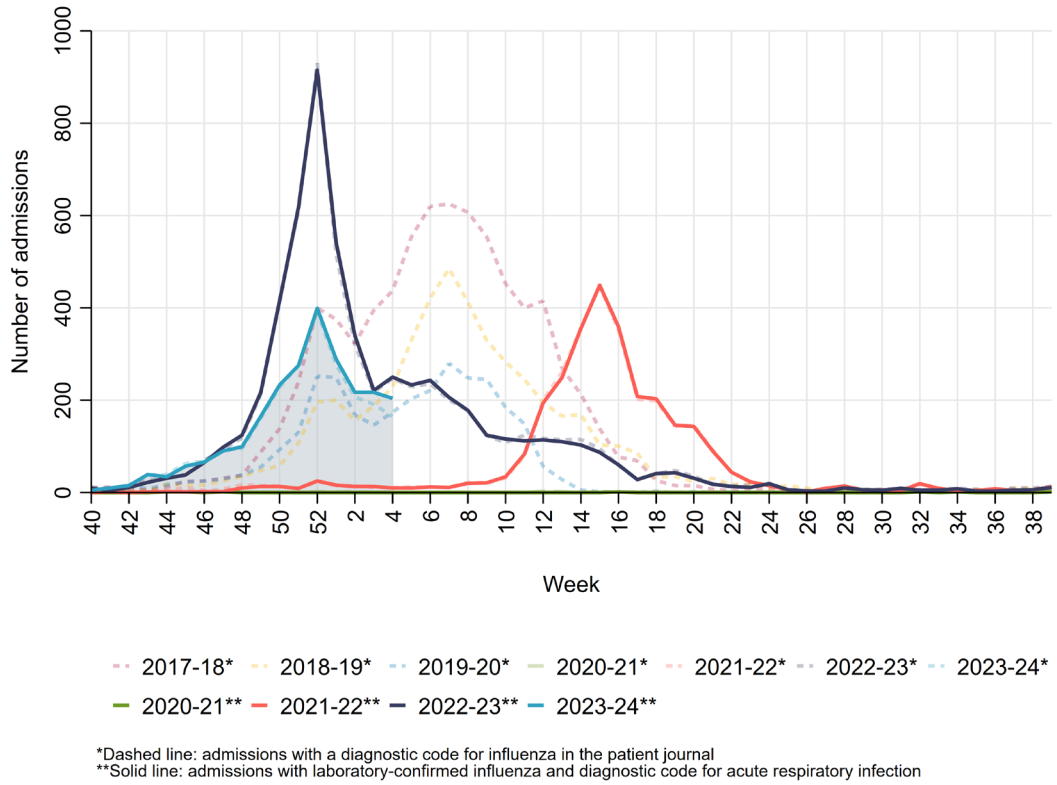
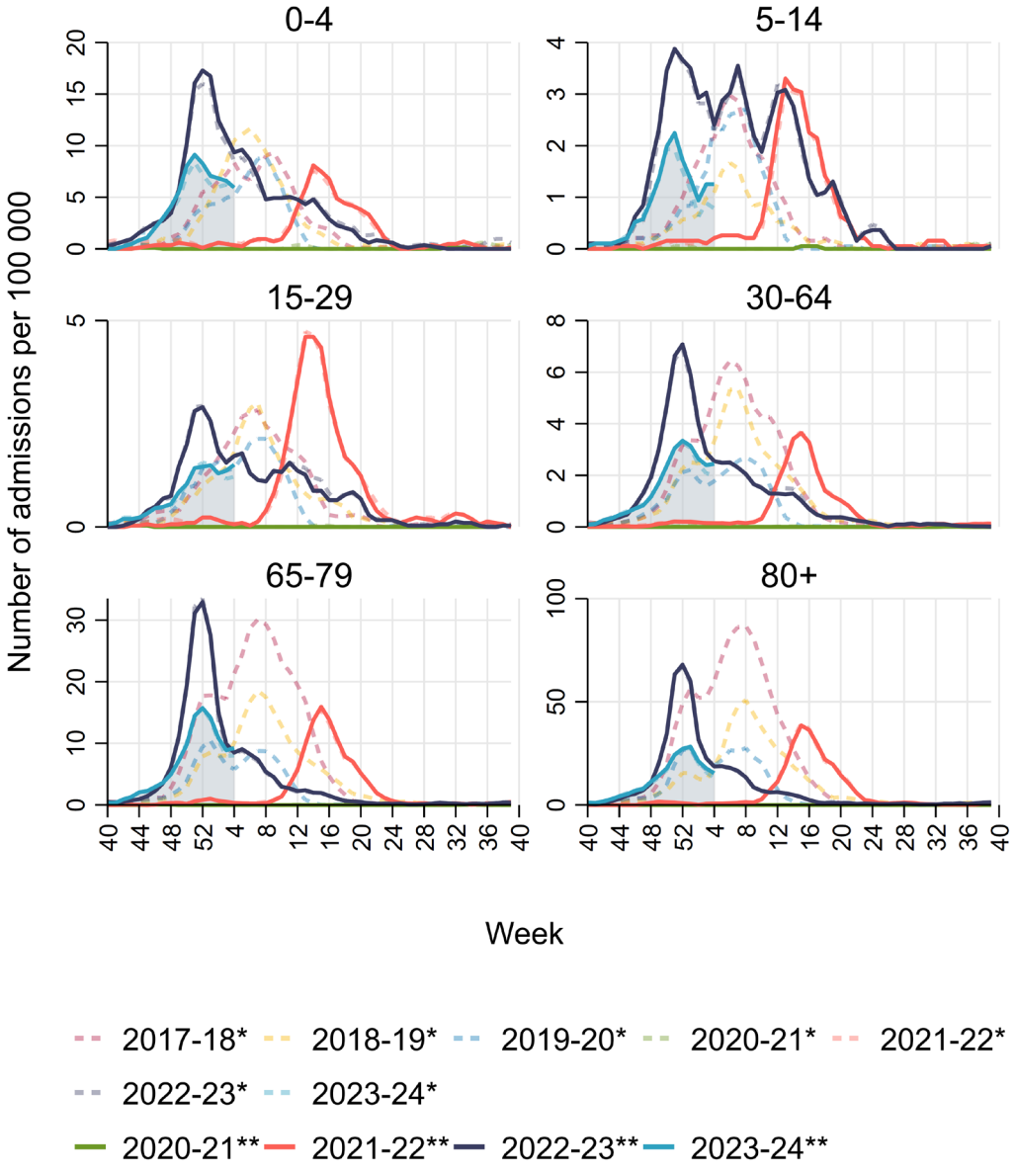


Figure 4. Weekly number of new hospital admissions with influenza by week and season, Norway, 2 October 2017 – 28 January 2024. Source: The Norwegian Emergency Preparedness Registry (Beredt C19) with data from the Norwegian Surveillance System form Communicable Diseases laboratory database and the Norwegian Patient Registry.

Table 1. Number of new hospital admissions with influenza by age group and influenza virus type, Norway, 2 October 2023 – 28 January 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. Note that the influenza type was not reported for all admissions.

	2023-w40 – 2024-w04					
	Total		Influenza A		Influenza B	
Age group	Admissions	Admissions per 100000	Admissions	Admissions per 100000	Admissions	Admissions per 100000
0-4 years	191	68.8	178	64.1	12	4.3
5-14 years	96	15.0	86	13.5	10	1.6
15-29 years	134	13.0	121	11.8	10	1.0
30-64 years	650	25.7	619	24.4	19	0.7
65-79 years	830	108.5	810	105.9	5-9	-
80+ years	513	208.2	501	203.4	1-4	-
Total	2414	44.0	2315	42.2	59	1.1



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

Figure 5. Weekly number of new hospital admissions with influenza by week and season, Norway, 2 October 2017 – 28 January 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 patients in intensive care units

Between 2023-w40 and 2024-w04, a total of 85 patients (1.5 per 100 000 inhabitants) were admitted to ICU with confirmed influenza, with a peak of 17 patients admitted in week 52. The median age of the patients was 60 years, and 46 % (39) were female.

In comparison, 143 patients were admitted to ICU with influenza in Norway between 2022-w40 and 2023-w04.

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 40-2023 and 4-2024 there were 100 recorded influenza-associated deaths in Norway, compared to 165 (2022/23), 6 (2021-2022), <5 (2020-2021), 39 (2019-2020), 35 (2018-2019), 119 (2017-2018) and 178 (2016-2017) for the same time period in the preceding seasons. The highest weekly rate of influenza-associated deaths during 2023/24 so far occurred in week 51. 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.

Laboratory confirmed influenza: Virological surveillance

Altogether, 127,081 patients in Norway were tested for influenza during weeks 40/2023-4/2024, resulting in 9,532 recorded detections of influenza A virus (94% of the influenza detections) and 609 influenza B virus (6 % of influenza detections) (Figure 6, Table 2).

Of these, 1,365 influenza A and 247 influenza B positive specimens have so far been referred to the NIC for further identification and characterisation. Among these 1,343 type A viruses were subtyped (781 H1(58 %) and 562 H3 (42 %). Two type A virus specimens were too weak for successful subtyping and 11 could not be confirmed as influenza A in the NIC. Two specimens contained both A(H1) and A(H3) viruses. All 229 lineage-typed influenza B viruses belonged to the B/Victoria/2/1987 lineage, 2 were confirmed as influenza B but contained too little viral RNA for lineage determination, and 11 initially influenza B positive specimens could not be verified in the NIC.

In addition to this, primary testing laboratories have identified 1,067 type A viruses as H1 and 26 as H3, of which 216 H1 and 1 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 and until reaching a peak in weeks 52/2023. This peak was, however, considerably lower than the 2022-2023 New Year peak; with 16 % influenza positives versus approx. 25 % one year earlier. There was a marked drop in the two first weeks of January, after which the proportion of influenza positives have stabilised or even increased slightly (Figure 4, 6). We consider intensity to be at medium level when the positivity rate in the overall national testing is between 10 and 20 %.

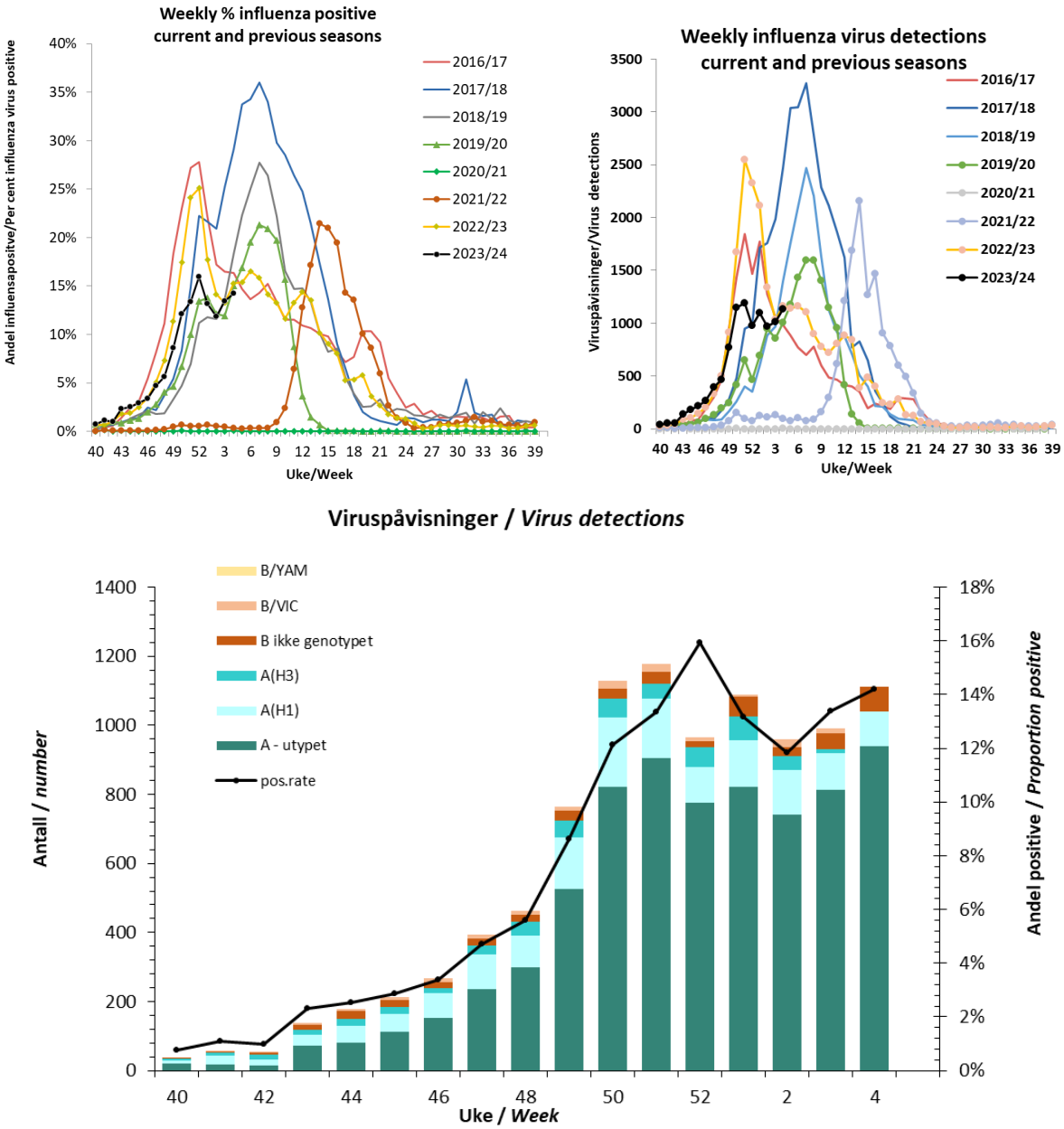


Figure 6. Laboratory detections, Norway 2022-2023. Upper left-hand panel: Weekly proportion of influenza virus positive specimens, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. Seasons impacted by Covid-19 are marked with symbols.
Lower panel: Weekly number of the different influenza viruses, displayed as stacked bars.

Type A viruses have been in strong majority over type B throughout the period. Among the type A viruses influenza A(H1N1) viruses were in clear majority in the beginning, but the proportions of subtype H1 and H3 were gradually evening out through late November and December an there is no sign that one subtype is taking predominance (Figure 7). Influenza B viruses have

been exclusively B/Victoria/2/87-lineage. 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.

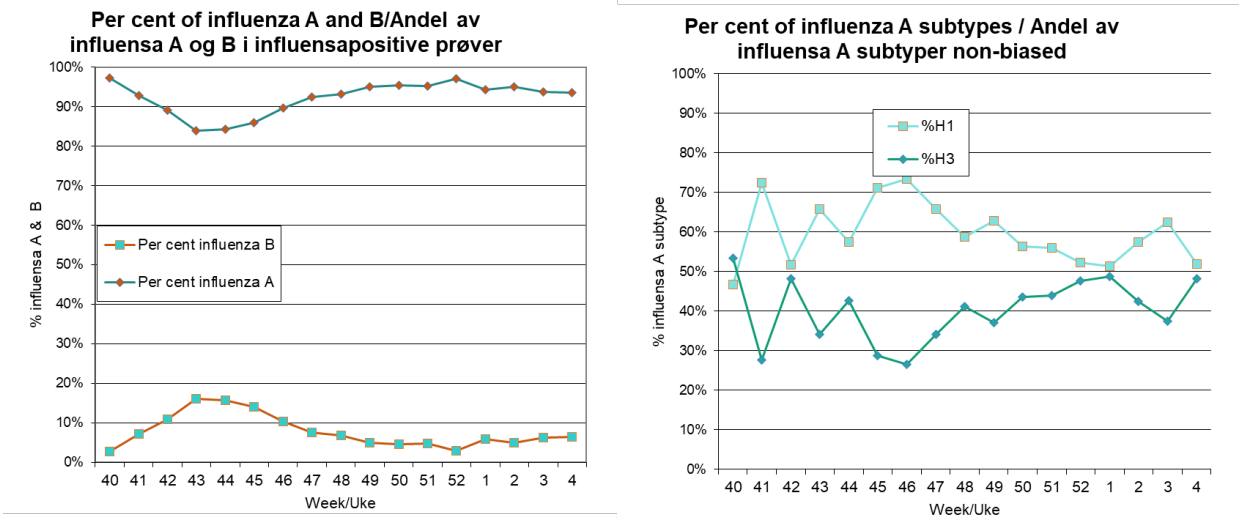


Figure 7. Influenza virus detections since week 40/2022, proportions per type A and B (left panel) and influenza A subtypes H1 and H3 (right panel). Only viruses tested for both subtypes are counted in the subtype analysis.

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

Pre-season seroprevalence and age distribution of viruses detected

In figure 8, 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.

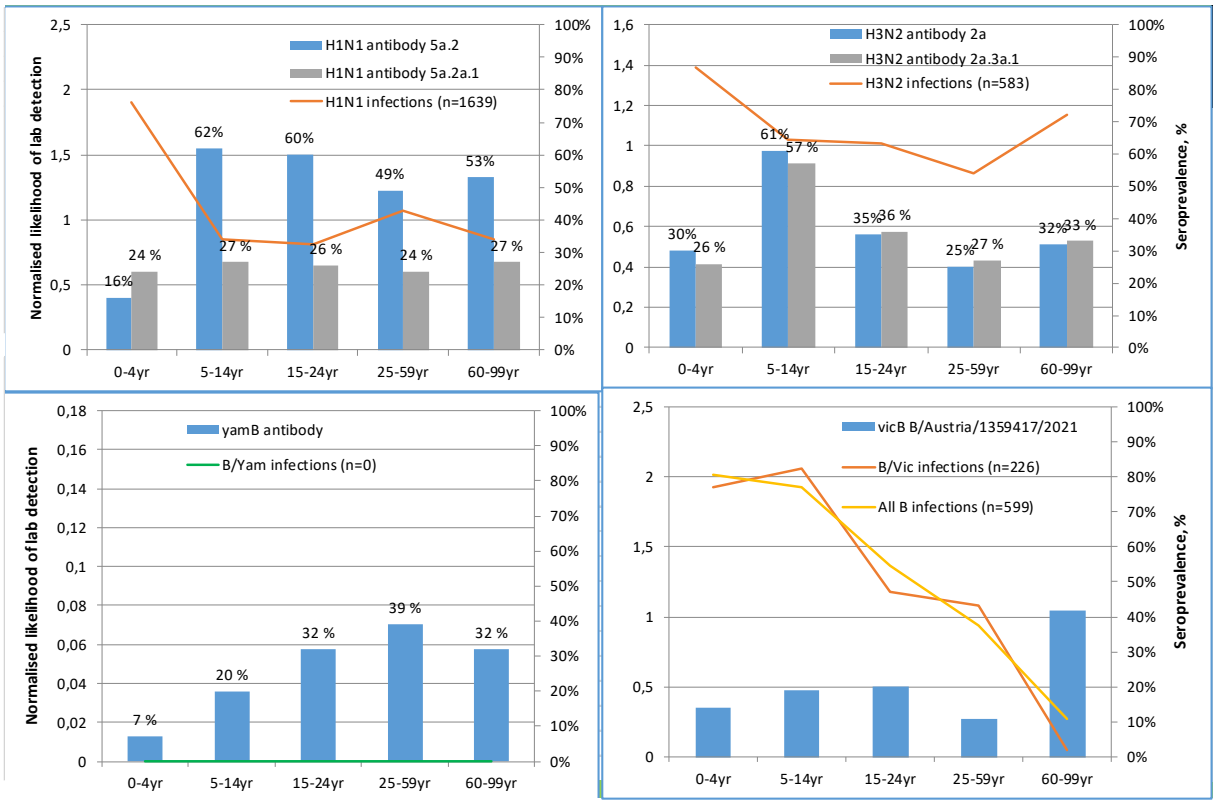


Figure 8. Prevalence of protective antibody to various influenza viruses in August 2023 (% seropositive, bars) and the age distribution of the corresponding influenza viruses in the 2023/2024 influenza season (up to week 4/2024, numbers of subtype/lineage detections per population in age group, normalised 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 suppressed incidence of infection. The correspondence between recorded incidence of A(H3N2) infections and pre-season seroprevalence is less clear. For influenza B/Victoria-lineage, children are twice as likely as the general population to get this diagnosis. Of note, there is a striking lack of recorded infections in the elderly, who also have the highest seroprevalence against the B/Victoria vaccine strain.

Table 2. Weekly total number of specimens tested for influenza, proportion of specimens positive for influenza virus, and influenza virus detections per type/subtype/lineage, in Norway from week 40/2022 through week 34/2023 (sentinel and non-sentinel data combined). 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	4941	0,7 %	20	8	8	1	0	0
41	5093	1,1 %	17	27	8	3	1	0
42	5615	1,0 %	17	18	14	4	2	0
43	6150	2,3 %	73	33	14	15	8	0
44	7322	2,5 %	81	52	23	23	6	0
45	7661	2,9 %	111	60	19	22	9	0
46	7979	3,4 %	154	72	17	17	11	0
47	8415	4,7 %	237	102	28	18	12	0
48	8353	5,6 %	301	94	42	20	12	0
49	8981	8,6 %	527	157	52	27	11	0
50	9462	12,1 %	823	209	64	27	25	0
51	8900	13,3 %	905	181	44	36	22	0
52	6120	15,9 %	776	110	61	17	12	0
1	8354	13,2 %	823	139	73	56	8	0
2	8222	11,8 %	747	134	45	25	23	0
3	7534	13,4 %	821	109	17	48	15	0
4	7978	14,2 %	960	99	2	73	0	0
Total	127081		7393	1604	531	432	177	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: 9528			Type B: 609			

Sentinel-based surveillance, primary care

From week 40/2023 through week 4/2024, 1,349 geographically representative sentinel specimens have been tested, with 154 detections of influenza virus A (82 subtype H1, 40 subtype H3, and 22 not yet subtyped), and 10 influenza virus B (of which 8 were Victoria-lineage, 2 are not yet lineage identified, and none were Yamagata-lineage). In addition, 230 SARS-CoV-2, 38 RSV, 155 rhinovirus, 21 human metapneumovirus (hMPV), 32 parainfluenza virus and 26 other human coronaviruses were detected (Fig 9, Table 3).

More than half of all sentinel surveillance samples are taken from the age group 25-59 with 797 (53.3%), the next biggest representatives in this dataset are the 60+ year olds with 18.4% or

275 samples and the 15–24-year-olds with 16,1% or 240 samples. The two least represented age groups were the youngest, 0-4 years, with 76 samples (5,1%), and the 5-14 year olds with 107 samples (7.2%).

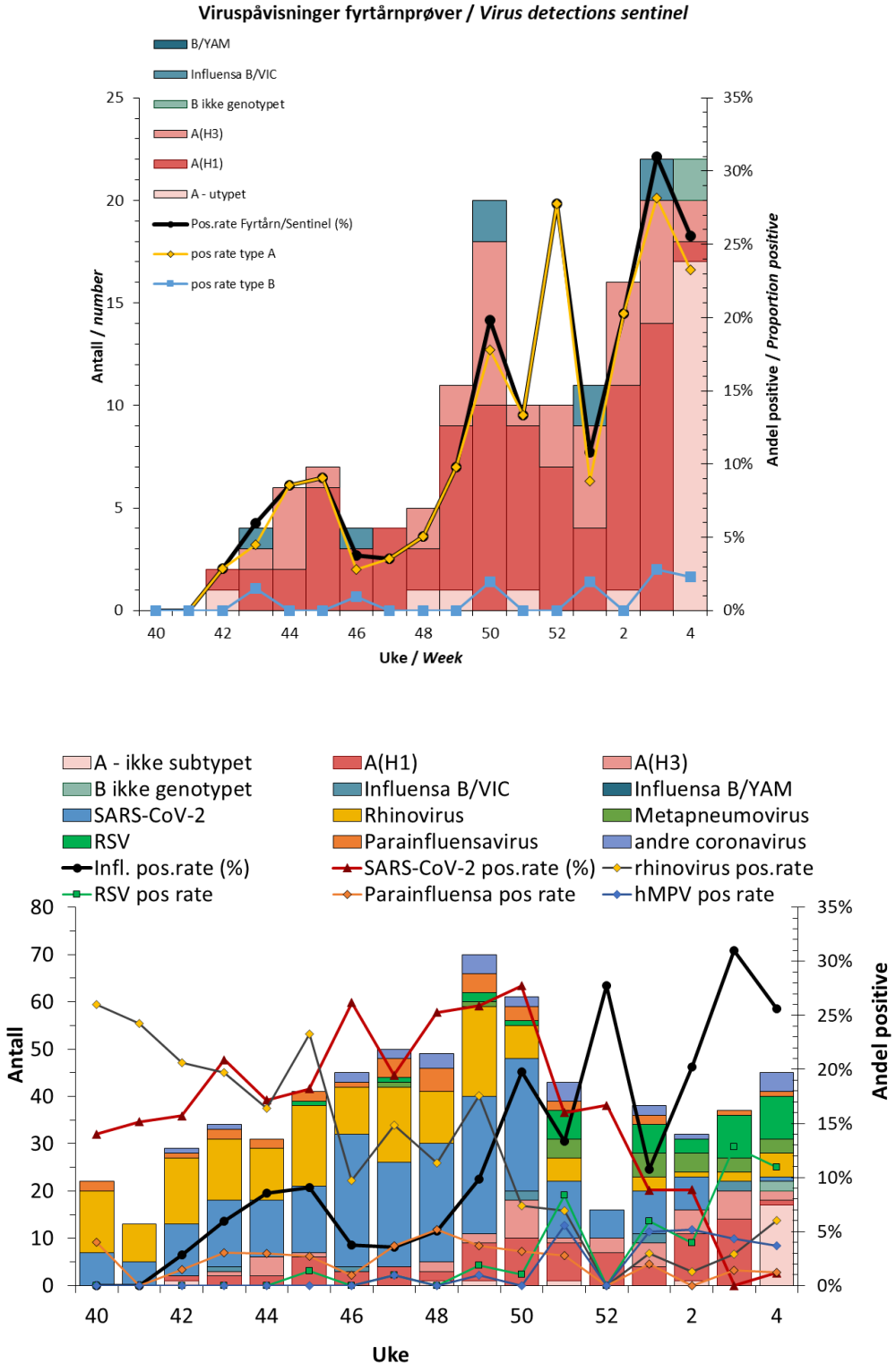


Figure 9. Weekly numbers of detections and per cent positives of influenza viruses (upper panel) and all surveyed respiratory viruses (lower panel) in the respiratory sentinel surveillance.

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

Week	Specimens tested	Influenza A - not subtyped	A(H1)	A(H3)	Influenza B untyped	B/Victoria	B/Yamagata	Influenza % positive	Influenza A % positive	Influenza B % positive	SARS-CoV-2 antall	% positive	RSV	% positive	Rhinovirus	% positive	Parainfluensa 1	Parainfluensa 2/4	Parainfluensa 3	All parainfl. % positive	Metapneumovirus	% positive	Other coronavirus	% positive
40	50	0	0	0	0	0	0	0 %	0 %	0 %	7	14 %	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	70	1	1	0	0	0	0	3 %	3 %	0 %	11	16 %	0	0 %	14	21 %	0	1	0	1 %	0	0 %	1	1 %
43	67	0	2	1	0	1	0	6 %	4 %	1 %	14	21 %	0	0 %	13	20 %	0	2	0	3 %	0	0 %	1	1 %
44	70	0	2	4	0	0	0	9 %	9 %	0 %	12	17 %	0	0 %	11	16 %	0	2	0	3 %	0	0 %	0	0 %
45	77	0	6	1	0	0	0	9 %	9 %	0 %	14	18 %	1	1 %	17	23 %	0	1	1	3 %	0	0 %	0	0 %
46	107	0	3	0	0	1	0	4 %	3 %	1 %	28	26 %	0	0 %	10	10 %	0	1	0	1 %	0	0 %	2	2 %
47	113	0	4	0	0	0	0	4 %	4 %	0 %	22	19 %	1	1 %	16	15 %	0	2	2	4 %	1	1 %	2	2 %
48	99	1	2	2	0	0	0	5 %	5 %	0 %	25	25 %	0	0 %	11	11 %	0	3	2	5 %	0	0 %	3	3 %
49	112	1	8	2	0	0	0	10 %	10 %	0 %	29	26 %	2	2 %	19	18 %	0	3	1	4 %	1	1 %	4	4 %
50	101	0	10	8	0	2	0	20 %	18 %	2 %	28	28 %	1	1 %	7	7 %	0	0	3	3 %	0	0 %	2	2 %
51	75	1	8	1	0	0	0	13 %	13 %	0 %	12	16 %	6	8 %	5	7 %	0	2	0	3 %	4	6 %	4	5 %
52	36	0	7	3	0	0	0	28 %	28 %	0 %	6	17 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	0	0 %
1	102	0	4	5	0	2	0	11 %	9 %	2 %	9	9 %	6	6 %	3	3 %	0	0	2	2 %	5	5 %	2	2 %
2	79	1	10	5	0	0	0	20 %	20 %	0 %	7	9 %	3	4 %	1	1 %	0	0	0	0 %	4	5 %	1	1 %
3	71	0	14	6	0	2	0	31 %	28 %	3 %	0	0 %	9	13 %	2	3 %	0	1	0	1 %	3	4 %	0	0 %
4	86	17	1	2	2	0	0	26 %	23 %	2 %	1	1 %	9	11 %	5	6 %	0	0	1	1 %	3	4 %	4	5 %
Sum	1348	82	40	22	82	82	0				230		38		155		0	20	12		21		26	

Genetic characterization of Influenza viruses in Norway

This season NIPH has received 1523 influenza viruses for analysis and 15% (234) of these have been characterized further with whole genome sequencing (Table 4). Furthermore, 68 viruses have so far been shared with the WHO Collaborating Centre in the UK (Worldwide Influenza Centre, Francis Crick Institute) and all 234 HA gene sequences have been submitted to the GISAID EpiFlu database as well as all NA and PA sequences that passed the quality threshold for submission.

H1N1 viruses

In the current season, the prevalence of genAH1/Sydney/5/2021-like viruses, characterized by substitutions K54Q, A186T, E224A, R259K, and K308R and belonging to clade 6B.1A.5a.2a, persists (Figure 10 and Figure 11). The viruses from this season align well with the sequences from the previous season, although they have acquired some additional substitutions. Several clusters have been identified within this genetic group, the recently growing clusters of genAH1/Sydney/5/2021-like viruses can be separated by these substitutions: P137S (8/147), V47I (9/147), T120A and K169Q (23/147), D94 and T216A (9/147). Notably, the P137S substitution was a key defining feature of the 6B.1A.5a.2a.1 viruses from last season and has been identified as an antigenic drift and immune escape substitution.

During the previous season, a prominent group of H1 viruses in Norway belonged to genAH1/Norway/25089/2022-like viruses (clade6B.1A.5a.2a.1). This season, this subgroup, defined by the substitutions P137S, K142R, D260E, and T227A, has been named the A/Wisconsin/67/2022 group. A subgroup of these viruses has also been identified: the A/Victoria/4897/2022-like viruses, characterized by an additional T216A substitution. In the latter group, a growing sizable cluster with added S85P and R113K substitutions has been observed, comprising 58 out of 147 of these viruses detected in Norway. This R113K substitution has been previously associated with a T-Cell epitope. Additionally, another cluster, constituting 22/147, is defined by an extra R45K substitution, while 6/147 viruses carry a T120A substitution.

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

While the majority of H1N1 viruses cluster similarly on hemagglutinin (HA) and neuraminidase (NA) trees, a subset of genAH1/Victoria/4897/2022 6B.1A.5a.2a.1-like +S85P viruses exhibit additional substitutions in the NA genes, namely I13V, S339L, and I241L. These variants were predominantly sampled in November and December 2023. (Figure 11).

The vaccine for the northern and southern hemispheres contains an A/Victoria/4897/2022-like (6B.1A.5a.2a.1) virus, genetically closely related to the circulating strains, and is expected to provide good protection.

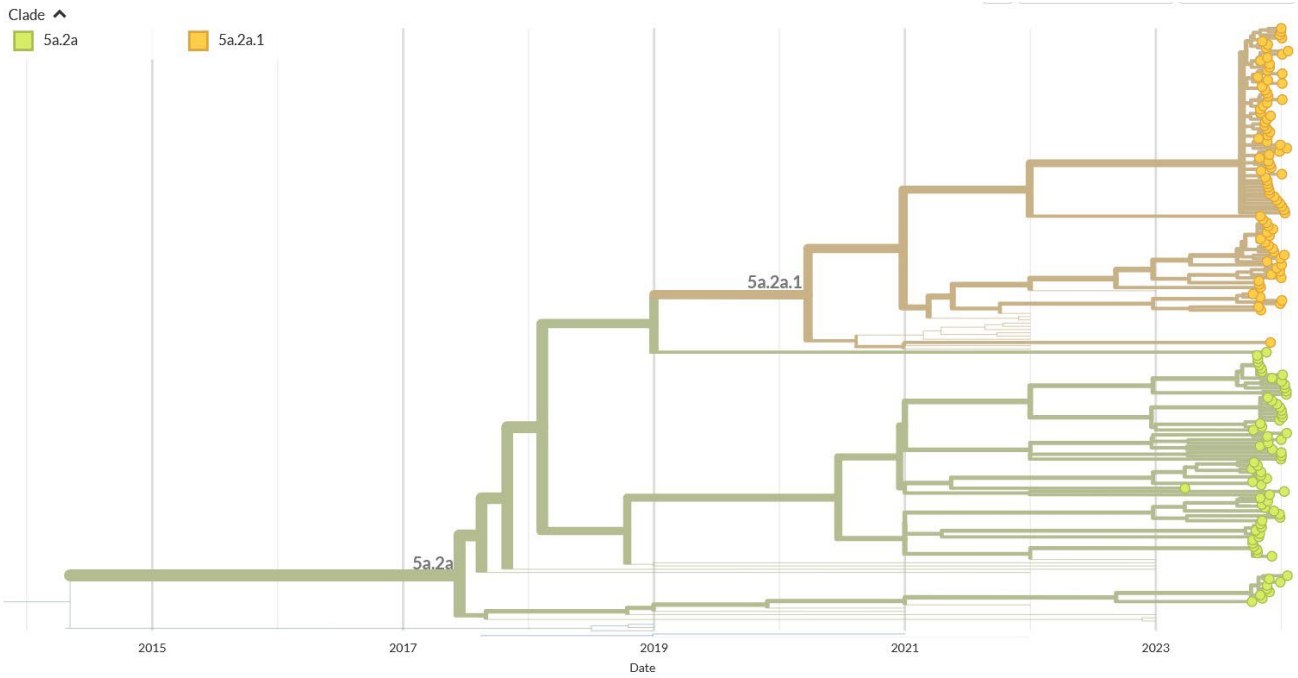


Figure 10. H1N1 NextClade phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2023 until week 5 2024, compared to the reference sequences for season 2023/24 provided by the ECDC/WHO Influenza characterization guidelines on a time axis indicating sampling date. Clades are indicated on key nodes as well as colors, the Norwegian viruses of this season are highlighted.

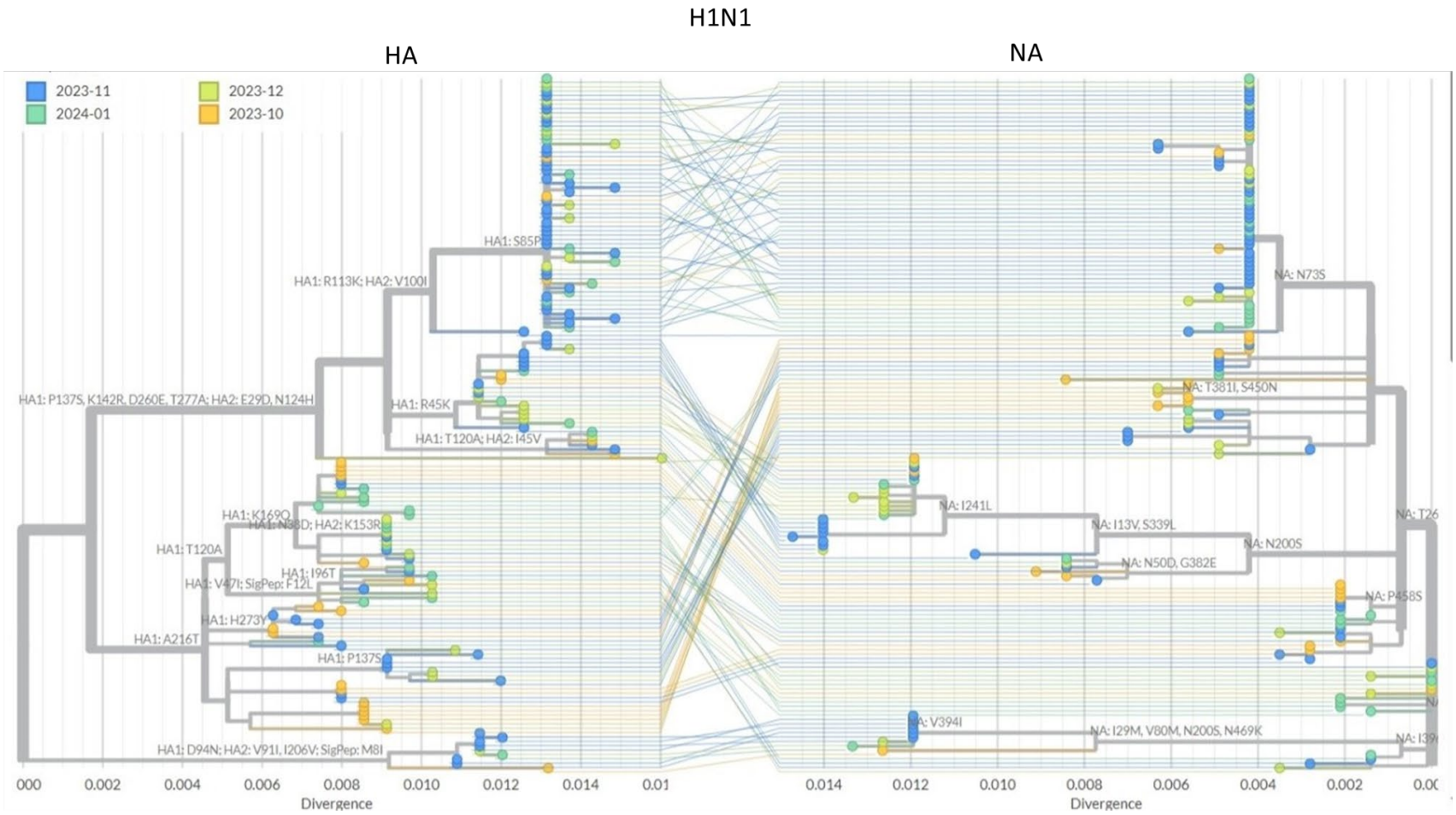


Figure 11. H1N1 NextClade phylogenetic tree of the haemagglutinin (left) and neuraminidase (right) of the H1N1 viruses from Norway season 2023/24. Clade defining amino acids indicated on key nodes. Colour of the nodes denote Sampling date by month-year.

H3N2 viruses

A(H3N2) virus continues to circulate, and the newer H3 viruses resemble the genH3/Darwin/9/2021 group of viruses, clade 3C.2a1b.2a.2a, that was less prevalent last season. This season, the genH3/Darwin/9/2021 group has further diversified into two distinct genotypes: genAH3/Finland/402/2023-like virus characterized by the substitutions E50K, D53N, N96S, I192F, belonging to clade 3C.2a1b.2a.2a.3a, and genAH3Thailand/8/2022 defined by D53N, N96S, I192F, and I140M, belonging to clade 3C.2a1b.2a.2a.3a.1. Almost all Norwegian viruses have been in the latter group.

The genAH3/Thailand/8/2022-like viruses have evolved into three distinct clusters with additional mutations. The largest cluster this season, comprising 48 out of 89 H3N2 sequences, carries additional substitutions N122D and K276E and clusters with reference strains A/Albania/289813/2022 and A/Sichuan-Gaoxin/1144/2023. This cluster has shown the most significant expansion in recent weeks. Another cluster, consisting of 34/89 sequences, exhibits an I25V substitution, with no associated reference strains. A smaller cluster with six sequences has acquired a Q173R substitution (Figure 12 and 13). Most hemagglutinin (HA) sequences cluster similarly with neuraminidase (NA) sequences (Figure 13). However, one virus, A/Norway/10243/2023, possesses an NA carrying an S331G substitution. This virus was sampled in October 2023 and could represent an earlier variant.

The vaccine component for the current northern hemisphere season remains an A/Darwin/9/2021-like virus (3C.2a1b.2a.2a). In contrast, the vaccine for the southern hemisphere in 2024 has been updated with the newer subdivided A/Thailand/8/2022-like (3C.2a1b.2a.2a.3a.1) group of viruses. Despite the genetic proximity of A/Thailand/8/2022-like viruses to the circulating strains in Norway, it is anticipated that the A/Darwin/9/2021-like component in the vaccine will confer effective protection, given the minimal genetic and antigenic differences between H3 viruses.

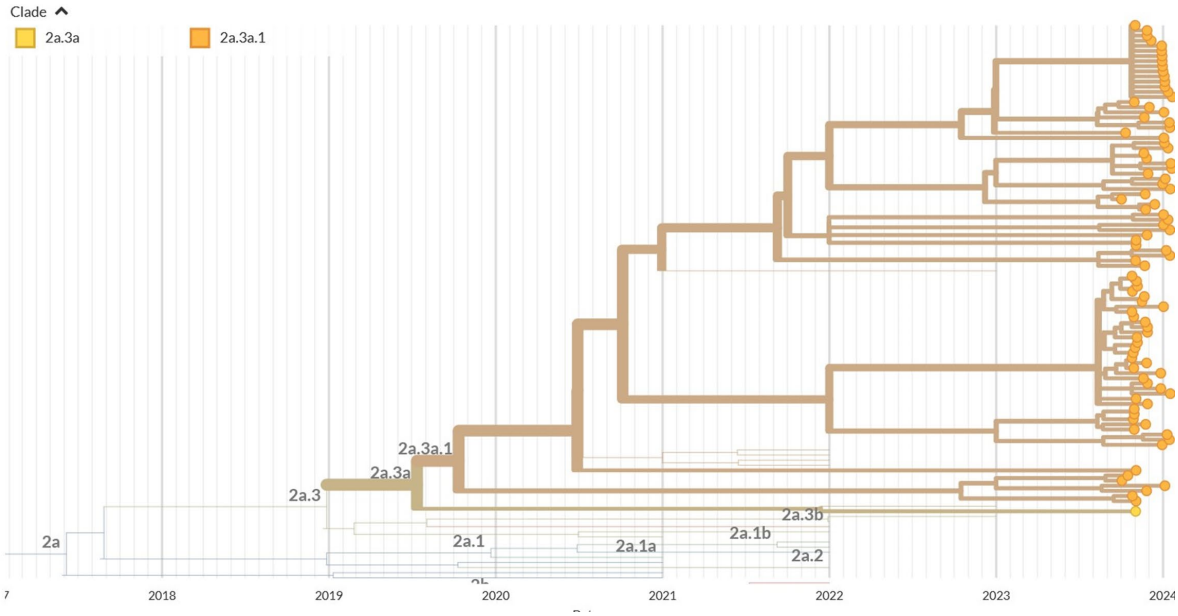


Figure 12. NextClade phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 40 2023 until week 5 2024, compared to reference sequences for season 2023/24 provided by the ECDC/WHO Influenza characterization guidelines on a time axis indicating sampling date. Clades are indicated on key nodes as well as colours, the Norwegian viruses of this season are highlighted.

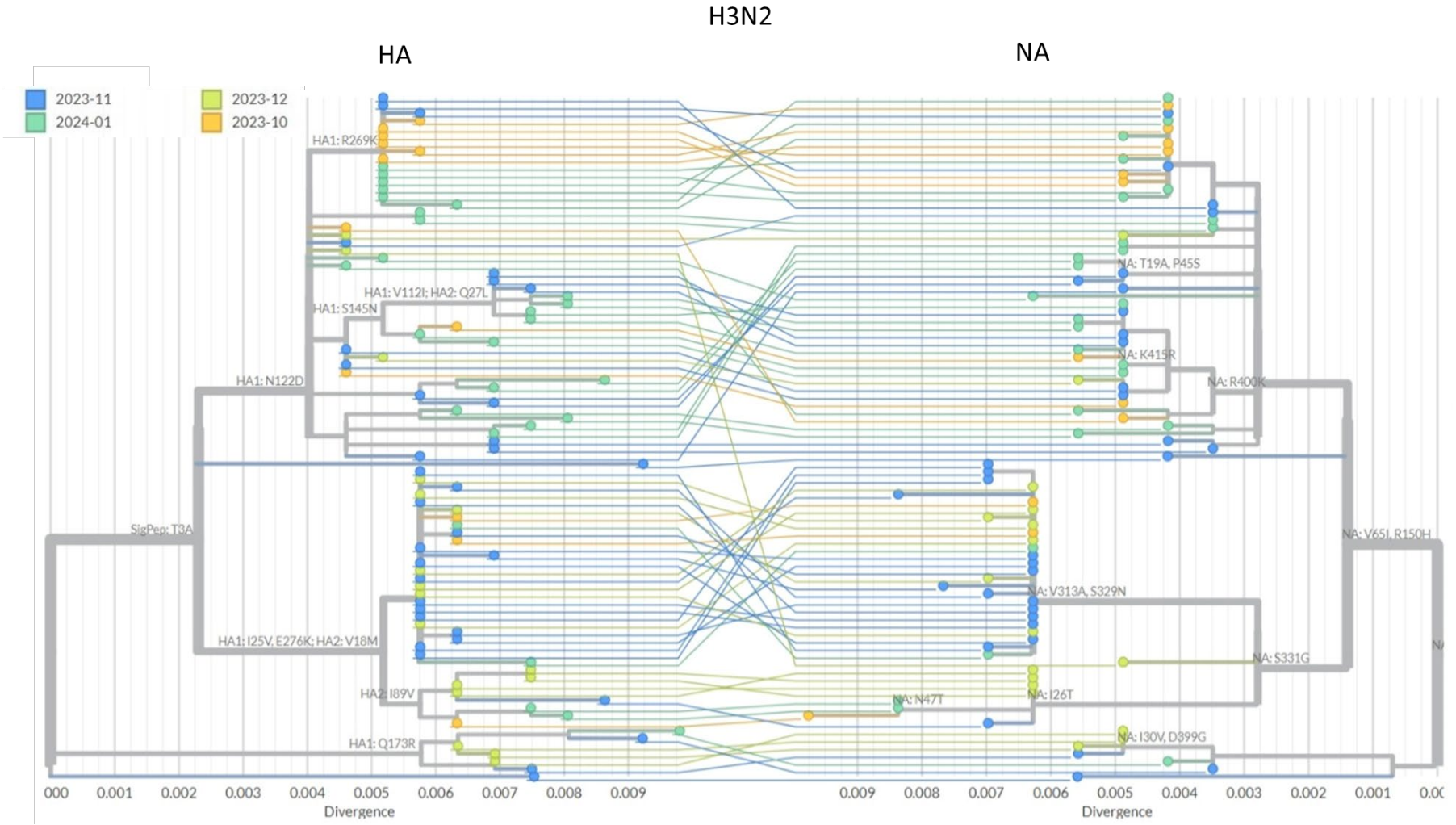


Figure 13. NextClade phylogenetic tree of the haemagglutinin (left) and neuraminidase (right) of the H3N2 viruses from Norway. Clade defining amino acids indicated on key nodes. Color of the nodes denote sampling date by month-year.

B/Victoria-lineage viruses

In the previous season, all B/Victoria viruses were categorized as genBVicB/Austria/1359417/2021-like viruses. This cluster has since undergone further subdivision, resulting in two distinct genetic clades: genBVicB/Connecticut/01/2021-like virus, characterized by the D197E substitution, and genBVicB/Catalonia/2279261NS/2023-like virus, defined by D197E and E183K substitutions. Both newly defined groups fall within the V1A.3a.2 clade.

In Norway, there has been a relatively low incidence of influenza B this season. Among the sequenced B/Victoria viruses, the majority belong to the group of genBVicB/Catalonia/2279261NS/2023-like viruses. However, there have also been a few findings of viruses belonging to the genBVicB/Connecticut/01/2021-like viruses. (Figure 14 and 15)

The vaccine component selected for the northern hemisphere for B/Victoria viruses is a genBVicB/Austria/1359417/2021-like virus. This vaccine strain demonstrates close genetic relatedness to the circulating viruses, ensuring optimal coverage against the prevailing strains.

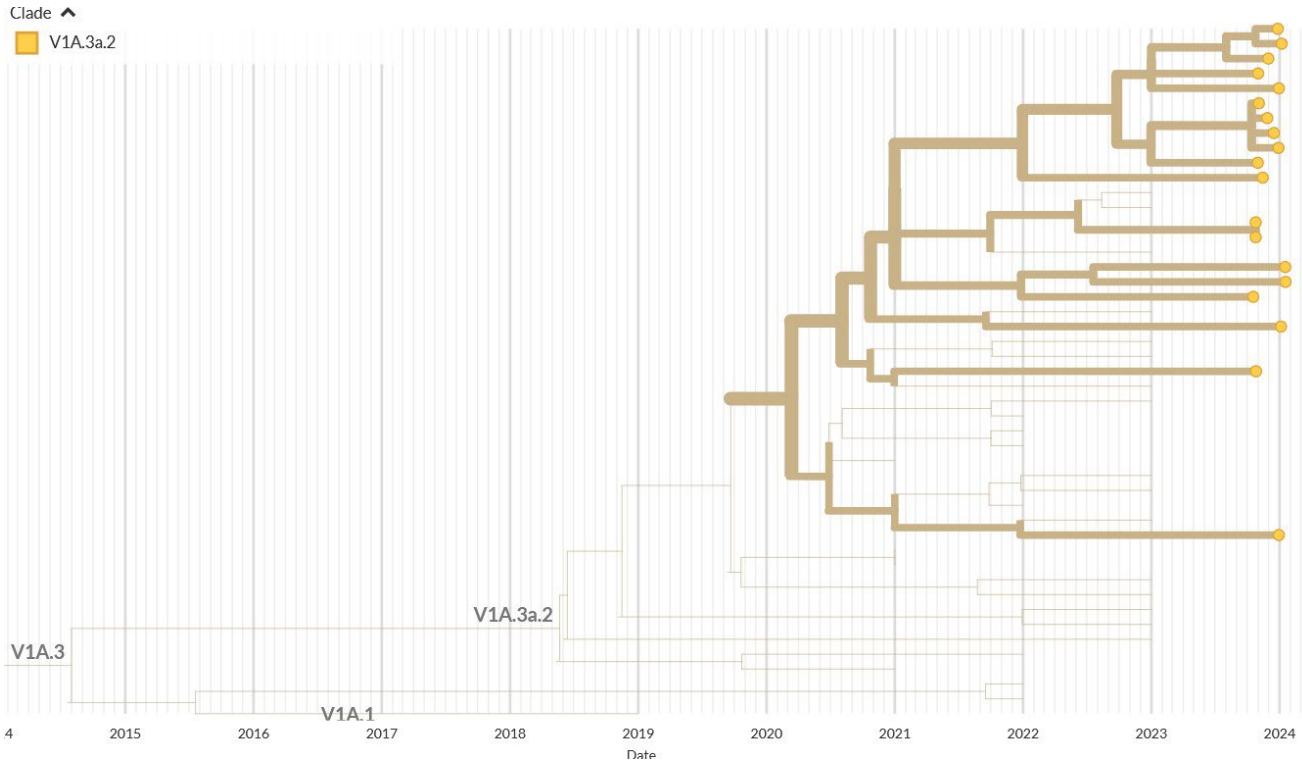


Figure 14. NextClade phylogenetic tree of the haemagglutinin of the B/Victoria viruses from Norway from week 40 2023 until week 5 2024, compared to reference sequences for season 2023/24 provided by the ECDC/WHO Influenza characterization guidelines on a time axis indicating sampling date. Clades are indicated on key nodes as well as colours, the Norwegian viruses of this season are highlighted.

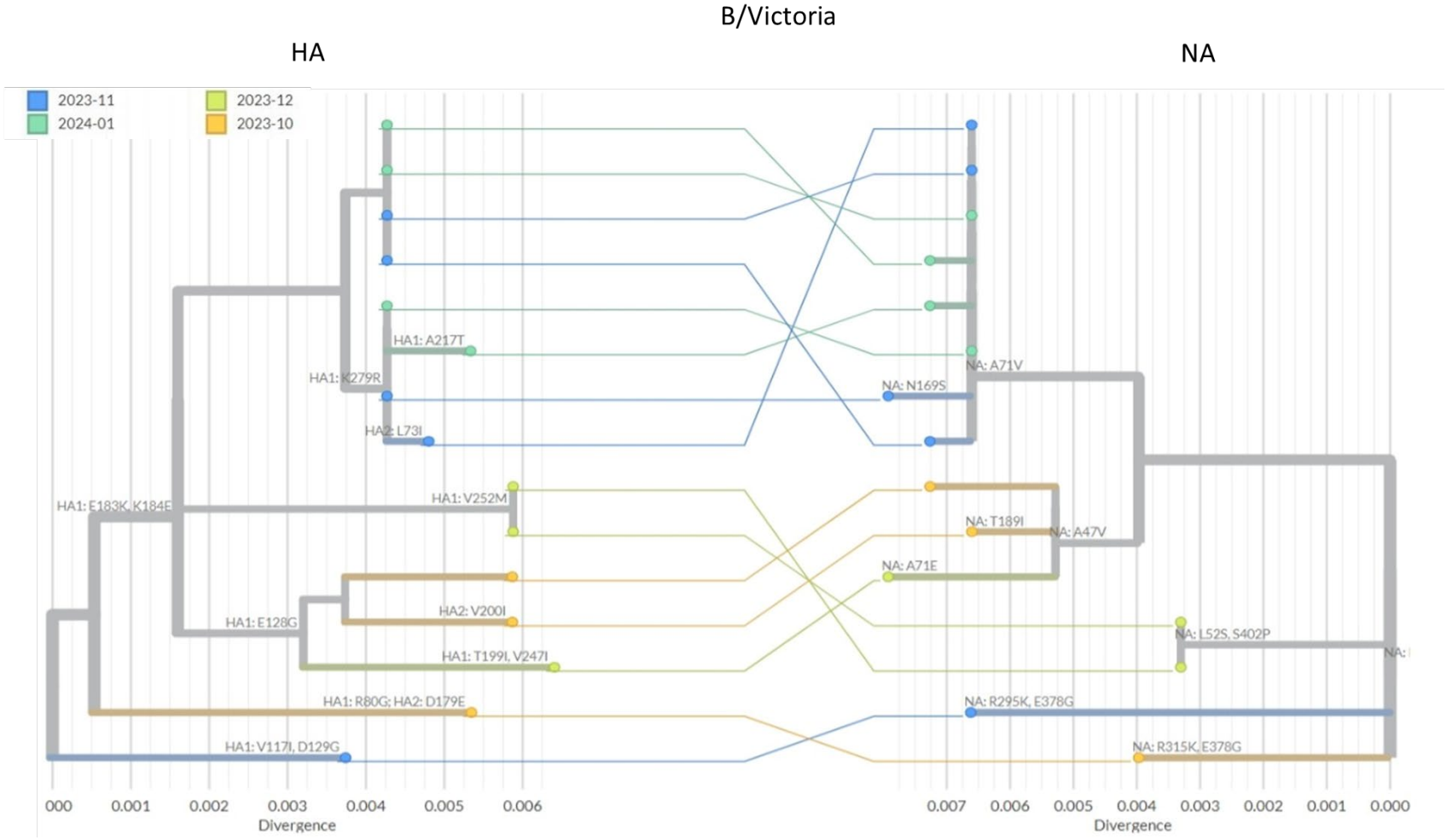


Figure 15. B/Victoria NextClade phylogenetic tree of the haemagglutinin (left) and neuraminidase (right) of the H1N1 viruses from Norway season 2023-24. Clade defining amino acids indicated on key nodes. Colour of the nodes denote sampling date by month-year.

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

Virus	2023 Oct	2023 Nov	2023 Dec	2024 Jan	Total
A/H1N1	26	73	30	31	160
6B.1A.5a.2a					
genAH1/Sydney/5/2021	73.1 %	35.6 %	40.0 %	48.4 %	
6B.1A.5a.2a.1					
genAH1/Wisconsin/67/2022	0.0 %	0.0 %	3.3 %	0.0 %	
genAH1/Victoria/4897/2022	26.9 %	64.4 %	56.7 %	51.6 %	
A/H3N2	17	35	12	27	91
3C.2a1b.2a.2a.3a					
genAH3/Finland/402/2023	0.0 %	2.9 %	0.0 %	0.0 %	
3C.2a1b.2a.2a.3a.1					
genAH3/Thailand/8/2022	100.0 %	97.1 %	100.0 %	100.0 %	
B/Victoria	5	5	5	4	19
V1A.3a.2					
genBVicB/Connecticut/01/2021	20.0 %	0.0 %	20.0 %	25.0 %	
genBVicB/Catalonia/2279261NS/2023	80.0 %	100.0 %	80.0 %	75.0 %	
Total	48	113	47	62	270

Surveillance of antiviral resistance in Influenza viruses

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

So far this season, 230 Influenza viruses have been tested for resistance (147 H1N1, 70 H3N2, 13 B-Victoria) to neuraminidase inhibitors such as oseltamivir and polymerase inhibitor Baloxavir. No resistance mutations have been detected and all viruses tested are sensitive to treatment with Tamiflu® and XOFLUZA®.

Population immunity against recent influenza viruses, August 2023

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. The main findings are shown in figure 16 in comparison to data from 2022, table 5, and summarised as follows:

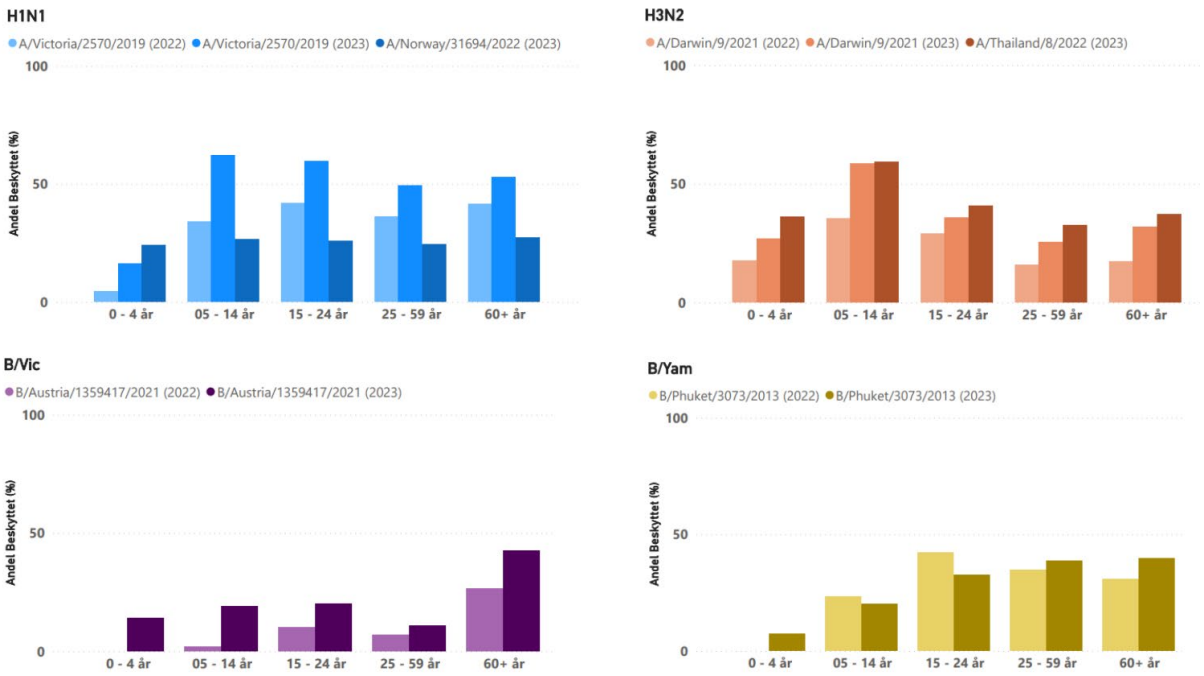


Figure 16. Seroprevalence in August 2022 and 2023 against current influenza A and B strains in various age groups. HAI was performed against A/Victoria/2570/2019 (H1N1, clade 6B.1A.5a.2), A/Norway/31694/2022 (H1N1, clade 6B.1A.5a.2a.1), A/Darwin/9/2021 (H3N2, 3C.2a1b.2a.2), A/Thailand/8/2022 (H3N2, 3C.2a1b.2a.2a.3a.1) 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. The seroprevalence was, however, ~ 25% against A/Norway/31694/2022 belonging to the drifted 5a.2a.1 clade, indicating more 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 a part of 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. 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 very 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 5. 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

A total of 1.56 million influenza vaccine doses have been distributed in the 2023/24 season both from NIPH and the other wholesalers; 1.12 million of these were distributed from the NIPH specifically intended for persons in medical risk groups and health care workers (HCW) involved in direct patient care. The number of distributed doses is approximately the same as in the 2022/23 season, but the number of discarded doses is not yet included as the possibility to get vaccination is still open. (Figure 17).

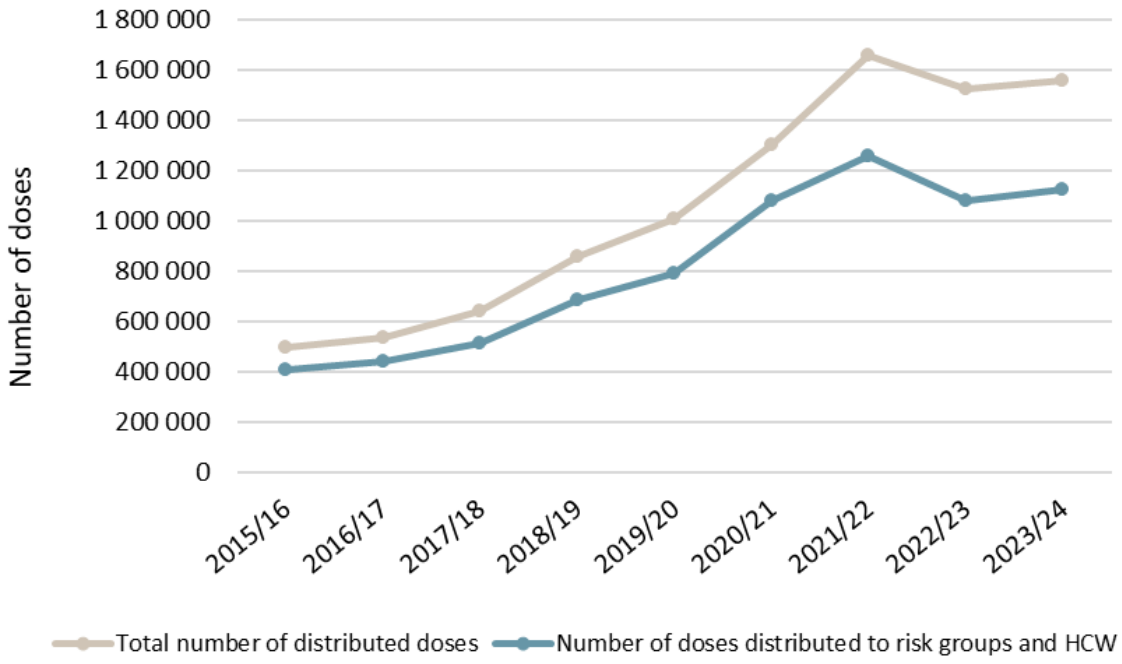


Figure 17. Influenza vaccine doses distributed in Norway, September 2015 through January 2024. HCW = Health Care Workers.

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

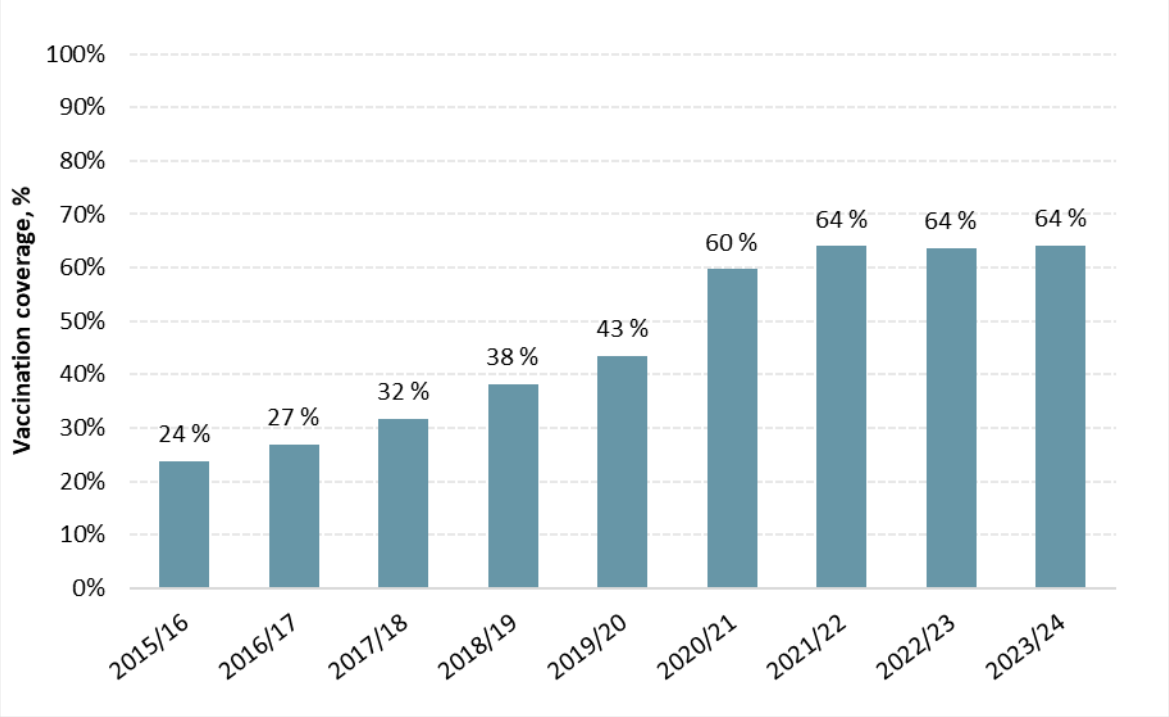


Figure 18. Vaccination coverage among residents above 65 years in Norway, 2015/16 season through to 2022/23 season as of January 2024.

According to the Emergency preparedness register for COVID-19 (Beredt C19), vaccination coverage in risk groups 18-64 years and 0-17 years per 28th of January2024 was 33% and 7%, respectively. Approximately 83% of the distributed doses are registered in SYSVAK, due to underreporting and technical issues. Vaccination coverage is therefore also estimated by survey data from Statistics Norway for the various risk groups and HCWs. However, these estimates will not be available until October 2024.

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 over 260,000 vaccinations in week 43 and then gradually declined to a few thousand doses weekly from week 52 (Figure 19). 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.

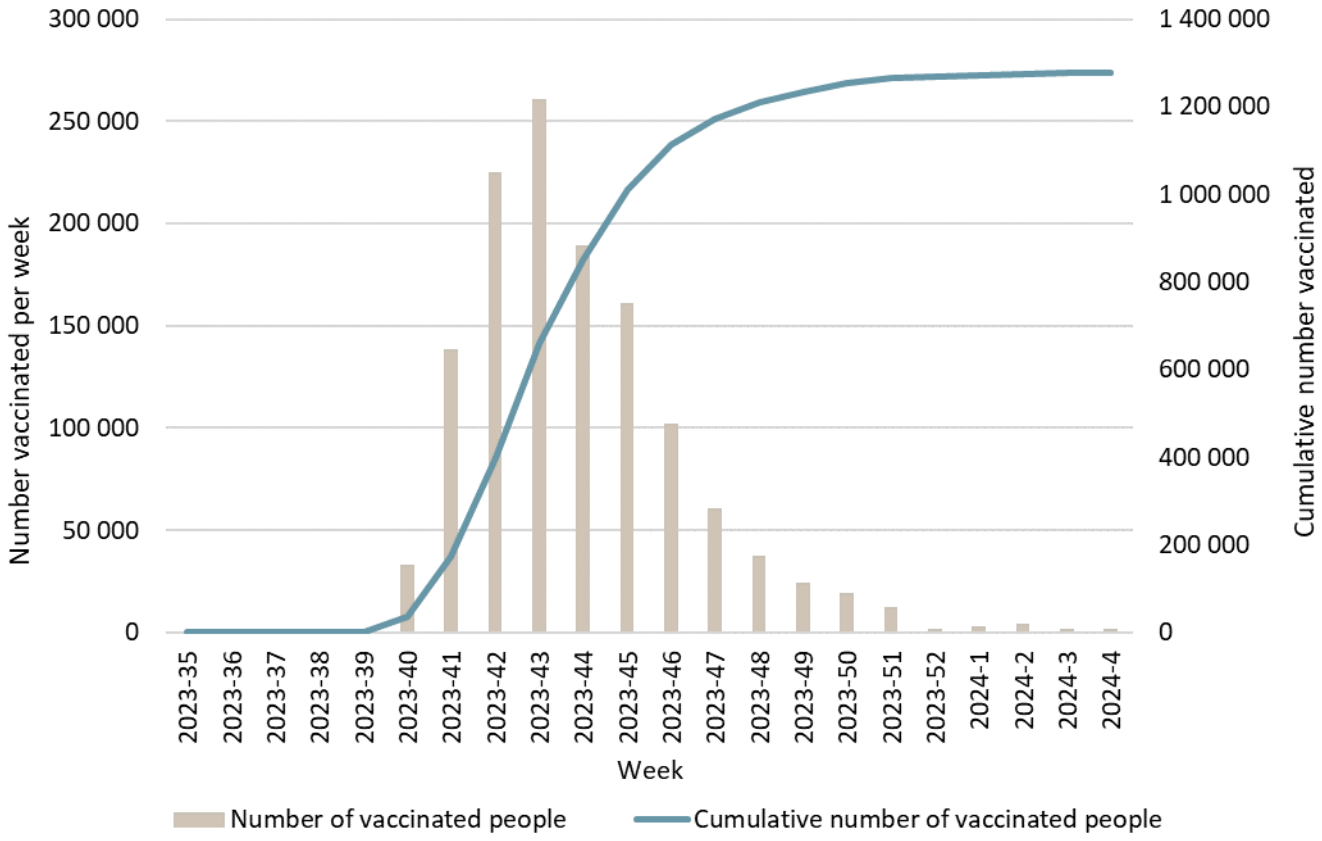


Figure 19: Number of vaccinated people per week and cumulatively in the 2023-24 season, 1. September 2023 – 28. January 2024. Source: National Population Registry and Norwegian Immunization Registry, SYSVAK.

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 four outbreaks of HPAIV H5N1 in commercial poultry flocks, two in small poultry backyard flocks, and two in municipal parks with captive birds. During autumn 2023 and winter so far in 2024, the Norwegian Veterinary Institute has reported detections of HPAIV H5N1 and H5N5, mainly in gulls and raptors (2). Detections have been from the mainland Norway and Svalbard.

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 (4), but increased awareness and precautionary infection control measures are recommended to prevent zoonotic infection.

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

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

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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 components

Influenza-like illness

Norwegian ILI surveillance data is provided by NorSyss (The Norwegian Syndromic Surveillance System, which receives data from the KUHR-system hosted previously by the Norwegian Directorate of Health and since 1.1.2024 by the Norwegian Institute of Public Health, which daily provides anonymised data on influenza diagnosed in primary health care consultations. The information is admitted to KUHR through doctors' reimbursement claims to the health authorities. NorSyss has been receiving KUHR data since 2014 and is supported by retrospective data from the 2006-07 season and onwards.

Virological surveillance.

Sentinel virological surveillance: 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 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.

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

Registry-based surveillance of influenza hospitalisations

In 2020-2021, a temporary registry-based system for surveillance of influenza hospitalisations was established in order to strengthen the influenza surveillance during the COVID-19 pandemic. In the beginning, individual-level data originating from the Norwegian Patient Registry (NPR) was used. Influenza hospitalisations were defined as inpatient hospital admissions combined with ICD-10 codes for influenza (J09-J11). Since the beginning of the monitoring season 2023-2024, the surveillance of hospital admissions with influenza has been more tightly integrated into the surveillance of severe acute respiratory infections (SARI), which

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

Influenza patients in intensive care units

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

Influenza-associated deaths

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

Influenza seroepidemiology

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

Vaccine distribution and coverage

Distribution data are reported by Department of Infection Control and Vaccine at NIPH and by IQVIA Solutions (distribution from other wholesalers). Vaccination coverage data are from the Norwegian immunisation registry SYSVAK. This electronic immunisation registry supplies national coverage estimates based on every individual's vaccination status. It is mandatory to

register all influenza vaccinations. However, in recent years the rate of registration has been around 75-80 % of the doses distributed (adjusted for the number of discarded doses). Coverage estimates from SYSVAK are therefore considered minimum estimates.

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

NIPH
Norwegian Institute of Public Health

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PO Box 222 Skøyen
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