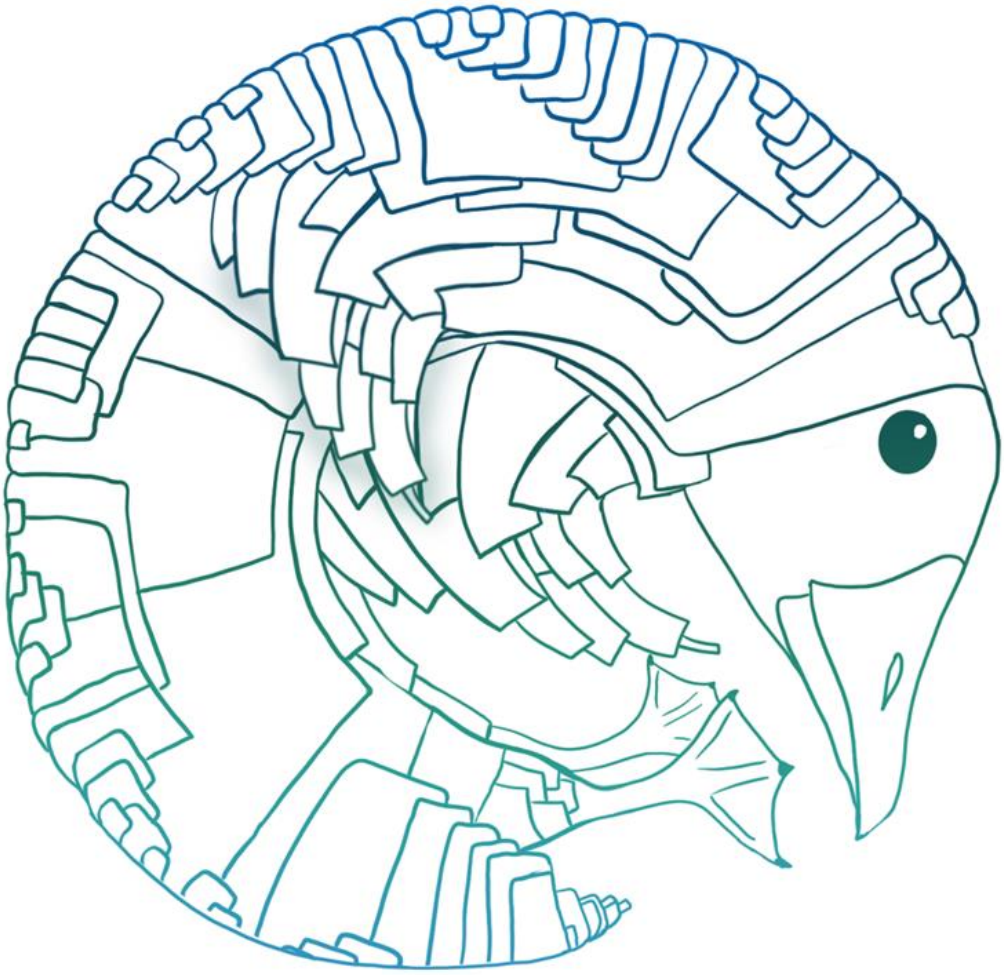
Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

Hôpitaux Universitaires Genève

Influenza virus surveillance in Switzerland
Season 2023–2024

(Weeks 40/2023-16/2024)



National Reference Centre of Influenza
Laboratory of Virology
Geneva University Hospitals
4 Rue Gabrielle-Perret-Gentil
1211 GENEVA 14 – SWITZERLAND

Cover image credit and description: Digital illustration using Procreate® by Lisa Spedaliero
Phylogenetic tree representing a wild goose.
Image definition: 2000x2000 pixels

Contacts

Ms Tania Spedaliero	Tel: +41/22 372 40 82 ✉ : Tania.Spedaliero@hug.ch
Dr Ana Rita Gonçalves Cabecinhas	Tel: +41/22 372 49 89 ✉ : agnv@hug.ch
Ms Patricia Boquete-Suter	Tel: +41/22 372 40 94 ✉ : Patrica.Suter@hug.ch
Dr Manuel Schibler	Tel: +41/22 372 40 96 ✉ : Manuel.Schibler@hug.ch
Professor Laurent Kaiser	Tel: +41/22 372 98 00 ✉ : Laurent.Kaiser@hug.ch

Contents

Abbreviations and Acronyms

ARI	acute respiratory infection
BM	baloxavir marboxil
CDC	Centers for disease control and prevention
CDV	canine distemper virus
COVID-19	coronavirus disease 2019
CPE	cytopathic effect
Ct	cycle threshold
EC_{50}	half maximal effective concentration
ECDC	European centre for disease prevention and control
EEA	European economic area
ENA	European Nucleotide Archive
EQAP	external quality assessment programme
EU	European union
FOPH	federal office of public health
GISAID	global initiative on sharing all influenza data
HA	hemagglutinin
HAI	hemagglutinin inhibition
HAdV	human adenovirus
HBoV	human bocavirus
HCoV	human coronavirus
HEF	hemagglutinin-esterase-fusion
L/HPAI	low/high pathogenic avian influenza
HMPV	human metapneumovirus
HPIV	human parainfluenza
IA, IB	influenza A, influenza B virus
ILI	influenza-like illness(es)
M	matrix
MDCK	Madin-Darby canine kidney cells
MDCK-SIAT1	sialic acid-enriched MDCK cells
NA	neuraminidase
NAI	neuraminidase inhibitor
NEP	nuclear export protein
NRCI	national reference centre of influenza
NS	non-structural
PA, PB	acidic protein, basic protein
RBC	red blood cell
RNA	ribonucleic acids
RNP	ribonucleoprotein
RV/EV	rhinoviruses/enteroviruses
RSV	respiratory syncytial virus
rRT-PCR	real-time reverse-transcription polymerase chain reaction
SARS-CoV-2	severe acute respiratory syndrome coronavirus 2

SPSP	Swiss pathogen surveillance platform
USA	United States of America
Vic, Yam	Victoria, Yamagata
VOC	variant of concern
VOI	variant of interest
VUM	variant under monitoring
WHO	world health organization
WIC	worldwide influenza centre
URTI	upper respiratory tract infection(s)

Acknowledgements

We would like to take this opportunity to extend our grateful thanks to:

- The Sentinel network and the participating medical practitioners.
- Fabienne Krauer, Nenad Torbica, Anton Labutin, Urs Mayr, Jean-Luc Richard, Anna Fesser, Ursina Roder, Hanna Hildenbrand, Rita Born; Federal Office of Public Health.
- Nicola Lewis, Ruth Harvey, Monica Galiano, Alex Byrne, Zheng Xiang, Christine Carr, Chandrika Halai, Karen Cross, Aine Rattigan, Alice Lilley, Michael Bennett, Becky Clark, Burcu Ermetal, Tanya Mikaeil, Abi Lofts, Alize Proust, and Lorin Adams; World Health Organization Collaborating Centre for Reference & Research on Influenza, the Crick Worldwide Influenza Centre, the Francis Crick Institute.
- Wenqing Zhang, Sylvie Briand, Maja Lièvre, Christian Fuster and all the members of the Global Influenza Surveillance and Response System; World Health Organization.
- The Global Initiative on Sharing All Influenza Data.
- Margaux Meslé, James Fielding, Amy Gimma, Mathias Leroy, and Mary Sinnathamby; World Health Organization Regional Office for Europe, and Eeva Broberg, Karen Nahapetyan, Angeliki Melidou, Maximilian Riess, Olov Svartstrom, and Maja Vukovikj; European Centre for Disease Prevention and Control.
- Pauline Vetter; Geneva Centre for Emerging Viral Diseases, Geneva University Hospitals and Faculty of Medicine.
- All members of the National Reference Centre for Emerging Viral Infections and the Centre for Emerging Viral Diseases, Geneva University Hospitals.
- All members of the Laboratory of Virology, Geneva University Hospitals.

Résumé – Zusammenfassung – Summary

Résumé de la surveillance de l'activité grippale 2023/2024

Pour la quatrième année consécutive au sein du réseau de surveillance Sentinella, les prélèvements nasopharyngés reçus au Centre National de Référence de l'influenza, ont non seulement été dépistés pour les virus de la grippe mais aussi pour le SARS-CoV-2, RSV A et B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV et HMPV. Parmi les 1'958 échantillons analysés, 1'247 se sont révélés positifs pour au moins un virus respiratoire. Les virus du SARS-CoV-2, de l'influenza A et les RV/EV étaient les plus fréquemment détectés durant cette saison (semaines 40/2023 à 16/2024).

La grippe a fait son apparition au sein du réseau Sentinella dès la semaine 41/2023. Sur les 1'958 échantillons dépistés, 352, soit 18%, étaient positifs pour un virus grippal. En Suisse l'activité de la grippe revient à des niveaux comparables aux saisons précédant la pandémie COVID-19. Les virus influenza de type A et B ont été co-détectés avec une dominance du sous-type A(H1N1)pdm09.

Les virus de sous-type A(H1N1)pdm09 appartenaient majoritairement au clade génétique 6B.1A.5a.2a et une minorité au groupe 5a.2a.1. Les isolats A(H1N1)pdm09 antigéniquement caractérisés étaient proches de la souche vaccinale recommandée pour l'hémisphère nord 2023/2024, soit A/Victoria/4897/2022. Seul un virus était mieux reconnu par l'antisérum dirigé contre la souche de référence A/Norway/25089/2022. Les virus influenza A de sous-type A(H3N2) détectés en Suisse appartenaient tous au sous-clade 2a.3a.1 du groupe génétique 3C.2a1b.2a. Ces isolats étaient bien reconnus par les antisera dirigés contre la souche vaccinale recommandée pour l'hémisphère nord pour 2023/2024, soit A/Darwin/9/2021 (3C.2a1b.2a.2) et par la souche vaccinale pour l'hémisphère nord 2024/2025 A/Thailand/8/2022 (clade 2a.3a.1). Quant aux virus de l'influenza B, tous appartenaient au clade V1A.3a.2 et tous étaient antigéniquement proches de la souche vaccinale recommandée pour l'hémisphère nord 2023/2024 B/Austria/1359417/2021.

L'activité grippale de 2023/2024 a été marquée par le retour d'un niveau de détection similaire aux saisons précédant l'émergence du SARS-CoV-2. Elle a débuté en semaine 49/2023 et a fini en semaine 10/2024, avec un pic en semaine 05/2024, soit 14 semaines.

A ce jour, et bien que le virus aviaire A(H5N1) soit détecté en Suisse chez les oiseaux sauvages, aucune infection grippale zoonotique n'a été recensée.

Chez les oiseaux sauvages, ainsi que chez la volaille, l'activité grippale reste particulièrement élevée dans plusieurs pays d'Europe, des Amériques et d'Asie. L'extension de la transmission de la souche H5N1 (clade 2.3.4.4b) à de nouvelles espèces aviaires et la multiplication des épisodes de transmission chez des animaux d'élevage et les éleveurs justifient une surveillance accrue, notamment afin de détecter rapidement une potentielle transmission interhumaine.

Zusammenfassung der Grippeüberwachung 2023/2024

Im vierten Jahr in Folge wurden im Rahmen des Sentinella-Überwachungsnetzes die im Nationalen Referenzzentrum für Influenza eingegangenen Nasopharynxproben nicht nur auf Grippeviren, sondern auch auf SARS-CoV-2, RSV A und B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV und HMPV getestet. Von den 1'958 analysierten Proben waren 1'247 positiv für mindestens ein respiratorisches Virus. SARS-CoV-2 Influenza-A-Viren und RV/EV wurden in dieser Saison am häufigsten nachgewiesen (Wochen 40/2023 bis 16/2024).

Die Grippe trat ab der Woche 41/2023 wieder im Sentinella-Netzwerk auf. Von den 1'958 gescreenten Proben waren 352, d.h. 18%, positiv für ein Influenzavirus. In der Schweiz kehrt die Grippeaktivität auf ein Niveau zurück, das mit den Saisons vor der COVID-19-Pandemie vergleichbar ist. Influenzaviren der Typen A und B wurden gemeinsam nachgewiesen, wobei das Influenzavirus A(H1N1)pdm09 dominierte.

Die Viren des Subtyps A(H1N1)pdm09 gehörten überwiegend der genetischen Klade 6B.1A.5a.2a und eine Minderheit der Gruppe 5a.2a.1 an. Die antigenischen charakterisierten A(H1N1)pdm09-Isolate standen dem empfohlenen Impfstamm für die nördliche Hemisphäre 2023/2024, A/Victoria/4897/2022, nahe. Nur ein Virus wurde von dem Antiserum, das gegen den Referenzstamm A/Norway/25089/2022 gerichtet war, besser erkannt. Die in der Schweiz nachgewiesenen Influenza-A-Viren des Subtyps A(H3N2) gehörten alle zu den Subkladen 2a.3a.1 der genetischen Gruppe 3C.2a1b.2a. Diese Isolate wurden von den Antiseren, die gegen den für die nördliche Hemisphäre empfohlenen Impfstamm 2023/2024 A/Darwin/9/2021 (3C.2a1b.2a.2) und gegen den Impfstamm für die nördliche Hemisphäre 2024/2025 A/Thailand/8/2022 (Klade 2a.3a.1) gerichtet waren, gut erkannt. Was die Influenza-B-Viren betrifft, so gehörten alle zur Klade V1A.3a.2 und alle waren antigenisch eng mit dem für die nördliche Hemisphäre empfohlenen Impfstamm 2023/2024 B/Austria/1359417/2021 verwandt.

Die Influenzaaktivität in den Jahren 2023/2024 war durch die Rückkehr zu einem ähnlichen Nachweisniveau wie in den Saisons vor dem Auftreten von SARS-CoV-2 gekennzeichnet. Sie begann in Woche 49/2023 und endete in Woche 10/2024, mit einem Höhepunkt in Woche 05/2024. Im Vergleich zur vorherigen Saison 2022/2023 kehrte das Tiefst Niveau der Aktivität 2023/2024 (<10%) eine Woche früher zurück.

Obwohl das Vogelgrippevirus A(H5N1) in der Schweiz bei Wildvögeln nachgewiesen wurde, sind bislang keine zoologischen Influenzainfektionen aufgetreten.

Bei Wildvögeln wie auch bei Geflügel ist die Influenza-Aktivität in mehreren Ländern Europas, Amerikas und Asiens weiterhin besonders hoch.

Die Ausweitung der Übertragung des H5N1-Stamms (Klade 2.3.4.4b) auf neue Vogelarten und die Zunahme der Übertragungsepisoden bei Nutztieren und Landwirten rechtfertigen eine verstärkte Überwachung, insbesondere um eine potenzielle Übertragung von Mensch zu Mensch frühzeitig zu erkennen.

Summary of surveillance of influenza activity 2023/2024

For the fourth year running within the Sentinella surveillance network, nasopharyngeal samples received at the National Influenza Reference Centre were tested not only for influenza viruses, but also for SARS-CoV-2, RSV A and B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV and HMPV. Of the 1,958 samples analysed, 1,247 tested positive for at least one respiratory virus. SARS-CoV-2 influenza A viruses and RV/EV were the most frequently detected viruses during this season (weeks 40/2023 to 16/2024).

Influenza returned to the Sentinella network in week 41/2023. Of the 1,958 samples screened, 352 (18%) were positive for an influenza virus. In Switzerland, influenza activity is returning to levels comparable to the seasons preceding the COVID-19 pandemic. Influenza A and B viruses were co-detected, with influenza A(H1N1)pdm09 predominating.

The majority of A(H1N1)pdm09 subtype viruses belonged to genetic clade 6B.1A.5a.2a and a minority to group 5a.2a.1. The antigenically characterised A(H1N1)pdm09 isolates were close to the recommended vaccine strain for the northern hemisphere 2023/2024, i.e. A/Victoria/4897/2022. Only one virus was better recognised by antiserum directed against the reference strain A/Norway/25089/2022. The influenza A viruses of subtype A(H3N2) detected in Switzerland all belonged to subclades 2a.3a.1 of genetic group 3C.2a1b.2a. These isolates were well recognised by antisera directed against the 2023/2024 northern hemisphere vaccine strain A/Darwin/9/2021 (3C.2a1b.2a.2) and the 2024/2025 northern hemisphere vaccine strain A/Thailand/8/2022 (clade 2a.3a.1). As for the influenza B viruses, they all belonged to the V1A.3a.2 clade and all were antigenically close to the recommended vaccine strain for the northern hemisphere 2023/2024 B/Austria/1359417/2021.

Influenza activity in 2023/2024 was marked by a return to a level of detection similar to the seasons preceding the emergence of SARS-CoV-2. It began in week 49/2023 and ended in week 10/2024, with a peak in week 05/2024. Compared with the previous 2022/2023 season, the 2023/2024 basal level of activity (<10%) returned one week earlier.

To date, although the avian A(H5N1) virus has been detected in wild birds in Switzerland, no zoonotic influenza infections have been recorded. Flu activity in wild birds and poultry remains particularly high in several countries in Europe, the Americas and Asia. The extension of the transmission of the H5N1 strain (clade 2.3.4.4b) to new avian species and the increase in transmission episodes in farm animals and farmers justify increased surveillance in view of to rapidly detect potential human-to-human transmission.

1. Introduction

Influenza virus infections are a major clinical and economic burden worldwide.[1] In Switzerland, influenza activity is yearly monitored through a mandatory laboratory reporting system, a hospital-based (CH-SUR) and a sentinel surveillance (Sentinella) networks.

Sentinella is a community-based network of primary care medical practitioners, who report influenza-like illnesses (ILI), defined as sudden onset of high fever (>38°C) and cough and/or sore throat, and acute respiratory infections (ARI), defined as the acute onset of illness with cough, sore throat, shortness of breath or rhinitis AND of infectious origin, as judged by a physician, to the Federal Office of Public Health (FOPH). A subgroup of sentinel practitioners also collects respiratory samples, which are sent to the National Reference Centre of Influenza (NRCI) for respiratory viruses' screening. Samples are tested for influenza, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), respiratory syncytial virus (RSV), human coronaviruses (HCoV) (NL63/HKU1/OC43/229E), human parainfluenza (HPIV) 1-4 viruses, human bocavirus (HBoV), human adenovirus (HAdV), human rhinovirus/enterovirus (RV/EV) and human metapneumovirus (HMPV).

This report summarizes the demographic, epidemiological and virological data gathered from samples processed and analysed by the NRCI from September 30, 2023, to April 19, 2024 (week 40/2023 to week 16/2024).

2. Influenza viruses

Influenza viruses are Orthomyxoviruses, a family of enveloped, negative, single-stranded ribonucleic acid (RNA) viruses (Figure 1), known to be causative agents of respiratory tract infections referred to as influenza disease or "flu". Influenza viruses are divided into four types, A, B, C and D. They are mainly transmitted via respiratory and contact routes.[1,2]

Influenza A (IA) viruses have a wide host tropism, while influenza B (IB) viruses are mainly found in humans[3], and seals[4]. These two influenza types are responsible for the annual influenza epidemics and can be further classified into A(H3N2) or A(H1N1)pdm09 subtype, and B/Victoria/2/87 or B/Yamagata/16/88 lineage. Of note, the B/Yamagata/16/88 lineage has not been detected since March 2020 worldwide.

Influenza C virus can be isolated from swine and humans in whom it mostly causes limited mild to moderate symptoms to all ages but primarily infects children.[5] Influenza D viruses are mainly found in swine and cattle.[6] While the pathogenic potential of influenza D virus in humans remains unknown, specific influenza D antibodies can be found in high proportions in individuals regularly in contact with cattle [7] and can cross-react with influenza C virus.[8] In addition influenza D has also been found in human nasal washes.[6]

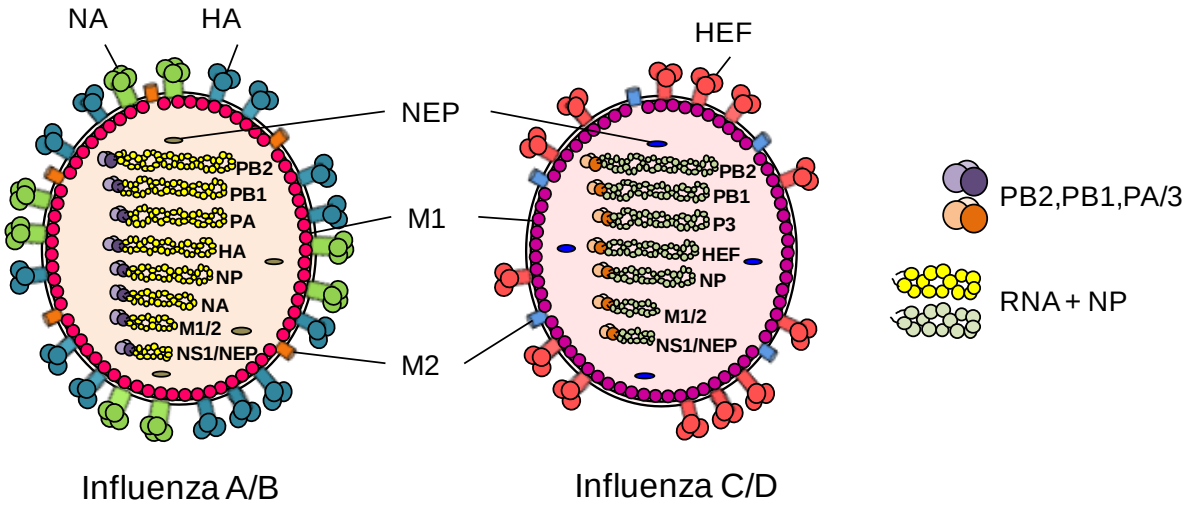


Figure 1. The structure of influenza viral particles. Basic protein 2 (PB2), 1 (PB1) and acidic protein or 3 (PA or P3) form a complex that corresponds to the RNA-dependent polymerase. The hemagglutinin (HA) and the hemagglutinin-esterase-fusion (HEF) play a role in virus attachment to sialic acids present at the surface of host cells and in fusion. The neuraminidase (NA) is crucial for virion detachment from the cellular surface by cleaving the HA on the virus surface. In influenza B, the NA gene also encodes the NB ion channel (not shown). The matrix protein 1 (M1) protein forms the viral capsid. The ion channel M2 allows virion acidification required for fusion. The nuclear export protein (NEP), also named “non-structural (NS) protein 2”, is implicated in the export of the virus polymerase + RNA + nucleoprotein (NP) complex to the cell nucleus. The RNA + NP is also called ribonucleoprotein (RNP). The RNA segments PB1, PB2, PA/3, HA or HEF, NP, NA (not present in influenza C and D), M and NS are present inside the viral capsid, protected by NPs. Only non-structural protein 1 is not present in the viral particle, but it is expressed upon infection of the host cell. Influenza D is structurally closer to influenza C than to A and B.

Influenza viruses are known to evolve rapidly through two major mechanisms called antigenic drift and shift. The first is the consequence of the accumulation of mutations in the hemagglutinin (HA) and neuraminidase (NA) genes encoding the two major surface glycoproteins targeted by neutralizing antibodies produced against the virus. The antigenic drift drives the annual evolution of the virus and is therefore responsible for the need to regularly adapt the seasonal influenza vaccine strains. The antigenic shift results from the exchange (reassortment) of the influenza A HA and NA genes from different non-human species. It drives the emergence of new variants with pandemic potential.[9]

Human infection with seasonal influenza A and B viruses can be asymptomatic or cause mild to severe diseases, which can be lethal. These viruses are of major concern in vulnerable individuals, such as the elderly (≥65 years old), pregnant women, children younger than 5 years old and individuals with underlying chronic diseases, in whom they represent an important health threat.

3. Other respiratory viruses

Respiratory viruses are often associated with mild or moderate acute respiratory diseases. However, they can also be linked to more severe syndromes and increased morbidity[10] in particular subpopulations.

3.1 Human coronaviruses (HCoVs)

Human coronaviruses are enveloped, single-strand, positive-sense 5′-capped and 3′-polyadenylated RNA viruses belonging to the subfamily *Orthocoronavirinae* of the Coronaviridae family. Their 30kb genome encodes more than 20 proteins.[11] *Orthocoronavirinae* are divided in four genera *: α-coronavirus, β-coronavirus, γ-coronavirus* and *δ-coronavirus. Alpha-* and *β-coronaviruses* infect mammalian species while *γ-* and *δ*-coronaviruses are avian viruses.[12]

Most HCoVs seem to peak during winter[13] and to display biannual epidemic patterns.[14]

HCoVs 229E, NL63, OC43, and HKU1 are known to cause mild to moderate diseases in humans while severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) are associated with more severe diseases.

The first cases of SARS-CoV and MERS-CoV were respectively identified in 2002 and 2012. SARS-CoV is currently not circulating in the human population, while sporadic laboratory-confirmed MERS-CoV infections continue to be reported to the WHO as of May 2024.[15]

HCoV 229E, NL63, OC43, and HKU1 can infect the upper and lower respiratory tracts of both adults and children, and are as many other respiratory viruses, often associated with common colds of mild to moderate intensity depending on the viral species. Nevertheless, in vulnerable individuals, both in children and adults, HCoV 229E, NL63,

OC43, and HKU1 may exhibit more severe diseases as bronchiolitis and pneumonia.[14] Neurological manifestations have also been reported.[16]

SARS-CoV-2 is a *β-coronavirus* responsible for the coronavirus disease (COVID-19) pandemic that emerged in China in December 2019.[17] Most of the first identified cases of COVID-19 were linked to Huanan Seafood Wholesale Market in Wuhan city where live-wild animals were also traded. However, the origin of the index case(s) remains unknown[18] and the virus "emergence process" in the human population remains controversial.[19] As of May 2023 the World Health Organization (WHO) has declared the end of the COVID-19 as a public health emergency [20] as it is "now an established and ongoing health issue which no longer constitutes a public health emergency of international concern (PHEIC)". Clinical manifestations of SARS-CoV-2 range from mild to severe diseases with non-specific symptoms like those caused by other respiratory viruses. Children usually manifest mild symptoms and the risk of hospitalisation or mortality is very low[21]. The disease burden varies with age, comorbidities, and depends on sex. Indeed, females are at slightly higher risk of severe outcomes than males.[22] Asymptomatic infections have also been occured.[11] Some individuals experience long COVID or Post-Covid conditions defined by the WHO as "the condition that occurs in individuals with a history of probable or confirmed SARS-CoV-2 infection, usually three months from the onset of COVID-19, with symptoms that last for at least two months and cannot be explained by an alternative diagnosis".[23] The central nervous system, the kidneys, heart, and blood vessels can also be affected.[24-28]

SARS-CoV-2 can be transmitted from human-to-human via respiratory droplets, fomites and by aerosols.[29] SARS-CoV-2 RNA has also been detected in blood[30], urine and faeces.[31] Some studies have observed viral RNA fragments in breast milk, raising the concern regarding the possibility of mother to child transmission via breastfeeding.[32] Wild and domestic animal infections by human SARS-CoV-2 have also been observed.[33-35]

As of May 2024, over 775 million confirmed cases and more than 7 million deaths have been notified globally.[36]

The SARS-CoV-2 virus continuously evolves into different genetic clades and subclades. Some genetic lineages were specifically identified as higher public health threats and classified in four risk groups, i.e. variant of concern (VOC), variant of

interest (VOI) and variant under monitoring (VUM). VOI is defined by the WHO as “a variant with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, virulence, antibody evasion susceptibility to therapeutics or detectability, and identified to have a growth advantage over other variants, with increasing relative prevalence alongside increasing number of cases over time, or other apparent epidemiological impacts to suggest an emerging risk to global health”. VOC variant is defined as a VOI and shares additional characteristics at a global public health scale such as “detrimental change in clinical disease severity, in COVID-19 epidemiology causing substantial impact on health system requiring major public health interventions or significant decrease in the effectiveness of available vaccines in protecting against severe disease.” The VUM definition is “a variant with genetic changes that are suspected to affect virus characteristics and early signals of growth advantage relative to other circulating variants, but evidence of phenotypic or epidemiological impact is unclear, requiring enhanced monitoring and repeat assessment pending new evidence. This includes variants with unusually large number of antigenic mutations but with very few sequences and/or it is not possible to estimate its relative growth advantage.”[37]

3.2 Respiratory syncytial virus (RSV)

RSV A and B, as well as their multiple respective genotypes[38], belong to the *Pneumoviridae* family, genus *Orthopneumovirus*. These enveloped viruses contain a non-segmented, single-stranded, negative sense RNA genome of ten genes encoding 11 proteins.[39] RSV is considered to be the most frequent causative agent of respiratory infections in children under 5 years old, but is also an important threat for adults with underlying medical conditions, the immunocompromised individuals[40], and the elderly.[41] Each year, around 33 million episodes of RSV-associated diseases are recorded in children under age 5 old as well as more than 118,000 deaths globally[42,43]; a large proportion in low income countries. Considering the high public health impact of RSV, the WHO has launched a pilot study ,currently on phase II, on the global surveillance of RSV using the already existing Global Influenza Surveillance and Response System.[44,45]

During RSV-associated upper respiratory tract infections (URTI), clinical manifestations are generally mild with symptoms such as runny nose, cough, nasal

congestion, low-grade fever, and decreased appetite. Most infants infected with RSV will develop an URTI, whereas 20 to 30% will develop potential severe lower respiratory tract infections such as bronchiolitis and pneumonia, sometimes leading to respiratory failure. RSV infections at early age are also suspected to be linked to the development of asthma.[46] Older children mostly present URTI symptoms. In adults and elderly, RSV symptoms can be similar to those caused by influenza virus.[41] Cases of RSV associated encephalitis[47], myocarditis[48,49], and hepatitis[50] have also been reported.

Two humanized monoclonal antibodies targeting RSV proteins, Palivizumab and Nirsevimab, are available for the prevention of acute lower respiratory tract infections/diseases due to RSV in neonates, infants, and toddlers in Switzerland.[51] Recommendations for use specific to each antibody are available. [52]

The U.S Federal Drug Administration (FDA) has recently licensed a vaccine meant to be administrated to pregnant women for the passive immunization of infants from birth to six months through. This vaccine can also be used in people aged ≥60 for the prevention of lower respiratory tract diseases caused by RSV.[53] Unfortunately, this latter is not yet available in Switzerland.

3.3 Human metapneumovirus (HMPV)

Like RSV, HMPV are enveloped single-stranded, negative-sense, non-segmented RNA viruses, which belong to the *Pneumoviridae* family, albeit to a distinct genus, namely the *Metapneumovirus*. Their 13 kbp genome contains 8 genes encoding 9 proteins. HMPV are divided in two genotypes A and B and two sub-genotypes A1-A2 and B1-B2.[54]

HMPV infections are prevalent in young children <5 years old; and are second in terms of association with hospitalisation rate after RSV infection. Reinfection throughout life is common but the disease is generally milder in young adults. As RSV, HMPV has a tropism for the upper respiratory tract, but can also lead to bronchiolitis, pneumonia, as well as acute asthma and chronic obstructive pulmonary disease exacerbation in adults. HMPV infections, as well as all the respiratory viruses described above, can be a major threat in vulnerable individuals such as the elderly, in whom they can also be fatal.[54]

3.4 Human parainfluenza (HPIV)

HPIV are enveloped, non-segmented, single-stranded, negative-sense RNA viruses belonging to the *Paramyxoviridae* family. Their 15,000 base-pairs genomes only encode 6 proteins. HPIV viruses are divided in four genotypes. Genotype 4 is further subdivided into a and b genotypes. HPIV 1 and 3 belong to the *Respirovirus* genus, while HPIV 2 and 4 belong to the *Rubulavirus* genus.

HPIV can infect both the upper and lower respiratory tracts of children, often <5 years old, and adults. HPIV, along with RSV, infections are major causes of morbidity and mortality in young children worldwide.[55] Even if they are generally considered as mild in healthy individuals, HPIV infections can also result in more severe respiratory diseases in immunocompromised individuals as well as in children.[56] HPIV-1 and HPIV-2 cause croup and cold-like symptoms, while HPIV-3 often results in bronchiolitis, bronchitis and pneumonia.[57] HPIV-4 is less well studied but seems to exhibit symptoms similar to HPIV-3 in children.[58] HPIV types may occur at specific seasons annually. HPIV-1 and -2 appear commonly in the fall. Although HPIV-2 is less common it occurs especially when the detection of HPIV-1 is low. HPIV-3 occurs in spring and early summer and is particularly high when the detection of HPIV-1 and -2 is low. The seasonal patterns of HIPV subtypes 4a and 4b are not well defined though they seem to occur in fall and winter yearly.[59]

3.5 Human bocaviruses (HBoV)

Human bocaviruses (HBoV) 1 to 4 are non-enveloped, non-segmented, single-stranded DNA viruses belonging to the family *Parvoviridae,* subfamily within the *Parvovirinae* family. Their approximately 5 kb genome encodes at least 8 proteins.[60]

After parvovirus B19, HBoV is the second parvovirus known to be pathogenic to humans. HBoV-1 considered as a causative agent for acute respiratory infection (ARI) is more common in respiratory specimens of young children[60], in whom disseminated infection can be observed, but it can also be detected in adults.[61] HBoV-2, -3 and -4 are commonly identified in stool samples.[62] They are also often found as co-infections. Their clinical presentation is similar to that of other respiratory viruses leading to either asymptomatic or mild URTI with HBoV1. However more severe clinical manifestations as, gastroenteritis, encephalitis, myocarditis[63], idiopathic lung fibrosis, as well as yet to

be confirmed carcinogenesis have also been associated with HBoV, particularly type 1.[64]

3.6 Human adenoviruses (HAdV)

Adenoviruses are non-enveloped, double-stranded DNA viruses of more than 26,000 base-pairs encoding several non-structural and structural proteins, that infect both animals and humans. HAdV belong to the *Mastadenovirus* genus of the *Adenoviridae* family and are further divided into species A to G, within 113 genotypes and more than 50 serotypes infect humans. HAdV B and E both infect the conjunctiva as well as the upper and lower respiratory tracts, while D and C are specific to only one of these anatomical sites, respectively. Finally, types A, F and G have a tropism for the gastrointestinal tract. Most HAdV infections are either asymptomatic or mild, particularly in young children. However, in vulnerable individuals (e.g. immunocompromised), the clinical manifestations are broader and more severe with possible fatal outcomes.[65,66] Occasionally, adenovirus' infection of the urinary tract in transplant recipients can cause haemorrhagic cystitis or allograft dysfunction.[67] Of note, HAdv has recently been suggested to be linked to acute hepatitis of unknown aetiology in children.[68] A recent study, based on a Wastewater-based epidemiology approach has highlighted that the genotypes of HADV-F40/F41 viruses could be involved in acute hepatitis cases in children.[69]

3.7 Rhinovirus/Enterovirus (RV/EV)

Picornaviruses can be pathogenic for both animals and humans. They are non-enveloped, single-stranded, positive-sense RNA viruses with genomes ranging from 7,200 to 8,500 bases long. RV (A-C) and EV (A-D) are species of the *Enterovirus* genus of the *Picornaviridae* family that are responsible for a high number of human infections annually.[70,71]

Due to their resistance to low pH and high temperatures (37°C), enteroviruses can survive the acidic gastric environment and infect the small intestine. In contrast, rhinoviruses being pH-sensitive and replicating optimally at the neutral pH and slightly lower temperature (~33°C) are found in the nasal mucosa. While rhinoviruses usually cause mild upper respiratory tract infections and enteroviruses usually cause non-severe diseases, such as hand, foot and mouth disease, these viruses can sometimes

cause more severe manifestations such as pneumonia, pancreatitis, hepatitis, myocarditis, encephalitis, flaccid myelitis, paralysis and even death.[70] It is notably the case of poliovirus, the causative agent of major poliomyelitis epidemics before the initiation of the Global Polio Eradication Initiative by the WHO in 1988. Of note, as of 26 June 2023, France, Croatia, Italy, Spain, Sweden, the United Kingdom of Great Britain, and Northern Ireland reported 26 cases of severe enterovirus-echovirus, including 11 infections in infants, some with a fatal outcome.

Rhinoviruses circulate annually with a peak between spring and early summer and are thus responsible for most of the ARI symptoms during this period.[72]

4. 2023/2024 surveillance period

Data gathered in the present report corresponds to the analysis of sentinel samples received at the NRCI from September 30, 2023 (week 40/2023) to April 19, 2024 (week 16/2024). Figure 2 summarizes the flow of analysis at the NRCI.

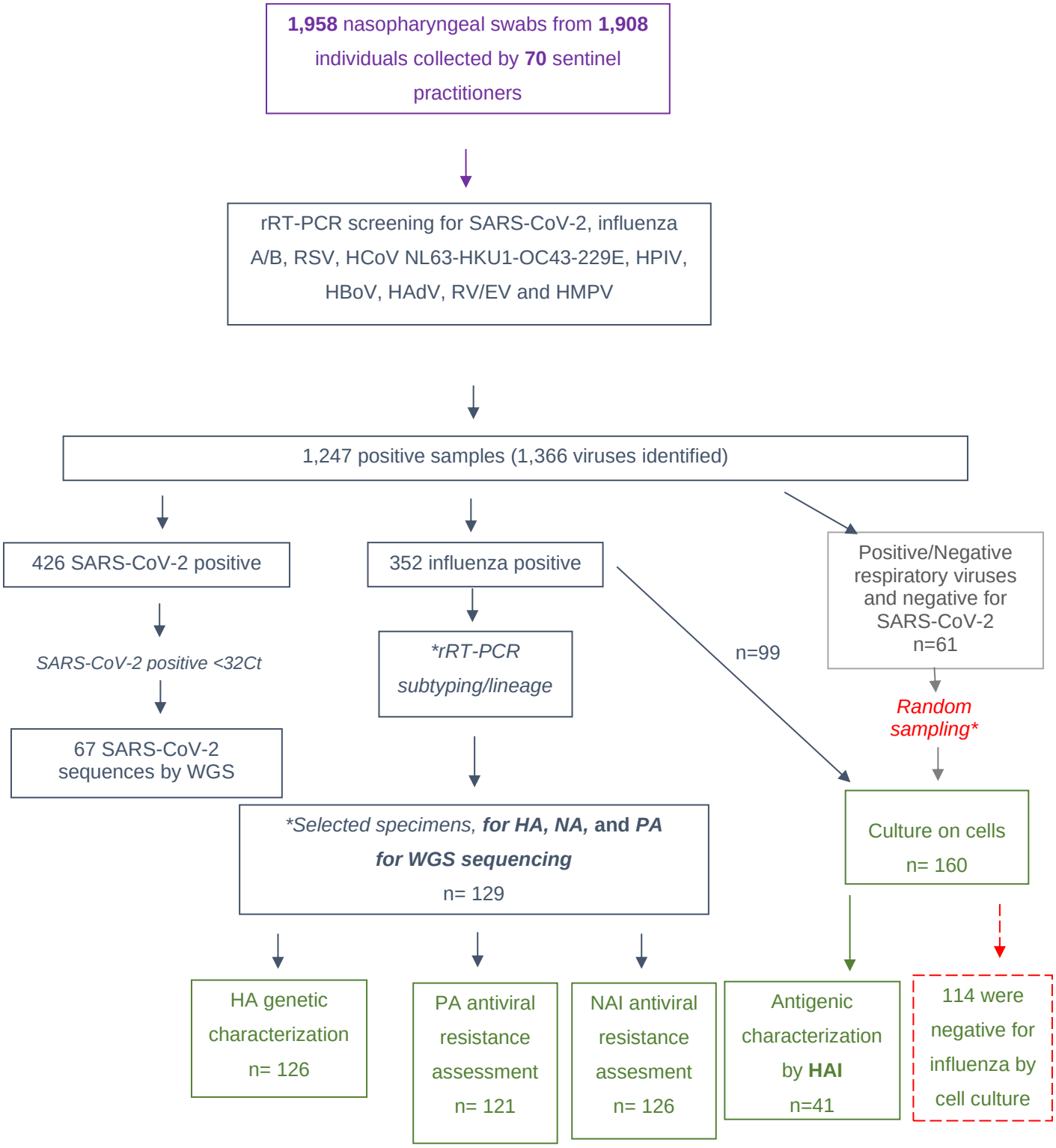


Figure 2. Flow chart of sentinel samples collection and processing. Starting in October 2023, influenza positive and negative samples that were also negative for SARS-CoV-2 were submitted to cell culture. Subtyping, antigenic, and genetic characterizations were only performed for influenza virus.

4.1 Demographic characteristics of the population tested within the Sentinella surveillance

From week 40/2023 to week 16/2024, 70 sentinel practitioners collected 1,958 nasopharyngeal samples from 1’908 individuals for screening at the NRCI. Among the 1,958 samples, 1,040 (53.1%) were from female and 918 (46.9%) were from male (Table 1).

4.1.1 Stratification by age

When further stratifying the population by age group (i.e., 0-4, 5-14, 15-29, 30-64 and ≥65 years old), samples were equally distributed amongst female and male (Table 1). Data on age was available for all individuals (median age 43 years old, range [0 to 98 years]; 95% confidence interval (CI) 42-44 years old). Median age for males was 42 years old (range [0 days to 95 years]; 95% CI 40-43 years old) and 44 years old for females (range [0 to 98 years]; 95% CI 42-45 years old) (Figure 3).

Table 1: Age and sex distribution of the Sentinella population, from weeks 40/2023 to 16/2024

Number of samples	***Male***	***Female***	***Totals***
	918	1040	1958
Age group distribution			
0-4	63	59	122
(%)	*6.9%*	*5.7%*	*6.2%*
5-14	55	55	110
(%)	*6.0%*	*5.3%*	*5.6%*
15-29	172	169	341
(%)	*18.7%*	*16.3%*	*17.4%*
30-64	473	542	1015
(%)	*51.5%*	*52.1%*	*51.8%*
≥65	155	215	370
(%)	*16.9%*	*20.7%*	*18.9%*

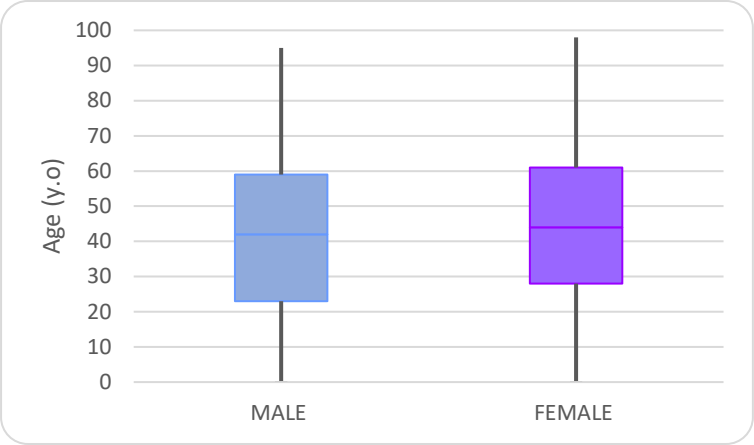


Figure 3. Age distribution of the sentinel population, from weeks 40/2023 to 16/2024. Distribution pattern for the entire population by sex. Median ages, 25% and 75% quartiles are shown in bold lines.

4.1.2 Attribution of samples to influenza and Covid-19 suspicion criteria

As mentioned previously samples tested in the Sentinella surveillance are based on clinical suspicion of ILI for influenza and ARI for COVID-19. One thousand two hundred forty-one (1,241) samples originated from individuals with both COVID-19 and ILI suspicions. Four hundred and fifty-five (455) and 109 swabs corresponded to COVID-19 and influenza suspicions, respectively. Suspicion criteria was unknown for 153 samples.

4.1.3 Influenza and COVID-19 vaccination status

Among the 1,958 samples received at the NRCI, influenza vaccination status was known for 1,723 of them. Of these 1',723 , 258 (15%) were vaccinated with the current influenza vaccine (northern hemisphere 2023/2024 WHO recommendation). Half of them were ≥65 years-old (Table 2). Concerning COVID-19, vaccination status was known for 1,883 individuals. Among them, 79 were vaccinated for 6 months or more ago, and 130 (6.9%) were vaccinated for less than 6 months ago. The latter were further stratified by age groups (Table 2).

Table 2: Influenza and COVID-19 vaccination by age in Sentinella individuals, from weeks 40/2023 to 16/2024

Influenza vaccination (*actual season*)	***Total*** 258	**COVID-19 vaccination** *(< 6 months)*	***Total*** 130
Age group distribution		**Age group distribution**	
0-4	6	0-4	0
(%)	*2.3%*	(%)	*0.0%*
5-14	9	5-14	1
(%)	*3.5%*	(%)	*0.8%*
15-29	16	15-29	11
(%)	*6.2%*	(%)	*8.5%*
30-64	98	30-64	56
(%)	*38.0%*	(%)	*43.1%*
≥65	129	≥65	62
(%)	*50.0%*	(%)	*47.7%*

4.2 Respiratory viruses detected in nasopharyngeal swabs

From week 40/2023 to week 16/2024, a total of 1,958 nasopharyngeal samples (NPS) were screened for influenza, SARS-CoV-2, RSV, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV, HBoV, HAdV, RV/EV and HMPV.

One thousand two hundred and forty-seven samples (1,247) (63.7%) were positive for at least one respiratory virus and 1,366 viruses in total were detected. Among these, the following pathogens were identified: SARS-CoV-2 (n=426; 31.19%), influenza A virus (n=325; 23.79%), RV/EV (n=273; 19.99%), RSV (n=70; 5.12%), HMPV (n=61; 4.47%), HAdV (n=39; 2.86%), HCoV OC43 (n=37; 2.71%), HCoV HKU1 (n=30; 2.20%), influenza B virus (n=27; 1.98%), HPIV 1/3 (n=27; 1.98%), HPIV 2/4 (n=23; 1.68%), HCoV 229E (n=15; 1.10%), HBoV (n=9; 0.66%), and HCoV NL63 (n=4; 0.29%) (Figure 4a).

A maximum positivity rate of 74.3% was observed during week 04/2024, the latter was close to the peak of ILI consultations for 2023/2024 (week 05/2024) in Switzerland (Appendix 1). A minimum positivity rate of 45.5% could be seen during week 15/2024. The median positivity rate for the 2023/2024 season was of 62.2% (range [45.5 to 74.3%]; 95% CI 59.6-64.8%) (Figure 4b). RV/EV, SARS-CoV-2, RSV, and HAdV were regularly detected throughout the surveillance period (Figure 5b). SARS-CoV-2 and

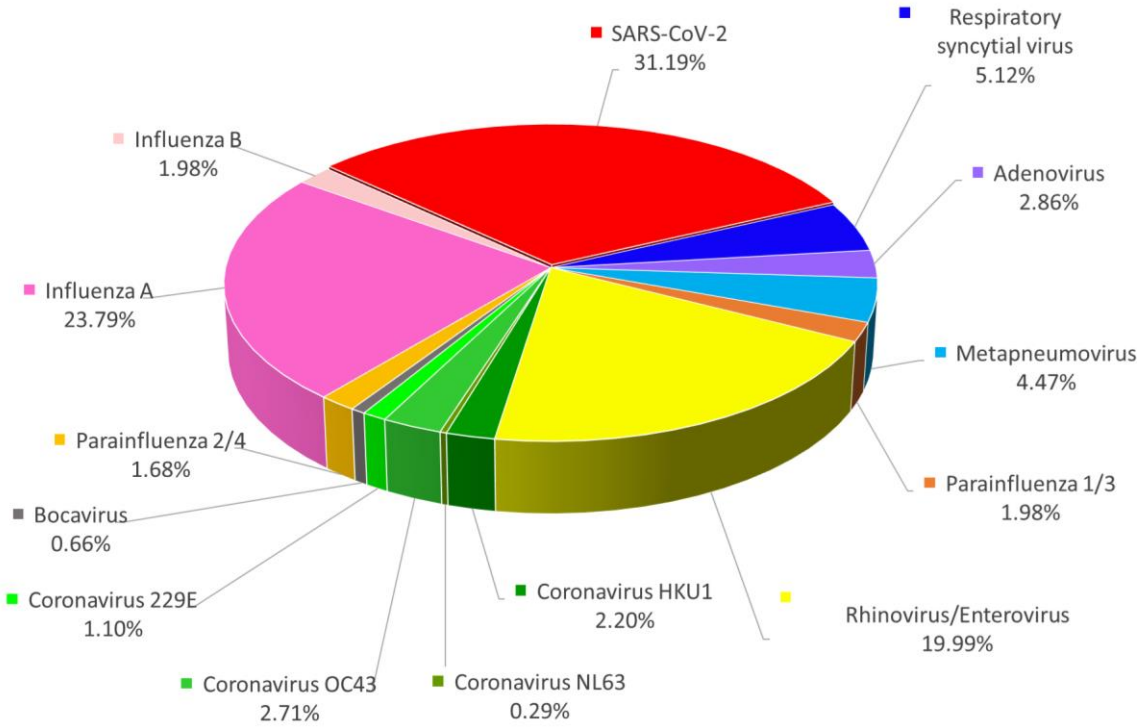
RV/EV were dominant at the beginning of the season. OC43 and HKU1 were regularly detected since week 42/2023 and 48/2023, respectively. Influenza virus detection started to increase in week 46/2023 and reached 50% of the total detected viruses during week 05/2024.

Even if at low numbers, HPIV2/4 was observed at the beginning of the season from week 40/2023 to week 01/2024, while HPIV1/3 started to increase in week 06/2024 and was dominant compared to HPIV2/4. The detection of HMPV started to increase from week 02/2024, while SARS-CoV-2 was declining. HBoV was sporadically detected during the season (Figure 4b).

From week 40/2023 to week 16/2024, more than one virus was detected in 99 (7.9%) out of 1,247 positive samples (Appendix 2). The highest number of co-detections (n=7; 21.2%) was observed in week 08/2024. Among the 99 co-detections, 53 concerned SARS-CoV-2 (53.5%); which were mainly observed with influenza virus (20/53), RV/EV (15/53) or RSV (8/53).

When stratifying positive specimens by age groups, we observed that RV/EV was present and at similar levels in all age groups (Figure 5a). SARS-CoV-2, and IA were dominant in the ≥ 65-year-old, adult (30-64), and teenage-young adult (15-29) groups. SARS-CoV-2 represented 44.7%, 35%, and 25.5% of each group, respectively, while IA accounted for 16%, 28.4%, and 25.5%, respectively (Figure 5a). In the children (5-14) and toddlers (0-4), HAdV and RSV were found in larger proportions compared to in adults and elderly, with 8.3% of each virus in the 5-14 years-old group and 14.5% for RSV and 11.3% for HAdV in the toddler group (Figure 5a-b). HBoV, human coronaviruses (NL63, OC43, E229, HKU1), HPIV1-4, IB were mainly detected in toddlers (Figures 5a-b).

a



b

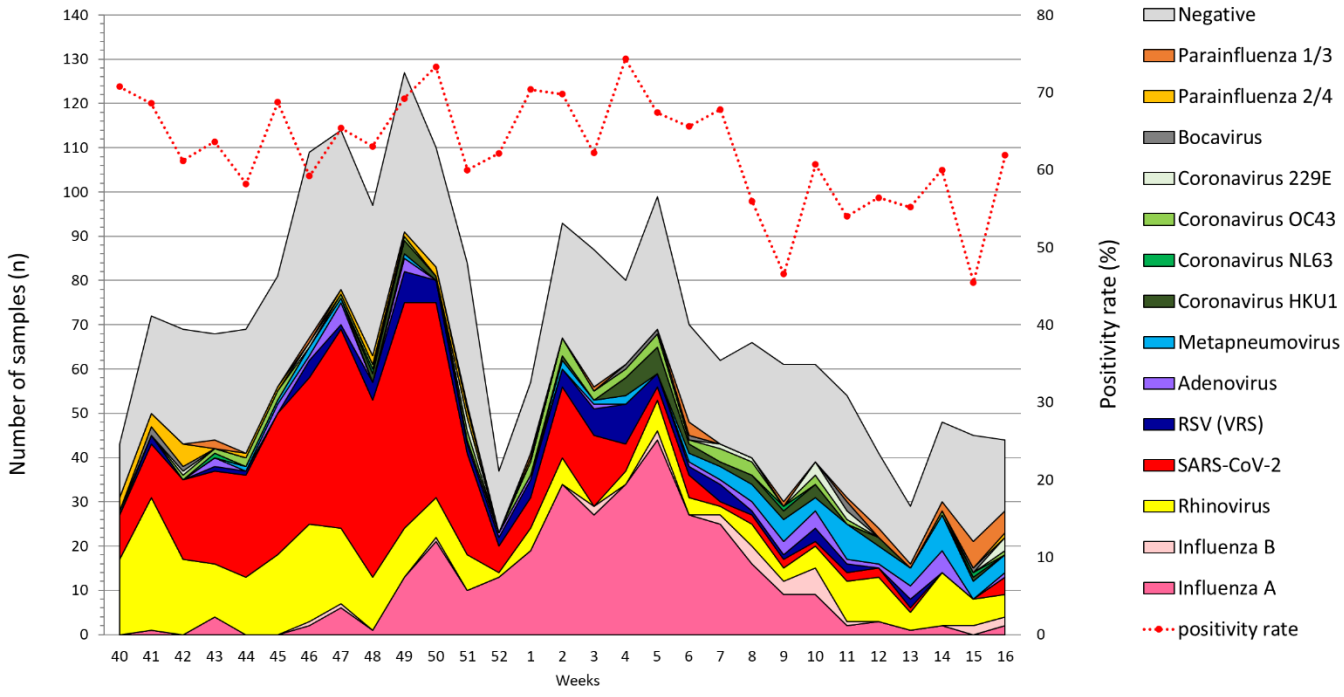
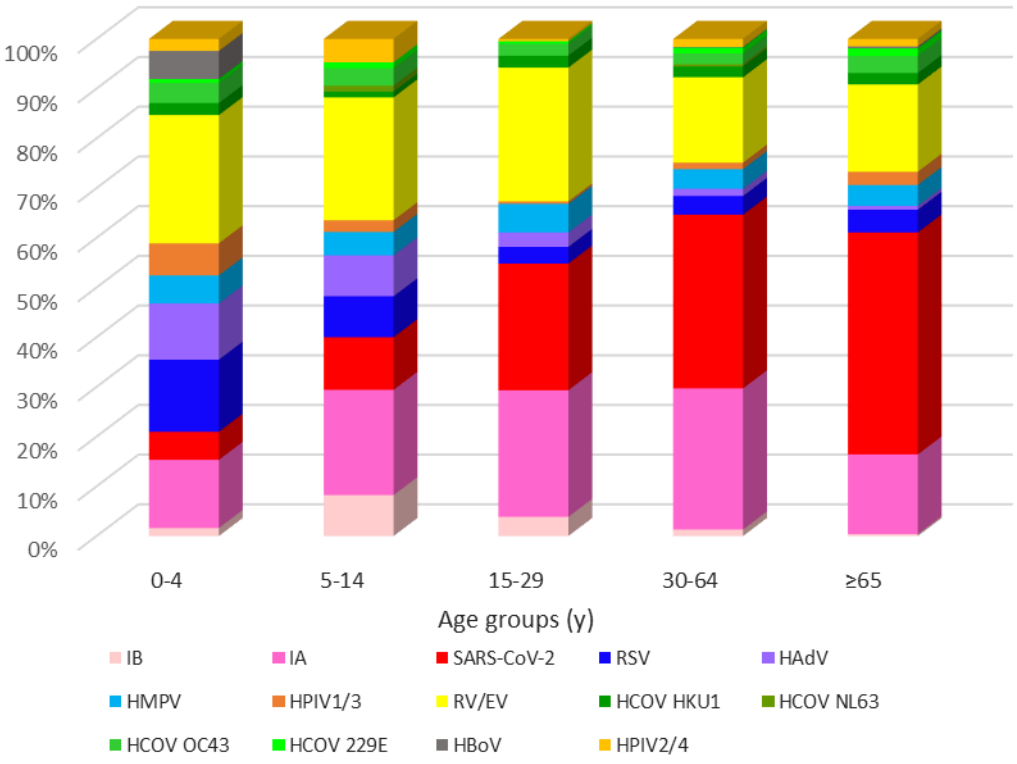
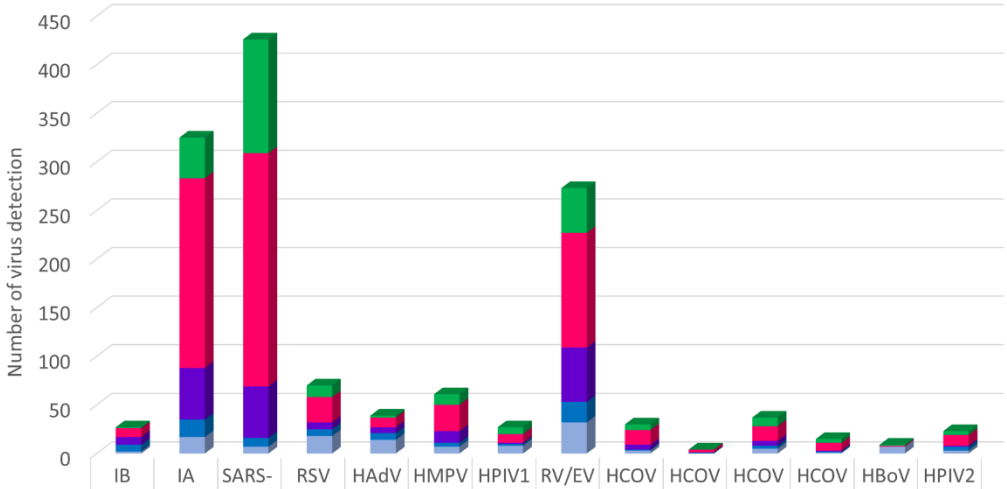


Figure 4. Percentage and temporal distribution of respiratory viruses detected in NPS collected from week 40/2023 to 16/2024. a. Percentages of the different respiratory viruses (n=1'366) detected in 1'958 NPS. **b**. Distribution of the detected pathogens throughout the surveillance period. Positivity rate is based on the number of positive samples per number of samples received each week.

a



b



	IB	IA	SARS-CoV-2	RSV	HAdV	HMPV	HPIV1/3	RV/EV	HCOV HKU1	HCOV NL63	HCOV OC43	HCOV 229E	HBoV	HPIV2/4
≥65	1	42	117	12	2	11	7	46	6	0	9	4	1	4
30-64	9	195	240	26	10	27	9	118	15	3	15	8	1	11
15-29	8	53	53	7	6	12	1	56	5	0	5	1	0	1
5-14	7	18	9	7	7	4	2	21	1	1	3	1	0	4
0-4	2	17	7	18	14	7	8	32	3	0	5	1	7	3

Figure 5. Respiratory viruses' distribution: a. by age group in percent **b.** by age group for each virus in absolute numbers of positive samples.

When stratifying the positive cases by age group and sex, no significant difference was observed between female and male (Figure 6).

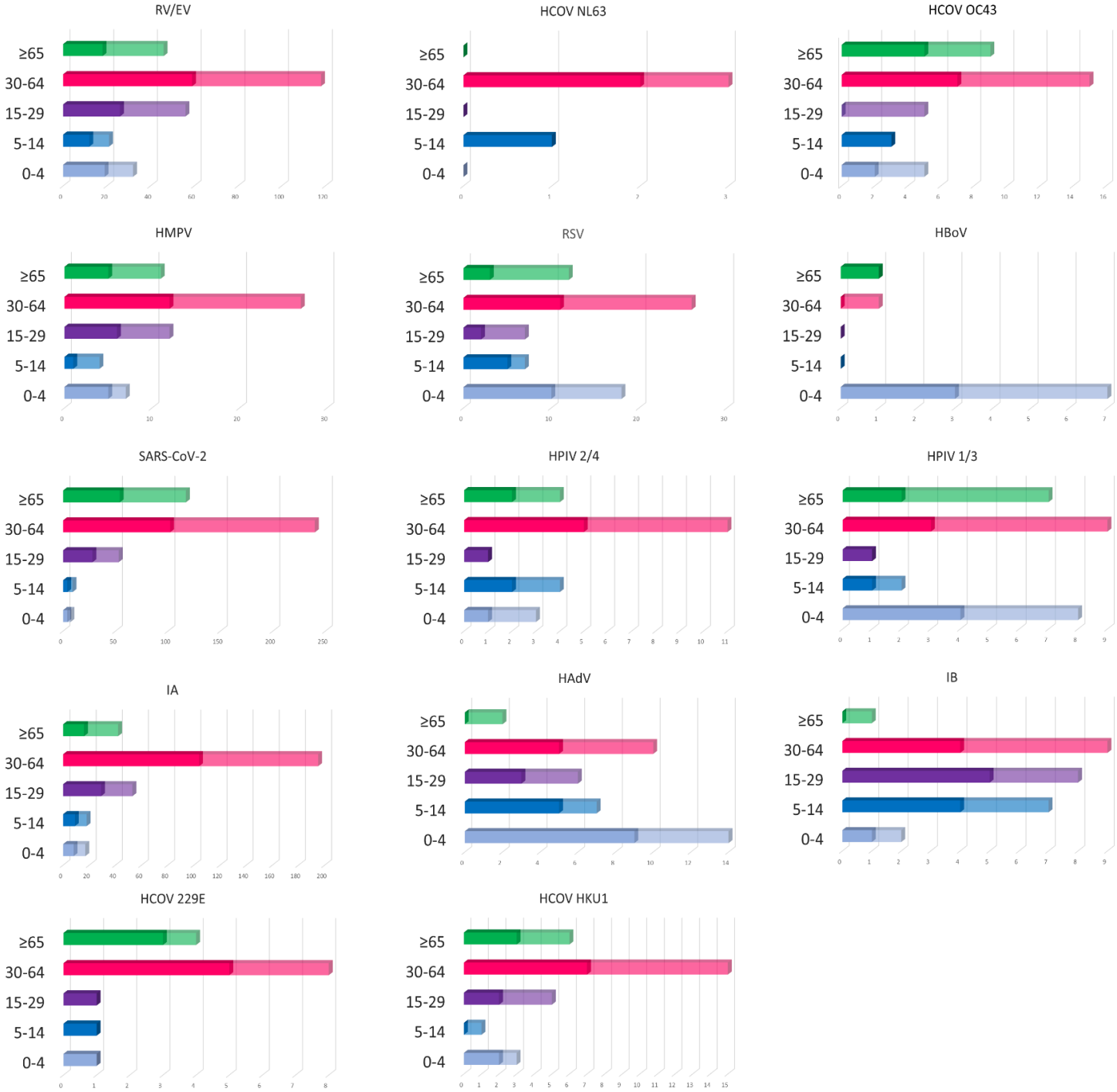


Figure 6. Respiratory viruses' distribution by sex and age groups in absolute number. Light and dark shades represent the female and male sex, respectively.

4.3 Influenza viruses' RT-PCR subtyping

Among the Influenza viruses detected (n=352), 325 IA and 27 IB viruses were identified from week 40/2023 to 16/2024 (Figure 7a). Among the IA viruses, a majority were subtyped as A(H1N1)pdm09 (n=260; 80%) and 64 (19.69%) as A(H3N2). Twenty-six (26) out of 27 IB viruses identified, belonged to the B/Victoria/2/87 lineage. One IA and one IB could not be subtyped due to low viral load. Within the Sentinella surveillance, influenza activity started from week 49/2023 overpassing the baseline threshold (>10%) defined by the European Center for Disease Control and Prevention (ECDC) and lasted 14 weeks until week 10/2024. The first IA and IB cases were detected in week 41/2023 and 46/2023, respectively (Figure 7b). The median positivity rate for influenza was of 9.5% (range [0 to 50%]; 95% CI (3.3-15.7%)) with a peak at 50% (n=46) during week 05/2024, which is also consistent with the maximum positivity rate for the surveillance period and consistent to the peak of ILI consultations in week 05/2024 (Appendix 1). A(H1N1)pdm09 virus was dominant along the surveillance period, while IB virus was detected later from week 03/2024, though at lower level.

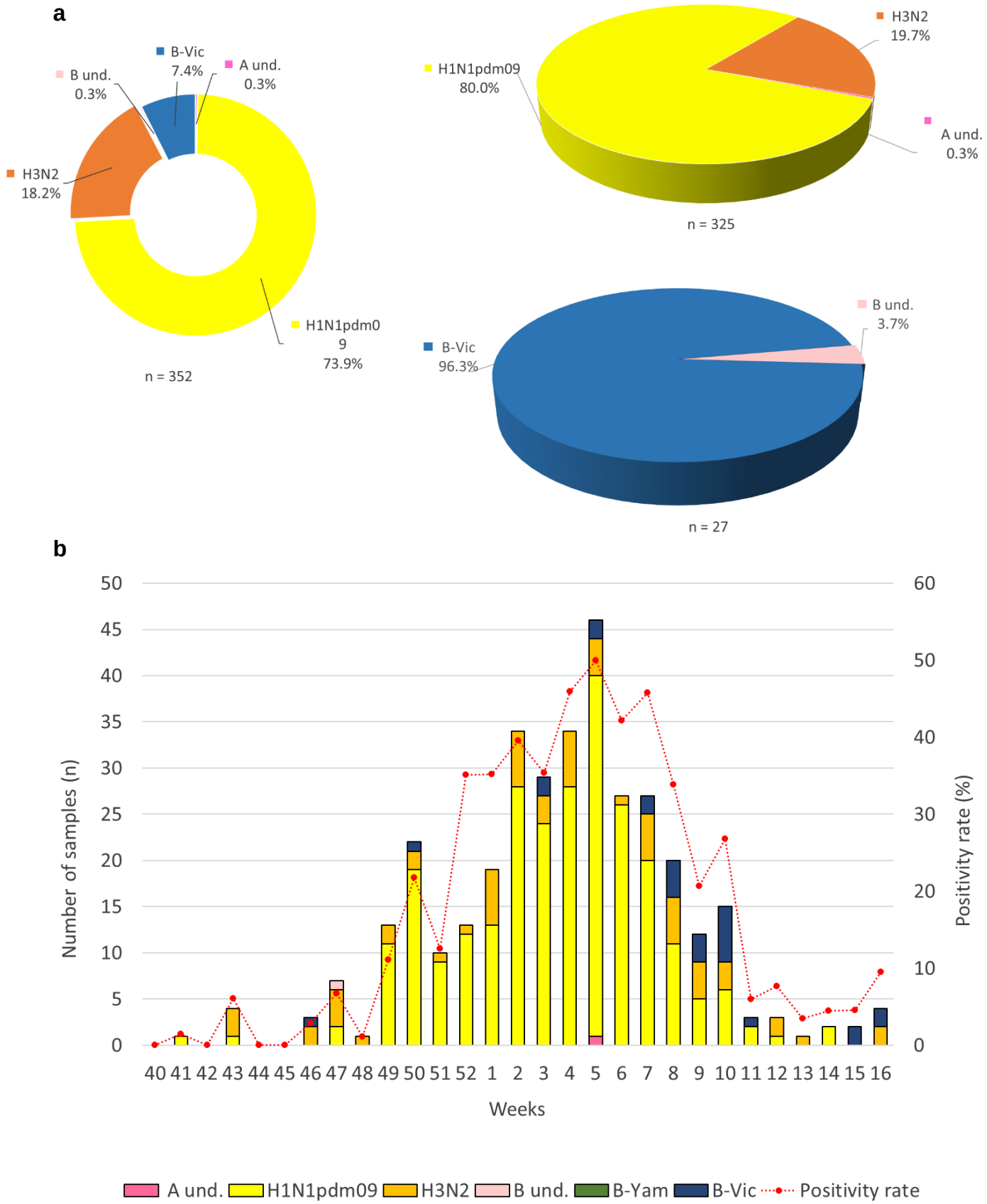


Figure 7. Percentage and temporal distribution of Influenza subtypes and lineages collected from week 40/2023 to 16/2024. a. Proportion of influenza viruses, subtypes and lineages **b**. Distribution of the detected influenza viruses throughout the surveillance period. Influenza viruses typing and subtyping done by real-time rRT-PCR. A und. and B und.: influenza A and B viruses that could not be further subtyped (undefined). H1N1pdm09 and H3N2 refer to influenza A(H1N1)pdm09 and influenza A(H3N2), respectively. B-Yam: influenza B virus of Yamagata lineage. B-Vic: influenza B virus of Victoria lineage. Positivity rate is based on the number of weekly positive influenza samples per the number of samples received each week.

4.4 Influenza viruses and SARS-CoV-2 characterisation

This chapter describes influenza viruses genetic and antigenic characterisations, as well as SARS-CoV-2 genetic analysis.

4.4.1 Antigenic and genetic characterization of influenza viruses

Cell culture on MDCK and MDCK-SIAT1 cells was attempted for 160 SARS-CoV-2-negative samples.

Among the 160 samples, 99 were influenza rRT-PCR positive (Ct values range from 13.3 to 37.9). Forty-five isolates positive influenza rRT-PCR samples grew up on cell culture. All influenza rRT-PCR negative samples remained negative in cell culture. Forty-four (21 A(H1N1)pdm09, 12 A(H3N2) and 11 B/Victoria/2/87 lineage) underwent HAI assay. Forty-one (41) out of 44 were antigenically characterized.

One hundred and twenty-nine (129) samples collected from October 2023 to May 2024 were submitted to genetic characterization. The obtained sequences were submitted to GISAID, including 79 isolates also submitted to the European Nucleotide Archive (ENA) (Appendix 4). One hundred and twenty-six (126) out of 129 HA sequences (97.7%) were successfully recovered. Among these, 83, 29 and 14 were from A(H1N1)pdm09, A(H3N2), and B/Victoria/2/87 lineage viruses, respectively (Figures 8-13).

Fifty-three samples (24 A(H1N1)pdm09, 21 A(H3N2), and 8 B/Victoria/2/87) were shared with the WHO Collaborating Centre Worldwide Influenza Centre (WIC) at Francis Crick Institute (London) for characterization. Sequencing and antigenic results are not available yet. Among them, 23 (10 A(H1N1)pdm09, 9 A(H3N2), 4 B/Victoria/2/87) samples were also sequenced at the NRCI (Figures 8-13).

4.4.1.1 Characterization of influenza A(H1N1)pdm09 viruses

A(H1N1)pdm09 viruses were the dominant subtype collected since October 2023 at the NRCI, as well as worldwide according to the WIC, ECDC and WHO.[73-75]

Among the 44 isolates characterized by HAI assay, 21 were A(H1N1)pdm09 viruses (47.7%). Eighteen (85.7%) of these isolates were well recognized by the reference antiserum directed against the egg-grown northern hemisphere vaccine strain 2023/2024 A/Victoria/4897/2022 (clade 5a.2a.1). One isolate showed reduced

reactivity to the antisera raised against A/Victoria/4897/2022 but was well recognized by the antiserum raised against the A/Norway/25089/2022 strain (clade 5a.2a.1) (Data not shown). Two viruses could not be characterized because they showed reduced reactivity (32- to 128-fold) to the antisera raised against both A/Victoria/4897/2022 and A/Guangdong_Maonan/SWL1536/2019 viruses. These were included in our shipments to the WIC.

Consistent with data from other European countries, most of the isolates (n=68) circulating in Switzerland belonged to the clade 6B.1A.5a.2a (5a.2a) and a smaller proportion (n=15) to the clade 6B.1A.5a.2a.1(5a.2a.1) (Figure 8). Within the clade 5a.2a, four subgroups were observed and characterized by specific amino acid mutations in the HA1 gene. Sixty-six (66) out of 68 sequenced isolates belonged to the subgroup C.1 (reference strain A/Sydney/5/2021) with clusters defined by amino acid P137S (n=12), including subgroup C.1.8 (n=24) with substitution V47I and A196T and subgroup C.1.9 (n=30) with K169Q mutation. The 2 remaining viruses were identified in the subgroup C.1.7.2 with amino acid substitutions D94N and T216A (no reference assigned yet) (Figure 9).

Regarding the 5a.2a.1 viruses (n=15), they were divided into two subgroups. The majority belonged to the subgroup C.1.1.1 (n=14) constituted of HA1 amino acid substitutions P137S, T277A, E356D+T216A, and a minor cluster, represented by A/Victoria/4897/2022 virus, with R45K substitution. The remaining isolate was identified in the subgroup C.1.1, represented by A/Wisconsin/67/2022 (Figure 9).

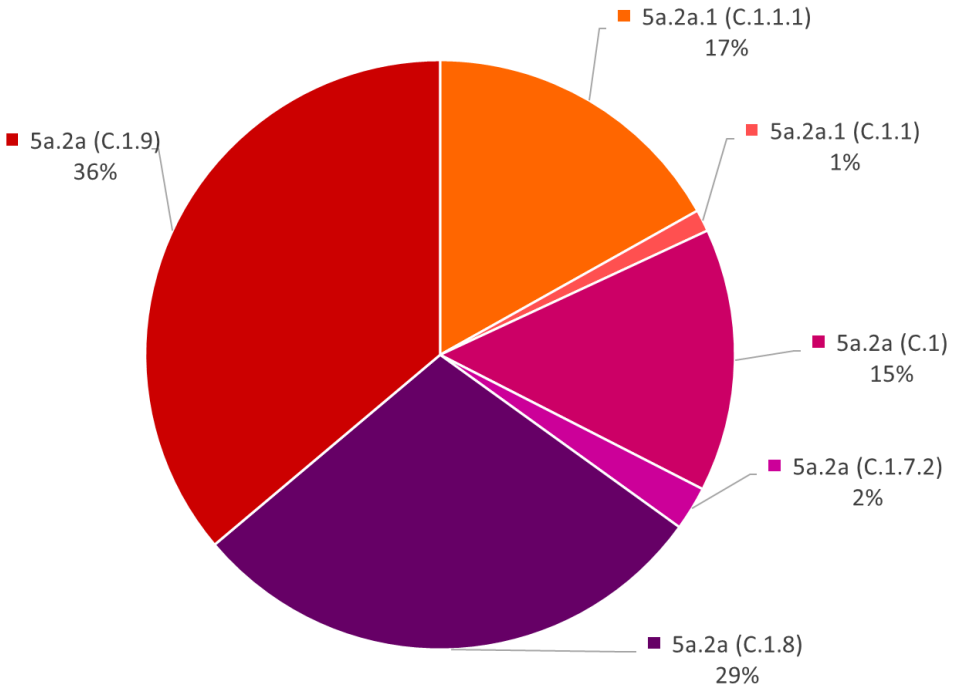


Figure 8. Distribution of influenza A(H1N1)pdm09 genetic clades viruses obtained with HA sequence and classified using Nexclade v3.8.1.

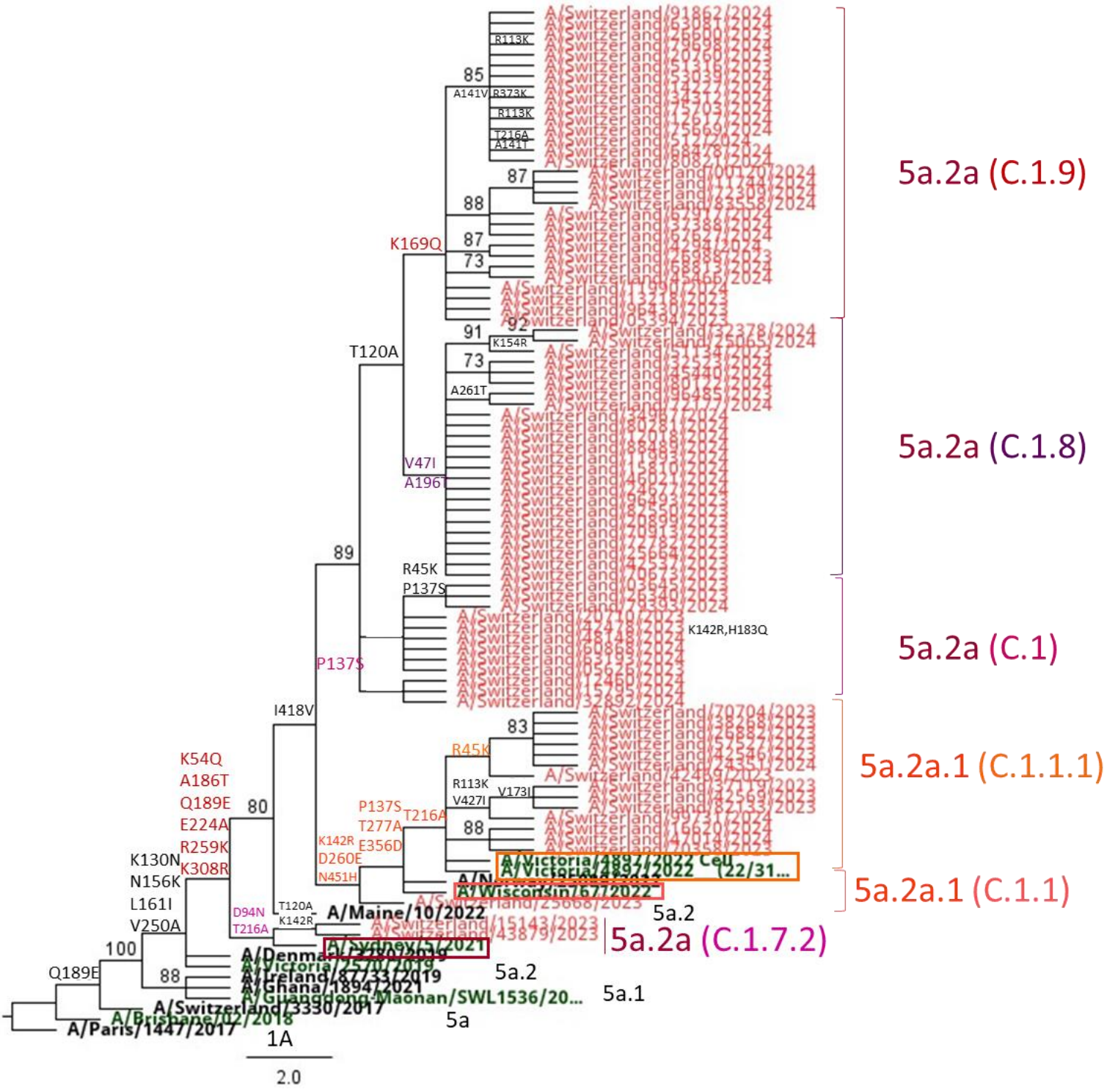


Figure 9. Phylogenetic analysis of the HA gene of A(H1N1)pdm09 viruses. Orange: influenza viruses detected in the Sentinella network during the 2023/2024 season. Green: vaccine strains for 2019-20 A/Brisbane/02/2018, 2020-21 A/Guangdong-Maonan/SWL1536/2019, 2021-23 A/Victoria/2570/2019 (egg-based), 2023 A/Sydney/5/2021(cell-/egg-based), 2023-25 A/Victoria/4897/2022. Bold: reference strains. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on which this research is based. The list is detailed in Appendix 6. Some typical amino acid substitutions characterizing the respective clusters described by the WIC and Nexclade v3.8.1 are displayed and highlighted in colors. Sequences were aligned using Geneious Prime 2022.1.1 MAFT alignment (v7.490) with default settings. A consensus tree was built from 1000 original trees in maximum likelihood (70% support threshold) using Geneious Prime 2022.1.1 PHyML (3.3.20180621) default settings.

4.4.1.2 Characterization of influenza A(H3N2) viruses

Twelve (12) A(H3N2) (27.3%) isolates were characterized by HAI. Seven (7) (58.3%) isolates reacted well (within 1- to 4-fold the homologous titer) with the antiserum raised against A/Thaïland/8/2022 (egg-based recommended vaccine strain 2024/2025; clade 2a.3a.1). Five (5) (41.6%) isolates showed good reactivity (within 1- to 4-fold titer reduction compared to the homologous) in presence of the antiserum raised against A/Darwin/9/2021-like reference virus (clade 2a) (Data not shown). All the 29 A(H3N2) isolates sequenced, belonged to clade 3C.2a1b.2a.2 (renamed as 2 since February 2023) and subclade 2a.3a.1. As observed in other countries, the A(H3N2) strains detected in Switzerland have further diversified into subgroups, all characterized by amino acid substitutions E50K, I140K, and I223V (reference and vaccine 2024/2025 strain A/Thailand/8/2022, clade 2a.3a.1).The isolates were further assigned to three different subgroups of clade 2a.3a.1. Five isolates belonged to the subgroup J.1 constituted of additional amino acid substitutions I25V and I418V, represented by the reference virus A/Sydney/856/2023. Twenty-three viruses belonged to the subgroup J.2, characterized by specific amino acid substitutions N122D and K276E (reference strain A/Sydney/878/2023). The remaining sample was attributed to the subgroup J (reference A/Thailand/8/2022 virus) (Figures 10-11).

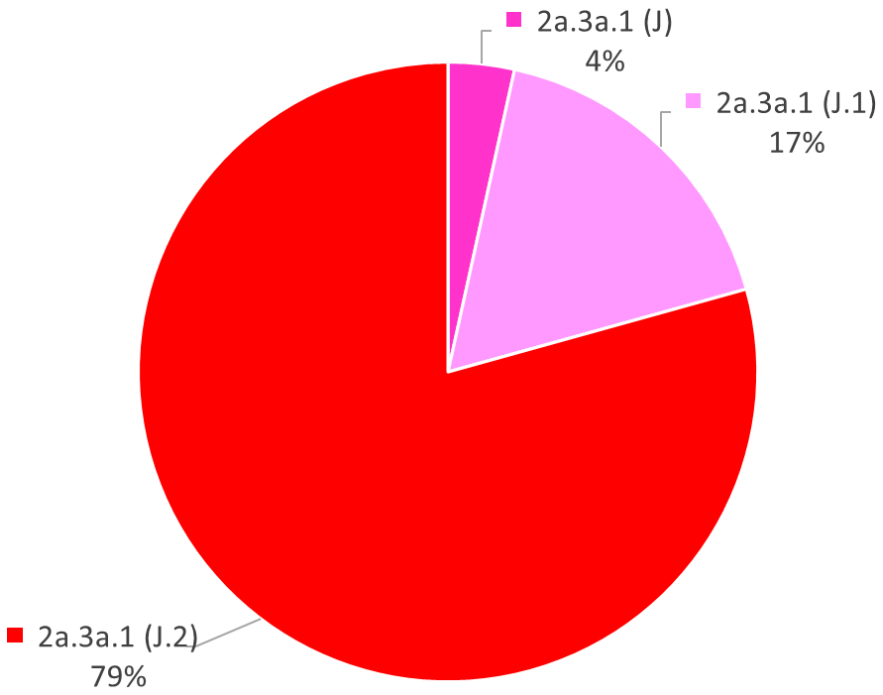


Figure 10. Distribution of influenza A(H3N2) genetic clades viruses obtained with HA sequence and classified using Nexclade v3.8.1.

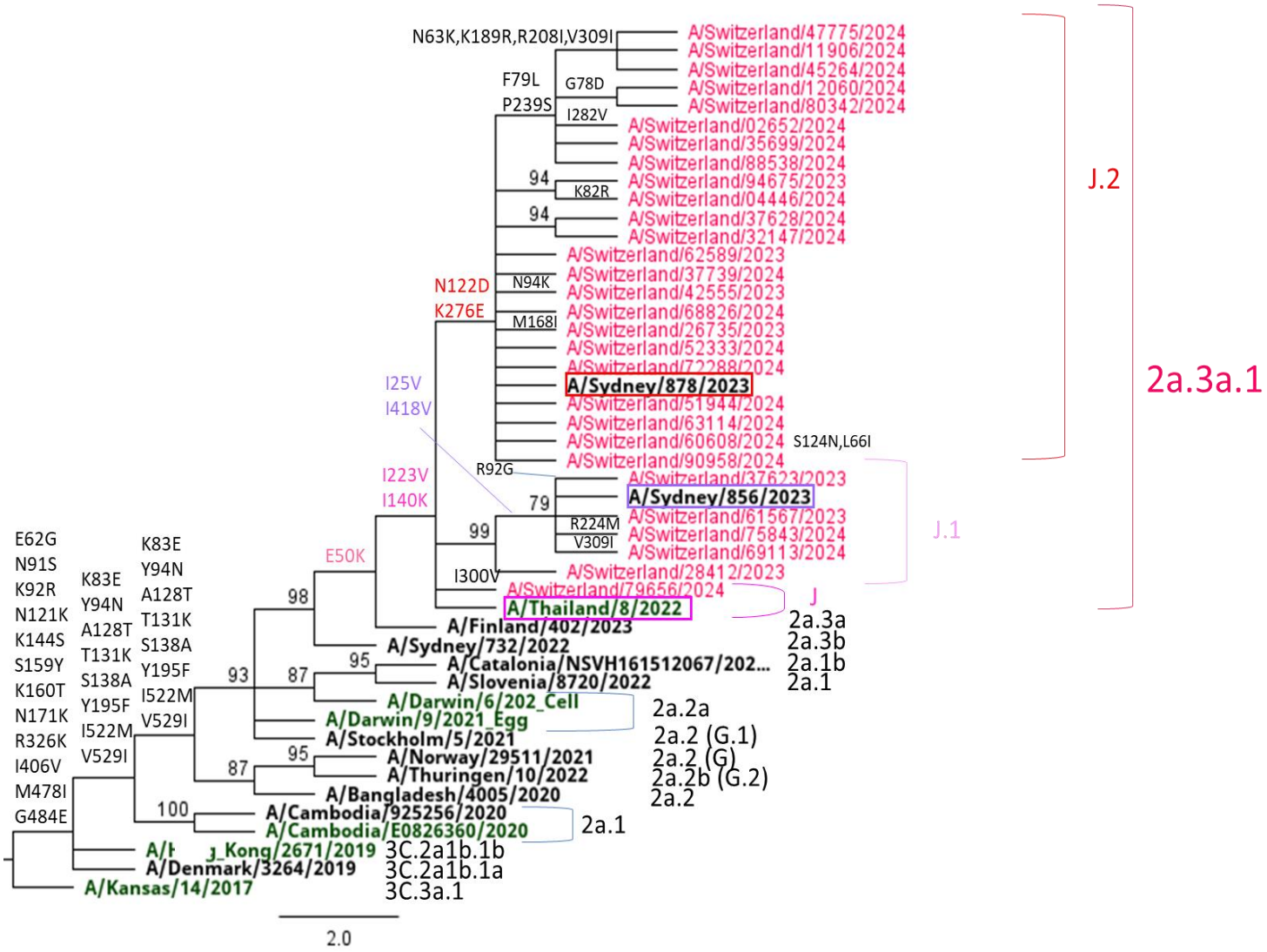


Figure 11. Phylogenetic analysis of the HA gene of A(H3N2) viruses. Pink: influenza viruses detected in the Sentinel network during the 2023/2024 season. Green: vaccine strains for 2019-20 A/Kansas/14/2017, 2020-21 A/Hong_Kong/2671/2019, 2021-22 A/Cambodia/E0826360/2020, 2022-24 A/Darwin/9/2021 (egg-based) and 2024-25 A/Thailand/8/2022. Bold: reference strains. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on which this research is based. The list is detailed in Appendix 6. Some typical amino acid substitutions characterizing the respective clusters described by the WIC and Nexclade v3.8.1 are displayed and highlighted in colors. Sequences were aligned using Geneious Prime 2022.1.1 MAFT alignment (v7.490) with default settings. A consensus tree was built from 1000 original trees in maximum likelihood (70% support threshold) using Geneious Prime 2022.1.1 PHyML (3.3.20180621) default settings.

4.4.1.3 Characterization of influenza B Victoria-like viruses

Eleven (11) (25%) B/Victoria/2/87 lineage viruses were subjected to HAI assay. All, except one (90.9%), reacted well with the antiserum raised against B/Austria/1359417/2021 virus (recommended vaccine 2023/2024, subclade V1A.3a.2). One isolate (B/Switzerland/29051/2024, clade C.5.7) was excluded from characterization due to low reaction with all antisera available (Figure 15) at the NRCI (Data not shown). This isolate was also sent to the WIC for assessment.

The 14 sequenced influenza B/Victoria/2/87 lineage viruses collected since October 2023 belonged to the clade V1A.3a.2 with the substituted amino acid residues A127T, P144L, and K203R (B/Austria/1359417/2021) (Figures 12-13). Within the V1A.3a.2 clade, the isolates were separated into three subclades. Five viruses belonged to the subclade C.5.6 represented by B/Norway/08717/2023 and characterized by amino acid substitution D129N. Five isolates were attributed to the subgroup C.5.1 with amino acid changes E183K and additional K128E substitution and represented by B/Catalonia/2279261NS/2023 reference strain. Four viruses belonged to the C.5.7 subclade characterized by amino acid substitutions E183K and additional E128G (no reference assigned yet).

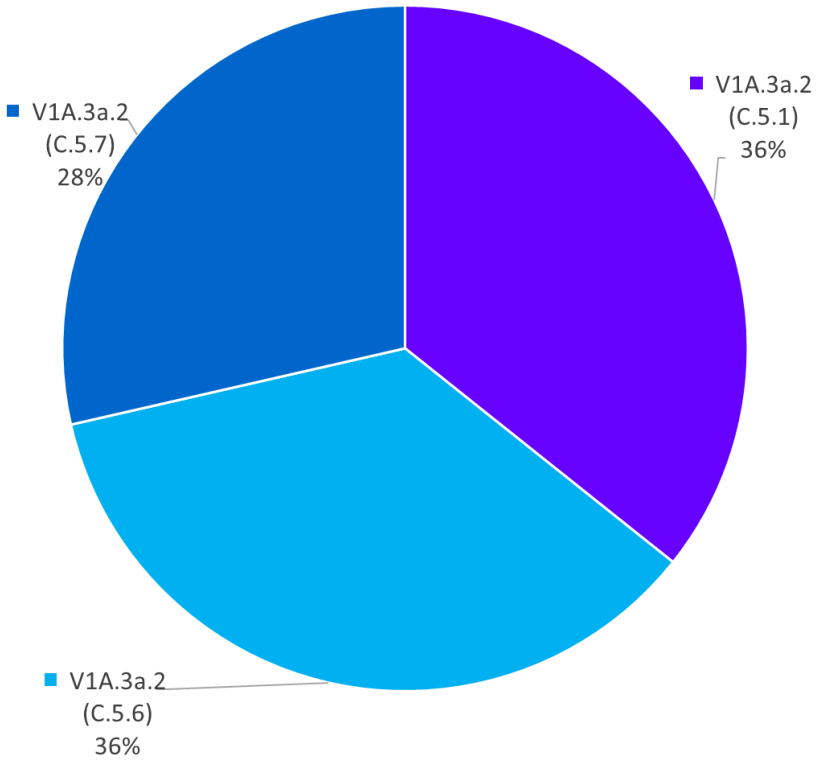


Figure 12. Distribution of influenza B/Victoria/2/87 lineage genetic clades viruses obtained with HA sequence and classified using Nexclade v3.8.1.

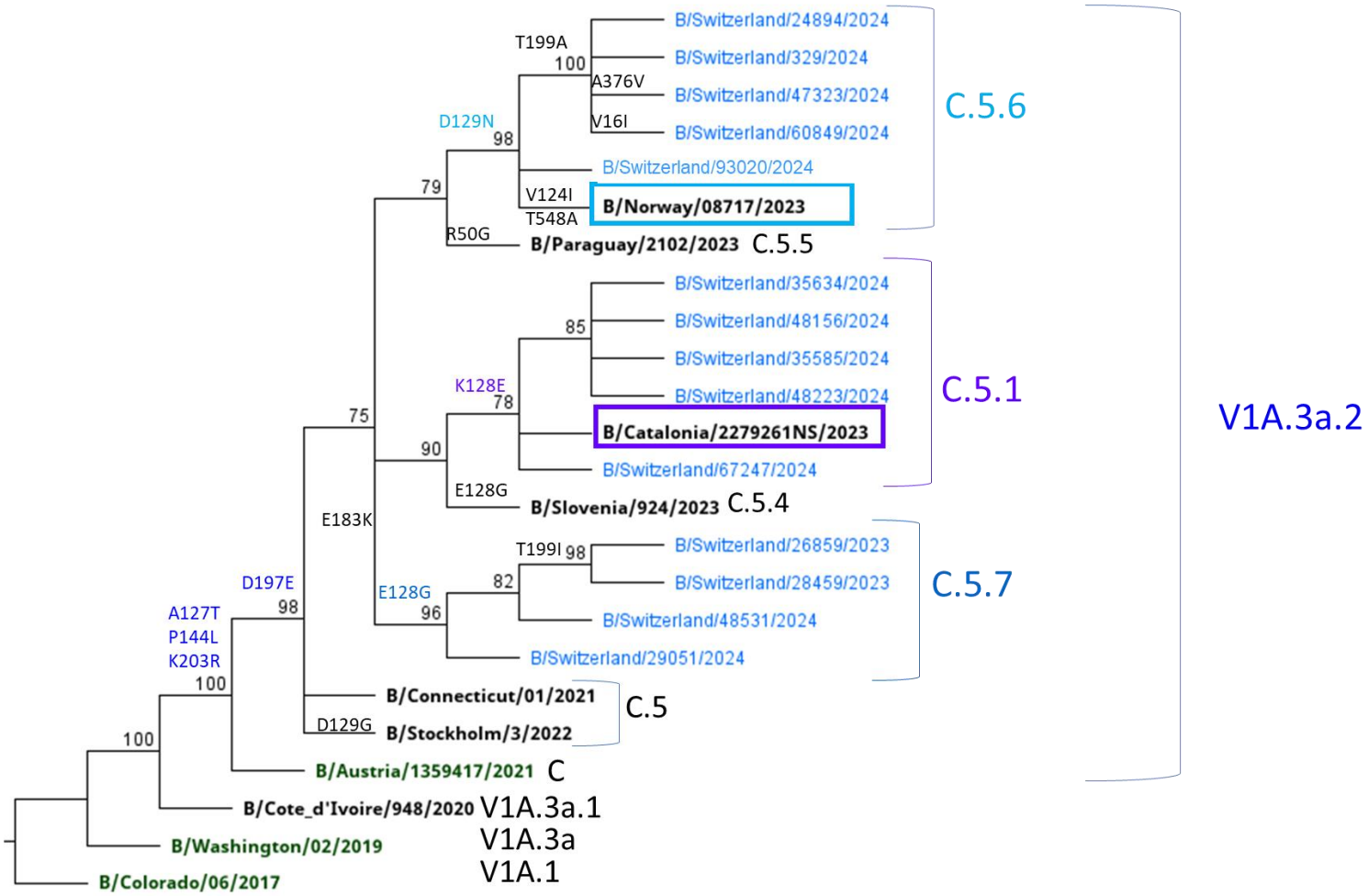


Figure 13. Phylogenetic analysis of the HA gene of B/Victoria/2/87 lineage viruses. Blue: influenza viruses detected in the sentinel network during the 2023/2024 season. Green: vaccine strains for 2018-20 B/Colorado/06/2017, 2020-22 B/Washington/02/2019, and 2022-25 B/Austria/1359417/2021. Bold: reference strains. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on which this research is based. The list is detailed in Appendix 6. Some typical amino acid substitutions characterizing the respective clusters by the WIC and Nexclade v3.8.1 are displayed and highlighted in colors. Sequences were aligned using Geneious Prime 2022.1.1 MAFT alignment (v7.490) with default settings. A consensus tree was built from 1000 original trees in maximum likelihood (70% support threshold) using Geneious Prime 2022.1.1 PHyML (3.3.20180621) default settings.

4.4.1.4 Characterization of influenza B/Yamagata-like viruses

No influenza B virus of the B/Yamagata/16/88 lineage was detected since January 2019 at the NRCI and since March 2020 worldwide.

4.4.2 Antiviral resistance

One hundred and twenty-six (126) (97.7%) NA sequences were successfully recovered: 83 were A(H1N1)pdm09, 28 A(H1N1)pdm09, and 15 B/Victoria/2/87 lineage (Data not shown). One hundred and twenty-one (121) (93.8%) PA sequences

were recovered: 78 A(H1N1)pdm09, 29 A(H3N2), and 14 B/Victoria/2/87 lineage (Data not shown).

Genotypic assessment of NA gene sequences from influenza viruses, analyzed within the Sentinella network, did not identify any mutation associated with reduced susceptibility to neuraminidase inhibitors (NAIs).

Of the 121 PA gene sequences available, genotypic assessment did not highlight any substitutions associated with reduced susceptibility to baloxavir marboxil (BM), except for one A(H3N2) isolate (A/Switzerland/04446/2024) for which the amino acid substitution A36V in the PA gene was identified. The latter may be associated with reduced susceptibility (6-fold change effective maximal concentration (EC_{50}) to BM.[76] Of note, amino acids 198E, and 199E were not covered for 2 influenza A(H1N1)pdm09 isolates thus not affording the assessment of antiviral susceptibility to BM.

Two clinical specimens from BM and oseltamivir treated hospitalized patients were sequenced for antiviral susceptibility assessment. One A(H3N2) sample displayed both NA substitution R292K and PA substitution I38T conferring highly reduced inhibition (HRI) to oseltamivir, reduced to highly reduced inhibition (R/HRI) to zanamivir and peramivir, and reduced susceptibility to BM.[76-78] The second clinical sample, an A(H1N1)pdm09, carried the double mutation NA I223R and S247G associated with RI to oseltamivir, normal to reduced inhibition (N/RI) to zanamivir and NI to peramivir. [79-81]

Phenotypic tests for antiviral resistance assessment were not performed at the NRCI. Phenotypic and genetic testing is being performed at the WIC and include samples collected from October 2023 to May 2024. The results are currently not available.

4.4.3 SARS-CoV-2 variants identification and genetic analysis

Sixty-seven (67) SARS-CoV-2 positive samples identified from week 40/2023 to week 16/2024, with Ct values lower than 32, were subjected to sequencing. Sixty-five (65) samples were characterized and fell into 28 distinct Pangolin[82] sub-lineages of variant of Interest (VOI) Omicron[83] (XBB.1.5-like, XBB.1.16-like, EG.5, BA.2.86 and JN.1-like*) (Table 3; Appendix 3).

Table 3. List of SARS-CoV-2 Pangolin sub-lineages within which Sentinella isolates were distributed

Pangolin [1] lineages (VOI)	Number of isolates	Pangolin lineages (VOI)	Number of isolates
BA.2.86	1	HV.1 (EG.5-like)	4
EG.10.1 (EG.5-like)	1	JN.1	11
EG.5.1 (EG.5-like)	2	JN.1.1 (JN.1-like)	1
EG.5.1.1 (EG.5-like)	8	JN.1.1.1 (JN.1-like)	1
EG.5.1.3 (EG.5-like)	2	JN.1.11 (JN.1-like)	1
EG.5.1.4 (EG.5-like)	3	JN.1.3 (JN.1-like)	3
EG.5.1.6 (EG.5-like)	1	JN.1.4 (JN.1-like)	2
EG.6.1 (EG.5-like)	1	JN.1.6 (JN.1-like)	1
FL.1.5 (XBB.1.9-like)	1	JN.1.7 (JN.1-like)	1
FL.1.5.1 (XBB.1.9-like)	3	XBB.1.16.11 (XBB.1.16-like)	2
GA.4 (XBB.1.17-like)	1	XBB.1.16.6 (XBB.1.16-like)	2
GK.1.1 (XBB.1.5-like)	1	XBB.1.41.1	1
GK.1.3(XBB.1.5-like)	1	XBB.1.5	1
HK.3 (EG.5-like)	7	NA	2
HK.5 (EG.5-like)	1	n	67

[1] Web-based lineage assessment: https://cov-lineages.org/lineage_list.html ; NA: not applied

At the beginning of the monitored season (week 40/2023 to week 04/2024), viruses from the lineages XBB.1.5-like, XBB1.16-like and EG.5 were dominant accounting for 55.2% (n=37) of the characterized isolates. Since week 02/2024, and despite the low detection number, viruses of JN.1-like lineage were replacing the previous sub-lineages and became dominant (n=21; 31.3%) (Figure 14). Of note, during the weeks 45/2023 to 01/2024, no SARS-CoV-2 positive samples were submitted to sequencing. Furthermore, Sentinella isolates were not evenly included in the national SARS-CoV-2 genomic surveillance programme. During weeks 14/2024 and week 15/2024, no SARS-CoV-2 were detected. In weeks 04/2024, 11/2024, 13/2024, and 16/2024, no SARS-CoV-2 samples were submitted to GISAID either. During week 07/2024, only one sample was submitted to GISAID, but sequencing was unsuccessful.

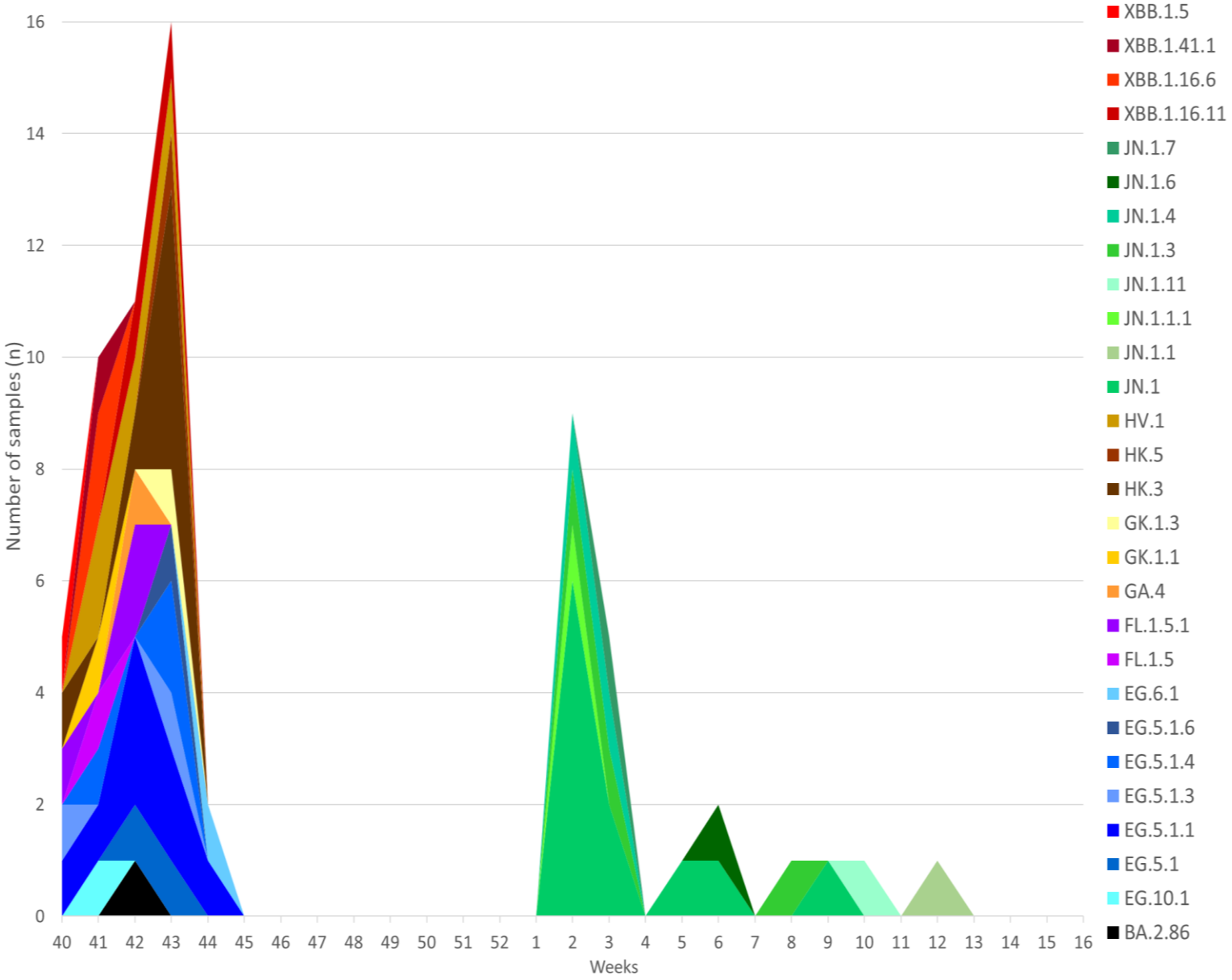


Figure 14. **Distribution of SARS-CoV-2 sub-lineages within the Sentinella surveillance (40/2023-16/2024).** Of note, no samples between weeks 45/2023 and 01/2024, in weeks 04/2024, 07/2024, 11/2024 and between 13/2024 and 16/2024 were sequenced.

4.5 Influenza circulation Worldwide

The global circulation of influenza viruses across the WHO regions was comparable in 2023/2024 and 2022/2023 seasons (GISRS monitoring system).[84] Overall, both IA and IB viruses have been detected globally with a dominance of IA. IA subtypes, A(H1N1)pdm09 and A(H3N2) dominance varied among influenza transmission zones.

In the Northern Hemisphere, week 47/2023 marked the start of the influenza activity, with a peak in week 52/2023 (22.4%). Except in Middle Africa, where IB virus was mostly detected, all the WHO regions reported a dominance of IA virus during

2023/2024 season. A(H1N1)pdm09 subtype was dominant in Central America and Caribbean, Tropical South America, Central and Southern Asia, North America, Northern and Southwest Europe. In Northern Africa, A(H1N1)pdm09 virus was primarily detected, followed by A(H3N2) from week 07/2024. A(H3N2) virus was dominant in Eastern Africa, Eastern Europe, and Western Africa. Influenza A(H3N2) and B viruses were co-detected in Eastern Asia, with a shift towards A(H1N1)pdm09 viruses from week 12/2024. In Western and South-East Asia, co-detection of A(H1N1)pdm09 and A(H3N2) subtypes was observed.

As expected, the influenza activity in the northern hemisphere declined by the end of the described period and raised from week 16/2024 up to week 26/2024 in the southern hemisphere with a dominance of IA virus.

Data from ECDC and WHO European regions collected from September 2023 to January 2024, showed that the global circulation of IA, subtype A(H1N1)pdm09 virus was attributed to clades 5a.2a and 5a.2a.1 with a global predominance of 5a.2a viruses.[74] Within the 5a.2a viruses characterised by the HA amino acid substitutions K54Q,A186T,E224A, R259K and K308R, a large subgroup defined by amino acid substitution I418V (reference strain A/Sydney/5/2021, subclade C.1) was observed in major parts of the world. Additional HA substitutions D94N and T216A were found leading to an emergence of a minor subclade not referenced yet, predominating mostly in New Zealand, Indonesia, and Australia. One minor subclade that was reported in Cambodia, Vietnam, and Thailand was referenced as the A/Maine/10/2022 strain, subclade C.1.2 and harbouring the A48P substitution. Concerning the 5a.2a.1 clade, represented by HA amino acid substitutions P137S, K142R, D260E, T277A, E356D, and N451H, two main subgroups were characterized. A major group with T216A substitution (reference A/Victoria/4897/2022 recommended vaccine strain 2023/2024, subclade C.1.1.1) and a minor clade represented by A/Wisconsin/67/2022 (cell-based recommended vaccine strain 2024/2025, subclade C.1.1). Most of the strains from both clades 5a.2a and 5a.2a.1 were well-recognised by the antiserum raised against both the recommended vaccines egg- and cell-based 2023/2024 A/Victoria/4897/2022 strain.

Antigenic analyses for A(H3N2) virus demonstrated that the clade 3C.2a1b.2a.2 (renamed as 2 since February 2023) dominated since the beginning of February 2023 worldwide. During the monitoring period 2023/2024, the great majority of A(H3N2)

viruses belonged to clade 2a.3a.1, which share the HA amino acid substitution E50K with clade 2a.3a but bears additional changes I140K, and I223V represented by the recommended vaccine 2024/2025 A/Thailand/08/2022, subclade J (previously assigned as H). Among the viruses belonging to clade 2a.3a.1, four main subgroups were identified with specific HA amino acid substitutions. One subclade J.1 (previously assigned as H.1), defined by I25V, V347M and some with I418V substitutions new reference strain A/Sydney/856/2023, was seen mainly in Europe, South-East Asia, and Australia. The viruses from subclade J.2 (previously assigned as H.2) with the N122D and K276E substitutions and represented by the new reference A/Sydney/878/2023 strain were predominating in the USA, the Middle East, and in Europe the virus from subclade J.2 strain. A minor subclade J.4 (previously assigned as H.4) (no reference strain assigned yet) was identified in Norway, West Africa and Central America. A minority of viruses reported in West Africa were attributed to the clade 2a.3a (reference strain A/Finland/402/2023), with substitutions K276E and V347M. Most of the viruses from subclade 2a.3a.1 were antigenically recognised by A/Thailand/08/2022 virus.

Despite the low number of detections during the reporting period, the clade V1A.3a.2 within the influenza B/Victoria/2/87 lineage remained predominant since 1st February 2023 in all geographic regions. The clade is characterized by HA amino acid substitutions A127T, P144L, N150K, G184E, N197D, K203R, and E279K (reference and recommended vaccine 2023/2024 B/Austria/1359417/2021 strain). Within this clade, recent viruses emerged with an additional substitution D197E, which is represented by the reference strain B/Connecticut/01/2021 (subclade C.5). Within the subclade C.5, 5 subgroups were identified around the world. The subclade C.5.1 defined by E183K and represented by B/Catalonia/2279261NS/2023 was dominant in the USA, Central America, Brazil and Europe. The subgroup C.5.4 with V117I, E128K, A154T, and K326R (reference B/Slovenia/924/2023) was mostly detected in the Americas. The subclade C.5.5 (represented by B/Paraguay/2102/2023) characterized by R80G, E184K was detected in the USA, Colombia, and Venezuela. The subclade C.5.6 with D129N (B/Norway/08717/2023) was abundant in Australia, South-East Asia, Middle East and Africa. A recent subclade, C.5.7 (no reference assigned yet) characterized by E183K and E128G mutations, emerged in China, Thailand, Europe, Middle East, and South Africa. All B/Victoria-lineage viruses collected since the beginning of the season were well-recognised by the antisera raised against

B/Austria/1359417/2021 and -like viruses (recommended vaccine 2023/2024, clade V1A.3a.2).

Antiviral resistance tests performed by 17 countries from week 40/2023 to 17/2024, showed that of the 4,562 viruses tested, 42 A(H1N1)pdm09 and 2 A(H3N2) displayed RI or HRI to oseltamivir, 2 A(H1N1)pdm09 and 2 A(H3N2) to zanamivir and 2 A(H1N1)pdm09 and 2 A(H3N2) to BM. Twenty-three (23) of them harboured the recent double mutation NA A(H1N1)pdm09 I223V and S247N, conferring RI to oseltamivir by 13- to 16- fold EC_{50} change.[85,86]

5. WHO recommendation for the composition of influenza virus vaccines for the 2024/2025 influenza season

Influenza vaccine recommendations are based on data collected within the Global Influenza Surveillance Response System network: virus antigenic and genetic characterization data, human serology data, virus fitness forecasting data, antiviral resistance data, vaccine effectiveness, and the availability of candidate vaccine viruses.

The vaccine strains recommended for the 2024/2025 northern hemisphere influenza vaccine by the WHO experts are shown in table 4.

Table 4. Recommended influenza vaccine composition for the 2024/2025 influenza season.
a: for egg-based vaccines. b: for cell-based vaccines

a	Vaccine strains 2024/25
A(H1N1)pdm09	A/Victoria/4897/2022 (H1N1)pdm09-like virus
A(H3N2)	A/Thailand/8/2022 (H3N2)-like virus
B/Victoria lineage	B/Austria/1359417/2021 (B/Victoria lineage)-like virus *
B/Yamagata lineage	B/Phuket/3073/2013 (B/Yamagata lineage)-like virus

**Only B strain included in the trivalent vaccine*

b	Vaccine strains 2024/25
A(H1N1)pdm09	A/Wisconsin/67/2022 (H1N1)pdm09-like virus
A(H3N2)	A/Massachusetts/18/2022 (H3N2)-like virus
B/Victoria lineage	B/Austria/1359417/2021 (B/Victoria lineage)-like virus *
B/Yamagata lineage	B/Phuket/3073/2013 (B/Yamagata lineage)-like virus

**Only B strain included in the trivalent vaccine*

6. Human infection with influenza viruses of zoonotic origin

Transmission of zoonotic influenza viruses to humans often leads to infections limited to a single individual and sometimes to their close contacts. However widespread

outbreaks and pandemics are also possible in the case of efficient human-to-human transmission. Recombination events between porcine/avian and human viruses due to concomitant circulation can drive human adaptation of zoonotic strains. To allow for the early identification and rapid containment of new potential animal-to-human transmission events, several countries, including Switzerland, have introduced regular screening of animals such as poultry, wild birds, and farm pigs for the presence of the respective influenza strains.

6.1 Swine-to-human influenza virus transmission

Human infections with IA viruses of porcine origin are identified as “variant” viruses and denoted with a letter “v”, such as A(H1N2)v, A(H3N2)v and A(H1N1)v.

6.1.1 In Switzerland

In 2001, the Federal Food Safety and Veterinary Office initiated a collaborative project with the Federal Office of Public Health, the Institute of Virology of the Vetsuisse Faculty of the University of Zurich, the Pig Health Service (SSP) of SUISAG, and the NRCI, which aimed at monitoring the swine influenza circulation in Switzerland. The project is named “Surveillance of swine influenza in pigs and humans”. In this context, specimens from farm pigs with respiratory symptoms are sent to, and analysed by, the National Veterinarian Institute (Vetvir, Zurich). In parallel, samples from pig breeders (or their employees), who have been in contact with influenza-infected animals and present with ILI symptoms, are sent to the NRCI. The latter are analysed using a rRT-PCR with the capacity to distinguish IA viruses of human and animal origin, both avian and porcine. Positive samples are further characterized by sequencing.

From week 40/2023 to week 16/2024 of the 3 non-sentinel samples originating from Swiss farmers having contact with pigs, one was real-time RT-PCR positive for an A(H1N1)v virus. The nanopore sequencing of this isolate (A/Switzerland/114/2023) confirmed the porcine origin of the virus, which likely belongs to an avian-like H1N1 swine lineage 1.C.2.2 circulating in Europe. Of note, no further human-to-human transmission has been observed.

6.1.2 Worldwide

Since 2010, 499 [439 A(H3N2)v, 18 A(H1N1)v, 40 A(H1N2)v, 1 A(H1)v, 1 A(H3)v] human cases of variant influenza virus have been reported in several states in the

USA.[87] These cases were often mild with no evidence of further human-to-human transmission. In 2024, influenza A(H1N2)v was reported in three individuals in the State of Pennsylvania who had contact with pigs. No human-to-human transmission was reported.[87-90] A new case of human A(H1N2)v infection was also reported in UK.[91] Overall, 27 cases of A(H1N2)v or A(H1N1)v have been reported globally since 2019 and, among them, 4 were from EU/EEA countries.[88]

6.2 Avian influenza A subtypes in humans

As for porcine influenza, human cases of infection with avian viruses are sporadically reported. Since the start of 2021, 28 detections of Highly Pathogenic Avian Influenza HPAI A(H5N1) in humans have been notified to WHO, of which 13 belonged to the recent clade 2.3.4.4b.[92] The cumulative number of confirmed human cases and deaths since 2003 are 887 and 462, respectively.[93] Since April 2024 and up to 26th July 2024, 13 human infections of A(H5) were reported in Texas, Michigan, and Colorado.[94,95] Nine out of 13 were confirmed to be A(H5N1). These cases were farm workers who had contact with poultry (n=9) or which were exposed to sick dairy cows (n=4). The individuals did not require hospitalisation and suffered from mild symptoms with conjunctivitis, although this virus can cause morbidity and mortality in mammalian species.[95] Furthermore, sequences from 6 humans in Colorado contain the amino acid mutation M631L in PB2 gene, which is the same marker of mammalian adaptation identified in more than 99% of dairy cow outbreak and also identified in the first human case in the US. However, none of them contain the mammalian adaptation marker in the PB2 gene E627K, except one so far.[95] Furthermore, no marker associated with antiviral resistance to NAIs was observed. One severe case of A(H5N1) infection, but who survived, was reported in Australia. He returned home from India on 24 May 2024.[96]

At the NRCI, we received one sample from a person with ILI symptoms who returned from Portugal. The individual mentioned that he stayed in a region where avian influenza was reported in birds. The individual tested negative for IA and IB as well as for an H5 specific real-time RT-PCR.

A lethal case of A(H5N6) virus infection was reported from China in a 50 years-old woman who had contact with backyard poultry.[96] A second human A(H5N6) case was notified in July 2024 in a 70 years-old woman also in China.[97]

In 2024, one case of A(H9N2) was detected for the first time in Vietnam on April 9th in an individual living near a poultry market.[98] Two additional cases were also reported in China[99] and India[100], respectively. Since December 2015, 101 cases, including 33 deaths, have been notified to the WHO in the Western Pacific regions.[99]

One Low Pathogenic Avian Influenza (LPAI) A(H10N3) infection was reported in China on 2 April 2024 in a poultry and livestock farmer. This is the third case detected in China and worldwide to date. [98,101]

One human LPAI A(H10N5) infection was reported in China with an onset date of 30 November 2023.[101]

As of 23 May 2024, one deadly case A(H5N2) was detected in a 59-years old man in Mexico. This is the first human laboratory-confirmed case ever reported globally.[102]

No human cases of avian influenza A(H3N8), A(H7N4), and A(H7N9) were reported for 2024.

7. Avian influenza A in animals

The primary reservoir for low and high pathogenic avian influenza A (L/HPAI) viruses is aquatic wild birds. Both virus types can cause subclinical to major outbreaks, with high mortality, in poultry and wild birds respectively.

The largest number of avian influenza outbreaks in Europe, since 2016/2017, was observed during 2022/2023.[103,104] In the ongoing season, the number of HPAI virus detections is the lowest since 2019/2020. Six hundred and fifty seven (657) detections in 30 countries and 344 detections in 22 countries were reported in wild and domestic birds, respectively.[104] HPAI A(H5), A(H5N1), A(H5N5) viruses were the most common subtypes identified in Europe during this season. In late 2023, HPAI A(H5N1) viruses were identified in new aquatic mammals such as elephant seal and fur seal in Antarctic, while a polar bear was infected by HPAI A(H5N1) virus in Alaska.[105,106] Cambodia also reported a first HPAI A(H5N1) outbreak in backyard poultry near the Vietnamese boarder in three years.[107]

In March 2024, the Centers for Disease Control and Prevention (CDC) reported for the first time HPAI A(H5N1) virus infection in juvenile goats, dairy cows, and alpacas in several US states.[105,108,109] Since May 2024, Australia reported 4 domestic birds infected with HPAI A(H7N3) and A(H7N9).[110]

In Switzerland, by the end of December 2023 and to date, one HPAI A(H5N1) virus was identified in a mute swan in the canton of Zürich.[111,112]

HPAI infections in birds and mammals with 2.3.4.4b clade viruses are widely distributed worldwide.

7.1 HPAI A(H5) outbreaks in the USA

HPAI A(H5) avian influenza viruses are circulating at high intensity in the US with, since March 2024, major outbreaks in dairy cows and poultry. A(H5) virus from the recent genotype B3.13 has been identified in 171 dairy cows' herds in 13 US states, including Michigan, Texas, and Colorado, where human A(H5) infections in farm workers were identified. Interestingly, in cows, the virus was detected mainly in the cow udders, which seem to constitute an ideal cell host for H5N1 propagation.[113] Since April 2024, there has been A(H5) detections in 35 commercial and 19 backyard flocks for a total of 18.4 million birds infected. [95]

8. Discussion

Sex and age groups distributions were comparable to previous years within the Sentinella population.

Concerning ILI and ARI suspicions, 310 positive respiratory viruses including 26 IA/IB were detected in samples declared as ARI syndromes. Regarding ILI declaration, 69 specimens positive for respiratory viruses, including 34 IA/IB were detected. According to the definitions, the ARI is more sensitive and would result in a larger number of cases compared to the ILI, which is more specific and has a higher positive predictive value for influenza.[114] The number of positive specimens associated with ILI syndromes reflects well the influenza season, while the positivity linked to ARI suspicions highlights the continuing annual circulation of other respiratory viruses (Appendix 1).

A low rate (13.2%), but similar compared to pre-COVID-19 pandemic season (12.6% in 2018/2019), of individuals tested in the context of the Sentinella surveillance were vaccinated against influenza during 2023/2024. Compared to 2018/2019 (41.8%), 50% of the tested elderly (≥65 years old), with a known vaccination status were vaccinated; among whom 11.6% were positive for influenza. A majority had an A(H1N1)pdm09 strain.

Our data are consistent with the ECDC technical report based on the previous surveys performed by the Vaccine European New Integrated Collaboration Effort (VENICE) on influenza vaccine recommendations and vaccination coverage data collection, indicating a low vaccine coverage, although there was an overall increase in vaccination uptake within the European countries.[115] This was also consistent with the ECDC report based on a survey of influenza vaccine effectiveness in European primary care and hospital centres from September 2023 to January 2024.[116]

For 2023/2024 vaccination rate against COVID-19 was of 6.6% among all age groups within Sentinella population. Not surprisingly vaccination rate was higher in adults (43.1%) and elderly (47.7%). Preliminary results from ECDC showed similar percentages of vaccination coverage by age groups, though there was high variation across countries. This difference may be due to different recommendations for COVID-19 vaccination, with variable target age groups during the 2023/2024 season.[117] Therefore, data have to be consolidated and actually have to be interpreted with caution.

For the fourth consecutive year, the NRCI monitored not only influenza viruses circulating in Switzerland but also a panel of other respiratory viruses. The number of samples (n=1,958) received from week 40/2023 to 16/2024 was comparable to the number (n=1,950) received in 2022/2023 for the same period.

The median positivity rate for the respiratory viruses during week 40/2023 to week 16/2024 was comparable (62.2%) to previous seasons, for 2022/2023 (69%), 2021/2022 (66%) and 2019/2020 (61.9%), but was higher than for 2020/2021 (49.2%). As usually observed, the increase in detection of respiratory viruses within the Sentinella network fitted well with the increase in the number of cases identified in the Swiss population (Figure 5b; Appendix 1).

As previously mentioned, data on respiratory viruses other than influenza is only available since 2019/2020 within the Sentinella network, and the emergence of SARS-CoV-2 in 2019 was shown to significantly impact the circulation of other respiratory viruses (Appendix 5).[118,119]

During the pandemic period, unusual circulation of some respiratory viruses such as RSV was observed. [120] Usually RSV was shown to alternate between low prevalence followed by high prevalence periods during annual epidemics in Switzerland.[121]

However, during the 2021/2022 season, RSV started to increase early in summer and showed prolonged circulation until fall, while in 2022/2023 it circulated mostly during fall until winter season. During the 2023/2024 season, RSV epidemic was observed during mid-fall until beginning spring in Switzerland (Figure 5b, Appendix 5). This phenomenon was also observed in other countries.[120,122-125] Indeed, the peak of RSV normally circulates during winter season in the temperate northern regions and during rainy seasons in the tropical and subtropical areas. This was observed that in temperate climate seasons, RSV is more prevalent when the temperature decreases.[126] We can speculate that climate change could be a factor that may contribute to perturbate the seasonal RSV circulation. Indeed, the permanent variation of temperatures could promote the prolonged occurrence of this virus.[127] In addition to this, RSV epidemic changed during COVID-19 pandemic.[120] Due to the hygiene measures and global lockdown restrictions, there was less proximity and more stringent health behaviours, thereby decreasing in long term the detection of RSV in the global population.[128] We could hypothesise that the waning of RSV immunity at the population level resulting from a lack of immune stimulation would increase the risk of infection and severity of disease, especially in vulnerable individuals, such as children. This has been showed in a Dutch study, where neutralising antibody levels against RSV decreased during 2020 and 2021 COVID-19 pandemic and during period of low RSV detection .[129] However, the association with decline of neutralising antibodies and immune protection remains to be determined.

The HMPV epidemic started beginning January 2024 with a prolonged circulation until spring. Even if delayed compared to 2022/2023 season (peak in week 2/2023), 2023/2024 HMPV circulation was consistent with the seasonality usually observed for this virus, which ranges from winter to late spring in temperate regions. [130-133]

During 2023/2024 season, SARS-CoV-2 virus co-dominated with RV/EV between week 40/2023 and week 51/2023, with a positivity peak at 43.6% (n=51) in week 49/2023, and decreased sharply thereafter, while influenza season was starting. SARS-CoV-2 continued to circulate at low levels during the second part of the period. Although there is a trend of SARS-CoV-2 seasonality displayed during fall, clear patterns have not yet been established and possible viral potential interference between SARS-CoV-2 and influenza needs to be further investigated.[134] Globally, the SARS-CoV-2 positivity rate reported to GISRS and to FluNet was of 7.3% from 79

countries during end 28 April 2024.[36] During 2023/2024 season, the total COVID-19 cases reported to the WHO decreased globally since week 17/2023.[135] JN.1-like lineage was the most reported VOI (from 130 countries) and accounted for 54.3% of sequences recovered during week 17, but declined from a prevalence of 69% in week 14/2024.[36] There are currently no SARS-CoV-2 lineages corresponding to the ECDC's VOC criteria.[136] A continuous update of SARS-CoV-2 variants evolution in Switzerland and in worldwide can be found on Covariants[137] and CoV-Spectrum.[138]

RV/EV remained the third most prevalent viruses after SARS-CoV-2 and influenza viruses during 2023/2024. As expected, RV/EV detection was consistent throughout the year with a peak of positivity reaching 42.9% at week 41/2023 (n=30). Regarding the other human coronaviruses, as for the previous season, only HCoV OC43 was regularly detected through the surveillance period (n=37). Although HCoV HKU1 was sporadically detected at a low rate during the spring 2023, cases were regularly reported during winter and mid-spring in 2023/2024 (n=30). In contrast, HCoV 229E was only sporadically detected (n=15) throughout the 2023/2024 season. Regarding HCoV NL63 virus, the 2023/2024 season was marked by a seldom detection with only 4 cases identified. This is the opposite of what has been observed during the previous season but consistent with the usual biannual circulations. HCoV NL63 virus accounted for 0.3% of the virus detected in 2023/2024, 2.1 % in 2022/2023, 0.1% in 2021/2022, 11.3% in 2020/2021, and 2.9% in 2019/2020. Human coronaviruses tend to exhibit seasonal circulation, with peaks mostly in winter in the Northern Hemisphere, however the prevalence pattern of each HCoV strain varies between countries and from year to year.[139,140]

In concordance with their seasonal pattern[59,141], HPIV1/3 and HPIV2/4 were mostly detected in winter-spring and autumn during 2023/2024 surveillance period, respectively. Interestingly, this was not the case for HPIV2/4 during 2019/2020, 2020/2021, and 2021/2022, where only sporadic cases were observed. Since 2022/2023, epidemics of parainfluenza viruses tend towards a return of seasonality for each serotype.[142]

Consistent with the observed prevalence in Europe[143], HBoV detection rate remained low during the four last surveillance periods (0.7%, in 2023/2024, 0.8% in 2022/2023, 1.4% in 2021/2022, and 0.3 % in 2020/2021). The virus was mainly found in children.[144]

Co-detections accounted for 7.9%, 10.5%, 11.3% and 7.2% of the positive samples in 2023/2024, 2022/2023, 2021/2022, and 2020/2021, respectively. This observation is consistent with existing literature.[145,146] In 2023/2024, the most common co-detection was SARS-CoV-2 (53.5%) combined with Influenza (20/53), RV/EV (15/53) or RSV (8/53). Consistent with what could be expected during the previous years, the co-detections occurred when the different viruses showed the highest positivity rate at their respective epidemic/circulation period.[147]

Of note, the rRT-PCR respiratory panel used at the NRCI does not target bacterial or fungal pathogens. However, the latter are also often co-detected along with respiratory viruses, particularly in hospitalized patients.[146]

During 2023/2024, influenza virus activity continued to display similar epidemic levels to those observed before the COVID-19 pandemic. Consistent with the European countries data [148], influenza season in Switzerland started in week 49/2023 overpassing the ECDC 10% positivity threshold, and lasted 14 weeks until week 10/2024, with a positivity peak at week 5/2024 (n=46; 50%). This was comparable to 2022/2023 season but with a shorter season (peak of positivity during week 52/2022; 53.1%; lasted 21 weeks).

In Switzerland, as in other European countries[148], influenza virus type A A(H1N1)pdm09 subtype predominated, followed by a small increase of influenza type B (B/Victoria/2/87 lineage), from week 7/2024 to week 17/2024. Compared with previous seasons, genetic data, as well as influenza detections reporting to TESSY/ECDC in 2023/2024, remained high although there was a decrease in antigenic data reporting compared to 2022/2023.[85] This may be due to the changes in the reporting forms that excluded antigenic characterization data from the total number of cases reporting.

Antigenic analyses from the NRCI showed that most of the A(H1N1)pdm09 isolates were well recognised by the antiserum raised against the Northern Hemisphere vaccine strain 2023/2024 A/Victoria/4897/2022 (clade 5a.2a.1) and one was antigenically characterized by the antiserum raised against the reference strain A/Norway/25089/2022 (clade 5a.2a.1). All isolates belonged to both 5a.2a and 5a.2a.1 subgroups with 5a.2a clade being dominant, and further divided into recent subgroups. Our genetic results were consistent with the WIC reports and the clades attributed to our samples were also found in other European countries.[148]

Most of the A(H3N2) tested samples were well recognised by both the antiserum raised against the Northern Hemisphere vaccine strain 2023/2024 A/Darwin/9/2021 (clade 2a.2) and the antiserum raised against the Northern Hemisphere vaccine strain 2024/2025 A/Thailand/8/2022. Furthermore, data from the WIC showed variable recognition by current 2a.3a.1 reference and vaccine antisera for 2a.3a.1 viruses collected since September 2024. Most of the 2a.3a.1 viruses were well recognised by the antiserum raised against the vaccine 2024/2025 A/Thailand/8/2022 and the reference strain A/Albania/289813/2022 (cell-propagated).[148] All A(H3N2) isolates belonged to the clade 2a.3a.1 and subsequently to J.2, J.1 and J subclades. This was consistent with the WIC analysis and the predominance of these clades globally.[148] The majority of B/Victoria/2/87 lineage viruses were well recognized by the antiserum raised against the Northern Hemisphere 2023/2024 vaccine strain B/Austria/1359417/2021. This was consistent with results from the WIC. All viruses belonged to the clade V1A.3a.2, subdivided into three subclades (C.5.1, C.5.6, C.5.7) which has predominated since 1st September 2022 globally.[148]

B/Yamagata/16/88 lineage viruses remained undetected since March 2020. This repeated lack of detection may suggest that the B/Yamagata/16/88 lineage may either be extinct, close to extinction or barely circulating.

The constant evolution and antigenic drift increase the risk that the antigens included in the vaccines will not represent the viruses that will circulate during the influenza season, thus reducing vaccine effectiveness.[149] This emphasises the importance of regularly monitoring influenza genetic and antigenic evolution.

During the 2023/2024 season, none of the viruses sequenced at the NRCI, in the context of the national surveillance program, exhibited mutations associated with reduced susceptibility to oseltamivir, peramivir nor zanamivir. Only one isolate had a PA sequence which displayed the amino acid substitution A36V as a marker of reduced susceptibility to BM. These results were consistent with those from the summary WHO Europe report.[148]

Even if already suspected from 2021/2022 influenza moderate circulation, 2023/2024 data from ECDC/Tessy, GISAID, GISRS and NICs confirms the return of influenza circulation to a similar level as pre-COVID-19 pandemic seasons and high genetic diversity through the emergence of new subclades.

During the five previous years, the number of H/LPAI epidemics in birds has never been as elevated, now reaching all five continents.

This high prevalence of avian influenza may increase the risk of outbreaks in domestic birds, mainly in poultry, resulting in high mortality rates both due to natural infection and massive culling. For instance, the prevention of recent bird flu outbreak among poultry and dairy cattle in the USA led to the elimination of about 2 million chickens in the state of Colorado.[150] This suggests not only an important economic loss but it also increases the risk to spread the disease amongst humans. Indeed, culling methods such as “dumping carcasses in landfills” have been observed in some farms in Colorado, which exposes the wild birds, poultry and farm workers to the virus, potentially contributing to the spread of the virus. [151]

Since 2020 HPAI A(H5N1), in particular 2.3.4.4b viruses, have emerged in and continue to spread to several animal species including, aquatic and terrestrial mammals.[103,152] The ability of those viruses, displaying a high mutation capacity, cross-genetic changes, and variable tropism (eg. virus detection in milk of dairy cows) to spread to various species is very concerning, as again, the recent outbreak in the USA highlights the increased risk of zoonotic transmission and raises fear of a possible human-human transmission.

After four years of the COVID-19 pandemic, which was demoted in May 2023 from its global health emergency status by the WHO, and after one year of significant decrease in detection (2021), influenza confirmed re-emergence. This emphases the importance of continuing the collection and analysis of influenza viruses and associated data. It remains crucial to choose the most appropriated influenza vaccine strains, as it is the best measure to mitigate the burden of severe diseases linked to influenza infections.

9. Methodology

9.1 Identification of cases

A network (Sentinella) of primary care practitioners voluntarily participates, on a yearly basis, in the national epidemiological and virological surveillance of influenza. Each week, they are requested to report ILI and ARI cases. According to ECDC and WHO criteria[153], ILI definition is declared as an acute respiratory infection with a fever measured to ≥38 C° and cough, with an onset within the last 10 days. Commonly with ILI definition, ARI also contains a sudden onset of symptoms with at least one of the respiratory symptoms such as cough, sore throat, shortness of breath, and coryza. This is accompanied with a clinical judgement that the illness comes from an infection.

A subgroup of these sentinel practitioners collects nasopharyngeal swabs from patients fitting the ILI and ARI case definitions for respiratory viruses screening. The practitioners are required to complete a brief case report form. The following data are collected: age; sex sample type; sample date; suspicion for a COVID-19 and/or Influenza, and Influenza (vaccine for the actual season) and COVID-19 (last dose since less than 6 months) vaccination status.

9.2 Molecular screening [1]

All nasopharyngeal swabs received at the NRCI are submitted to rRT-PCR screening for influenza, SARS-CoV-2, RSV, HCoVs NL63/HKU1/OC43/229E, HPIV, HBoV, HAdV, RV/EV and HMPV.

Except for SARS-CoV-2, all respiratory viruses were screened using a combination of eight custom rRT-PCR mixes produced by Eurogentec. Mixes' targets are grouped as follows:

- RSV/ canine distemper virus (CDV, our RNA/DNA extraction efficiency and PCR inhibitors control),
- HCoV NL63/OC43
- HCoV 229E/HKU1

[1]The evaluation of the proficiency of the Laboratory of Virology at Geneva University Hospitals in performing molecular detection of influenza viruses is accessed through the World Health Organization (WHO) External Quality Assessment Programme for the Detection of Influenza Viruses by RT-PCR and was initiated in 2007 by the WHO (https://www.who.int/influenza/gisrs_laboratory/external_quality_assessment_project/en/).

- HBoV/HPIV2/4 (does not distinguish between HPIV 2 and 4)
- HMPV/HPIV1/3 (does not distinguish between HPIV 1 and 3)
- RV/EV
- HAdV/CDV
- FluA/B rRT-PCR

Briefly, 800 µl of the initial respiratory specimens are extracted using the QiaSymphony magnetic-particle system (Qiagen, Basel, Switzerland) and viral RNA/DNA is recovered in 100 µl of elution buffer AVE. rRT-PCR reactions were performed using 5 µl of extracted RNA/DNA and 15 µl of reaction mix and run on Quantstudio 5 thermocycler.

Influenza A and B screening rRT-PCR is adapted from 2007 and 2009 USA CDC protocols. The duplex rRT-PCR targets are the matrix (M) protein and the non-structural (NS) protein genes for influenza A and B viruses, respectively. IA positive samples are further subtyped using an in-house-developed quadruplex rRT-PCR targeting the HA (H1 and H3) and the NA (N1 and N2) genes discriminate between influenza A(H1N1)pdm09 and A(H3N2) strains. H1 and N2[2] primers-probe combinations were designed in-house. H3 CDC primers-probe combination was part of 2007 CDC protocol and N1 primers-probe combination was adapted from Henritzi *et al* [154]. The quadruplex detection limit is similar to that of the diagnostic rRT-PCR. The N1 combination can detect H1N1v[2], swH1N1[3] and H5N1[4] isolates tested during the assay validation process. The H3 and N2 rRT-PCR combinations are also able to detect the A/Wisconsin/12/2010 H3N2 triple reassortant (H3N2tr),[155] although the latter virus is not known to circulate in Switzerland. Nevertheless, if needed, additional tests are available at the NRCI to discriminate seasonal H3N2 from H3N2tr viruses. Influenza B/Yamagata/16/88-like (Yam) and B/Victoria/2/87-like (Vic) lineages are distinguished using a duplex rRT-PCR adapted from Schweiger et al. 2000.[156] rRT-PCR reactions were performed using 5 µl of extracted RNA and 20 µl of SuperScript™

[2] H1N1v: A/Switzerland/***2244/2011 and A/Berne/****6552/2017, variants isolated from Swiss pig breeders.
[3] swH1N1 35 (2008): virus isolated from a Swiss pig.
[4] H5N1: A/Hong Kong/6841/2010 (EQAP panel 16) and A/goose/Qinghai/1A/05*A/PR8/34(INT).

III Platinum™ One-Step qRT-PCR Kit w/ROX (Invitrogen™) reaction mix and run on Quantstudio 5 thermocyclers.

SARS-CoV-2 viruses were screened using the Cobas® SARS-CoV-2 reagents on a Cobas® 6800 instrument according to the manufacturer's conditions. In some rare cases GeneXpert® Xpress SARS-CoV-2 (Cepheid) test was also used.

9.3 Antigenic and genetic characterization of influenza virus

A selection of influenza viruses is submitted to phenotypic and genotypic analysis. In general, five RT-PCR positive samples with cycle threshold (Ct) values <30 are chosen per week for further characterization and are submitted to a hemagglutination inhibition (HAI) assay. This latter allows assessment of the antigenic similarity between reference and circulating influenza strains.

A subset of influenza positive samples with Ct values <30 is also sequenced to assess the phylogeny of the circulating viruses and to determine genetic proximity to reference vaccine strains. Sequencing also allows for the detection of key mutations previously described as conferring resistance to NA inhibitors (NAIs) or BM treatments, while M and NS genes sequencing allows to check the adequacy of rRT-PCR primers and probes used for influenza A and B screening.

9.3.1 Cell culture

Both influenza positive and negative samples are cultured on MDCK and MDCK-SIAT1 cells. This allows to ensure that a low positivity rate for influenza is not due to a rRT-PCR detection defect. For example, this could be the case in the presence of viruses carrying mutations in the genomic regions targeted by rRT-PCR screening. For biosafety reasons, only negative-SARS-CoV-2 samples were submitted to cell culture.

Briefly, 400 µl of transport medium containing nasopharyngeal swabs are incubated at 33°C on MDCK cells and 37°C on MDCK-SIAT1. The presence of a cytopathic effect (CPE) is monitored for a period of up to 7 days. If CPE is present, samples are submitted to an hemagglutination and hemagglutination inhibition (HAI) assays. If CPE is absent or low after 7 days, the cells are screened for influenza viruses by immunofluorescence using monoclonal influenza A and B antibodies combined with

mouse fluorescein isothiocyanate-conjugate (Merck-Millipore, Chemicon®, Schaffhausen, Switzerland).

9.3.2 Hemagglutination inhibition (HAI) assay

A two-fold serial dilution is performed using 50 µl of viral suspension buffer in SALK solution (5%) and 25 µl of glutaraldehyde-fixed guinea pig red blood cells (RBC) (1.5%) are added for 1 h incubation at 4°C. The HA titer is defined as the last dilution in which the complete hemagglutination is still observed. After titer determination, HAI assay is performed as follows: 25 µl of reference antisera are added in the first two wells of a 96-well plate. Two-fold dilutions are prepared by adding 25 µl of SALK solution (5%) in the second well. 25 µl are then collected from the same well and the procedure is repeated to the end of each line. 25 µl of viral suspension containing 4 HA units are added to the antisera dilution and incubated for 1 h at room temperature. 25 µl of guinea pig RBC are then added to each well. The plates are incubated, then, for 1 h at 4°C. The HAI titer corresponds to the last antiserum dilution for which HA is still inhibited. This titer is compared to the homologous titer obtained with reference strains submitted to their corresponding antigenic antisera (antigenic table). The antigenic tables are influenza strain-specific (Figure 15) and are thereby, adjusted yearly. Since the serum is initially diluted 1/8, the titers provided in figure 15 should be multiplied by 8 to obtain the final titers.

Reference antisera and corresponding viral strains are kindly provided by the World Health Organisation (WHO) Collaborating Centre Reference Laboratory at the Francis Crick Worldwide Influenza Centre (WIC, London, UK). HAIs are performed with glutaraldehyde fixed guinea pig Red Blood Cells (RBC) (Charles River, Lyon, France).

IB		Reference Antisera			
		B/Brisbane/60/2008	B/Washington/02/2019	B/Austria/1359417/2021	B/Phuket/3073/2013
Reference Strains	B/Brisbane/60/2008	**2048**	128	32	<16
	B/Washington/02/2019	256	**512**	16	<16
	B/Austria/1359417/2021	64	<16	**1024**	<16
	B/Phuket/3073/2013	64	32	64	**256**

H3N2		Reference Antisera		
		A/Cambodia/e0826360/2020	A/Darwin/9/2021	A/Thailand/08/2022
Reference Strains	A/Cambodia/e0826360/2020	**1024**	256	32
	A/Darwin/9/2021	64	**64**	256
	A/Thailand/08/2022	256	512	**1024**

H1N1		Reference Antisera	
		A/Guangdong-Maonan/SWL1536/2019	A/Victoria/4897/2022
Reference Strains	A/Guangdong-Maonan/SWL1536/2019	**2048**	16
	A/Victoria/4897/2022	64	**2048**

Figure 15. Antigenic tables for the 2023/24 influenza season. These tables correspond to the HI titers of reference influenza strains (first column of the tables) incubated with ferret reference antisera (first row of the tables) provided by the WHO. The HI titers correspond to the highest dilution where an inhibition is still observed. The titer obtained after incubation of a given strain with the corresponding ferret antiserum is known as the homologous titer (in bold). In red: 2023-2025 influenza vaccine strains. IB (Victoria-lineage in yellow, Yamagata-lineage in orange,) H3N2 in green, and H1N1 in purple correspond to the influenza virus antigenic tables, respectively.

9.3.3 Genetic characterization of influenza viruses

Positive samples, with a Ct value <30, selected for sequencing in two batches/year are processed as follows: for the first batch, 400 µl of the initial respiratory specimens were extracted using the NucliSens EMAG magnetic bead system (BioMérieux, Geneva, Switzerland) and viral RNA is recovered in 50 µl elution volume. QiaSymphony (Qiagen, Basel, Switzerland) extracted, viral RNA in 100 µl elution buffer, obtained from 800 µl of clinical sample, was used for the second sequencing batch. Whole genome sequencing of influenza is performed by Microsynth AG. Influenza A and B segments are pre-amplified using, for influenza A[157], a mix of two forward primers and a single reverse primer located in the conserved regions of the viral genome segments; and for influenza B[158], a primer cocktail of 13 different forward and reverse primers. Libraries were prepared using Illumina Nextera kits and were then run on the Illumina platform MiSeq using 2*150 reads. Data is quality-filtered and de-multiplexed by Microsynth AG before being sent to the NRCI for in-house sequence analysis and

shared through GISAID and ENA. Optimal sequencing results are obtained for samples with Ct values <25 (Appendix 4).

9.4 Genetic characterization of SARS-CoV-2 virus

Genetic characterization of SARS-CoV-2 is done by whole genome sequencing by the Genome Centre (Campus Biotech, Geneva, Switzerland) within the SARS-CoV-2 national genomic surveillance program. The resulting consensus sequences are shared nationally via the Swiss Pathogen Surveillance Platform (SPSP) and internationally through GISAID.

10. Collaborative projects and publications

As for 2023, the NRCI continued to support the laboratory of virology and the National Reference Centre for Emerging Viral Infections (CRIVE), regarding SARS-CoV-2 variant detection and genetic characterization as part of the national genomic surveillance of SARS-CoV-2.

10.1 Ongoing projects

10.1.1 Whole genome sequencing of respiratory viruses

The NRCI collaborated with the Health 2030 Genome Centre DNA Sequencing and Data Analytics and Interpretation Platforms' team in order to evaluate the Illumina Respiratory oligo panel performance. A report containing the results of this evaluation was shared with the FOPH early 2024.

10.1.2 Co-infections of respiratory viruses within the Sentinella population

As a complement to the surveillance program, we recently decided to study the prevalence of respiratory viral co-infections (VRI) in Switzerland and their impact on viral activities in the post-pandemic context, using Sentinella data collected from August 2022 to end of July 2024 (corresponding to the two first post pandemic years). This study is currently being conducted in collaboration with two members of the Geneva Centre for Emerging Viral Diseases: Dr Manel ESSAIDI-LAZIOSI (from the research group of Prof. Isabella Eckerle at the Faculty of Medicine of Geneva), and Dr Francisco PEREZ (from the Reference Centre for Emerging Viral Infections). The idea came from the unique situation at early post COVID-19 pandemic period, where the progressive lifting of the sanitary restrictions (that began around spring 2022) has been followed by the resurge, although with a certain unexpected seasonality, of pre-pandemic respiratory viruses, after more than one year of absence. This situation was unpredictable, as their co-circulation alongside the novel SARS-CoV-2 might impact the global landscape of VRI in the future. The study of the interaction between respiratory viruses in the context of co-infection is of strong interest for predicting future trends and developing effective management strategies for respiratory viral infections. Preliminary data from the first year (August 2022 to July 2024) showed that co-detections, while rare, were observed year-round and were more common in children. Their incidence seems to be more important with specific viruses, that are not

necessarily the most prevalent. The presence of a second virus is likely impairing infections by SARS-CoV-2 and RSV, but not influenza viruses, especially in early adults and middle-aged individuals. These observations need to be confirmed by the analysis of the second post-pandemic year, which is still ongoing.

10.1.3 Sharing of materials prepared by the NRCI

1. Shared material: four *RNA of reference influenza A and B strains*

   With whom: *Dr. Jolinda de Korne, Dr. Christian Stamm, Dr. Frederik Hammes, Department Environmental Microbiology, Dübendorf, Switzerland*

   Project*: Wastewater-based surveillance of hospitals for respiratory pathogens*

2. Shared material: *MRC-5/24 cells*

   With whom: *Dr. Olha Puhach, Department of Molecular Medicine and Microbiology, Faculty of Medicine, University of Geneva, Switzerland*

   Project*: Investigation of immune responses to endemic human coronaviruses*

3. Shared data: *Sentinella data on respiratory viruses' detection during seasons 2022-2023 and 2023-2024*

   With whom: *Dr Manel Essaidi, Department of Molecular Medicine and Microbiology, Faculty of Medicine, University of Geneva, Switzerland*

   Project*: To study the co-infections/detections of respiratory viruses within the Sentinella population in Switzerland*

4. Shared material: *PCR protocols*

   With whom*: Spiez Labor*

   Project*:* Assay updating and validation

11. References

1. Hutchinson E.C, Yamauchi Y. Understanding Influenza. In: Yamauchi Y, ed. Influenza Virus: Methods and Protocols. Springer New York; 2018:1-21

2. Krammer F, Smith G.J.D, Fouchier R.A.M, et al. Influenza. *Nature Reviews Disease Primers*. Jun 28 2018;4(1):3. doi:10.1038/s41572-018-0002-y

3. Taubenberger J.K, Morens D.M. The Pathology of Influenza Virus Infections. Annual Review of Pathology: Mechanisms of Disease. 2008;3(1):499-522. doi:10.1146/annurev.pathmechdis.3.121806.154316

4. Bodewes R, Morick D, de Mutsert G, et al. Recurring Influenza B Virus Infections in Seals. *Emerging Infectious Diseases*. 2013;19(3):511-512. doi:10.3201/eid1903.120965

5. Sederdahl B.K, Williams J.V. Epidemiology and Clinical Characteristics of Influenza C Virus. *Viruses*. Jan 13 2020;12(1)doi:10.3390/v12010089

6. Hause B.M, Collin E.A, Liu R, et al. Characterization of a Novel Influenza Virus in Cattle and Swine: Proposal for a New Genus in the Orthomyxoviridae Family. *mBio*. May 1 2014;5(2)doi:10.1128/mBio.00031-14

7. Asha K, Kumar B. Emerging Influenza D Virus Threat: What We Know so Far! *Journal of Clinical Medicine*. 2019;8(2):192. doi:10.3390/jcm8020192

8. Su S, Fu X, Li G, Kerlin F, Veit M. Novel Influenza D virus: Epidemiology, pathology, evolution and biological characteristics. *Virulence*. Nov 17 2017;8(8):1580-1591. doi:10.1080/21505594.2017.1365216

9. Hyunsuh K, Webster R.G, Webby R.J. Influenza Virus: Dealing with a Drifting and Shifting Pathogen. *Viral Immunology*. 2018;31(2):174-183. doi:10.1089/vim.2017.0141

10. Mombelli M, Lang B.M, Neofytos D, et al. Burden, epidemiology, and outcomes of microbiologically confirmed respiratory viral infections in solid organ transplant recipients: a nationwide, multi-season prospective cohort study. *American Journal of Transplantation*. 2021;21(5):1789-1800. doi:10.1111/ajt.16383

11. Long Q-X, Tang X-J, Shi Q-L, et al. Clinical and immunological assessment of asymptomatic SARS-CoV-2 infections. *Nature Medicine*. Jun 18 2020;doi:10.1038/s41591-020-0965-6

12. Chen Y, Liu Q, Guo D. Emerging coronaviruses: Genome structure, replication, and pathogenesis. *Journal of Medical Virology*. 2020;92(4):418-423. doi:101002/jmv.25681

13. Masse S, Capai L, Villechenaud N, Blanchon T, Charrel R, Falchi A. Epidemiology and Clinical Symptoms Related to Seasonal Coronavirus Identified in Patients with

Acute Respiratory Infections Consulting in Primary Care over Six Influenza Seasons (2014–2020) in France. *Viruses*. 2020;12(6):630

14. Liu D.X, Liang J.Q, Fung T.S. Human Coronavirus-229E, -OC43, -NL63, and -HKU1 (Coronaviridae). *Encyclopedia of Virology*. 2021:428-440. doi:10.1016/b978-0-12-809633-8.21501-x

15. World Health Organization. Regional Office for the Eastern Mediterranean Region. MERS situation update: May 2024. 2024

16. Desforges M, Le Coupanec A, Brison E, Meessen-Pinard M, Talbot P.J. Neuroinvasive and neurotropic human respiratory coronaviruses: potential neurovirulent agents in humans. *Advances in Experimental Medicine and Biology*. 2014;807:75-96. doi:10.1007/978-81-322-1777-0_6

17. Zhu N, Zhang D, Wang W, et al. A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*. 2020;382(8):727-733. doi:10.1056/NEJMoa2001017

18. Zhou P, Yang X.L, Wang X.G, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. Mar 2020;579(7798):270-273. doi:10.1038/s41586-020-2012-7

19. Gostin L.O, Gronvall G.K. The Origins of Covid-19 - Why It Matters (and Why It Doesn't). *New England Journal of Medicine.* June 22 2023;388(25):2305-2308. doi:10.1056/NEJMp2305081

20. World Health Organization. Statement on the fifteenth meeting of the IHR (2005) Emergency Committee on the COVID-19 pandemic. 5 May 2023, 2023. https://www.who.int/news/item/05-05-2023-statement-on-the-fifteenth-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-coronavirus-disease-(covid-19)-pandemic Accessed 15.05.2024

21. Bundle N, Dave N, Pharris A, et al. COVID-19 trends and severity among symptomatic children aged 0-17 years in 10 European Union countries, 3 August 2020 to 3 October 2021. *Eurosurveillance*. Dec 2021;26(50)doi:10.2807/1560-7917.ES.2021.26.50.2101098

22. Sudre C.H, Murray B, Varsavsky T, et al. Attributes and predictors of long COVID. *Nature Medicine*. Apr 2021;27(4):626-631. doi:10.1038/s41591-021-01292-y

23. World Health Organization. A clinical case definition of post COVID-19 condition by a Delphi consensus. 2021. COVID-19: Clinical care. 2021; https://www.who.int/publications/i/item/WHO-2019-nCoV-Post_COVID-19_condition-Clinical_case_definition-2021.1. Accessed: 25.08.2023

24. Vitalakumar D, Sharma A, Kumar A, Flora S.J.S. Neurological Manifestations in COVID-19 Patients: A Meta-Analysis. *ACS Chemical Neuroscience*. Aug 4 2021;12(15):2776-2797. doi:10.1021/acschemneuro.1c00353

25. Marinho P.M, Marcos A.A.A, Romano A.C, Nascimento H, Belfort R.Jr. Retinal findings in patients with COVID-19. *Lancet*. May 23 2020;395(10237):1610. doi:10.1016/s0140-6736(20)31014-x

26. Landecho M.F, Yuste J.R, Gándara E, et al. COVID-19 retinal microangiopathy as an in vivo biomarker of systemic vascular disease? *Journal of Internal Medicine*. Jan 2021;289(1):116-120. doi:10.1111/joim.13156

27. Riotto E, Mégevand V, Mégevand A, et al. Retinal Manifestations in Patients with COVID-19: A Prospective Cohort Study. *Journal of Clinical Medicine.* Mar 25 2022;11(7)doi:10.3390/jcm11071828

28. Markan A, Bansal R, Gautam N, et al. Longitudinal analysis of cotton wool spots in COVID-19 with high-resolution spectral domain optical coherence tomography and optical coherence tomography angiography. *Clinical & Experimental Ophthalmology.* May 2021;49(4):392-395. doi:10.1111/ceo.13919

29. Hamilton F, Arnold D, Bzdek B.R, et al. Aerosol generating procedures: are they of relevance for transmission of SARS-CoV-2? *The Lancet Respiratory Medicine*. doi:10.1016/s2213-2600(21)00216-2

30. Cappy P, Candotti D, Sauvage V, et al. No evidence of SARS-CoV-2 transfusion transmission despite RNA detection in blood donors showing symptoms after donation. *Blood*. 2020;136(16):1888-1891. doi:10.1182/blood.2020008230

31. Jones D.L, Baluja M.Q, Graham D.W, et al. Shedding of SARS-CoV-2 in feces and urine and its potential role in person-to-person transmission and the environment-based spread of COVID-19. *Science of The Total Environment*. Dec 20 2020;749:141364. doi:10.1016/j.scitotenv.2020.141364

32. World Health Organization. Breastfeeding and COVID-19. Jun 23 2020. https://www.who.int/publications/i/item/WHO-2019-nCoV-Sci_Brief-Breastfeeding-2020.1 Accessed: 25.08.2023

33. Goryoka G.W, Cossaboom C.M, Gharpure R, et al. One Health Investigation of SARS-CoV-2 Infection and Seropositivity among Pets in Households with Confirmed Human COVID-19 Cases — Utah and Wisconsin, 2020. *bioRxiv*. 2021:2021.04.11.439379. doi:10.1101/2021.04.11.439379

34. Halfmann P.J, Hatta M, Chiba S, et al. Transmission of SARS-CoV-2 in Domestic Cats. *New England Journal of Medicine*. 2020;383(6):592-594. doi:10.1056/NEJMc2013400

35. Sit T:H:C, Brackman C.J, Ip S.M, et al. Infection of dogs with SARS-CoV-2. *Nature*. Oct 01 2020;586(7831):776-778. doi:10.1038/s41586-020-2334-5

36. World Health Organization. COVID-19 epidemiological update-17 May 2024. 2024

37. World Health Organization. Tracking SARS-CoV-2 variants. 2023; https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/ Accessed:25.08.2023

38. Muñoz-Escalante J.C, Comas-García A, Bernal-Silva S, Noyola D.E. Respiratory syncytial virus B sequence analysis reveals a novel early genotype. *Scientific reports*. 2021;11(1):3452.

39. Coultas J.A, Smyth R, Openshaw P.J. Respiratory syncytial virus (RSV): a scourge from infancy to old age. *Thorax*. 2019;74(10):986-993. doi:10.1136/thoraxjnl-2018-212212

40. Chatzis O, Darbre S, Pasquier J, et al. Burden of severe RSV disease among immunocompromised children and adults: a 10 year retrospective study. *BMC Infectious Diseases*. 2018;18(1):111-111. doi:10.1186/s12879-018-3002-3

41. Carvajal J.J, Avellaneda A.M, Salazar-Ardiles C, Maya J.E, Kalergis A.M, Lay M.K. Host Components Contributing to Respiratory Syncytial Virus Pathogenesis. 10.3389/fimmu.2019.02152. *Frontiers in Immunology*. 2019;10:2152.

42. Shi T, McAllister D.A, O'Brien K.L, et al. Global, regional, and national disease burden estimates of acute lower respiratory infections due to respiratory syncytial virus in young children in 2015: a systematic review and modelling study. *The Lancet*. Sep 02 2017;390(10098):946-958. doi:10.1016/s0140-6736(17)30938-8

43. Li Y, Wang X, Blau D.M, et al. Global, regional, and national disease burden estimates of acute lower respiratory infections due to respiratory syncytial virus in children younger than 5 years in 2019: a systematic analysis. *The Lancet*. May 28 2022;399(10340):2047-2064. doi:10.1016/s0140-6736(22)00478-0

44. World Health Organization. WHO strategy for global respiratory syncytial virus surveillance project based on the influenza platform. 2019; https://cdn.who.int/media/docs/default-source/influenza/rsv-surveillance/who-rsv-surveillance-strategy-phase-26mar2021.-final.pdf?sfvrsn=d8b1c36a_9 Accessed 25.08.2023

45. Pebody R, Moyes J, Hirve S, et al. Approaches to use the WHO respiratory syncytial virus surveillance platform to estimate disease burden. *Influenza and Other Respiratory Viruses*. 2020;14(6):615-621. doi:10.1111/irv.12667

46. Rosas-Salazar C, Chirkova T, Gebretsadik T, Chappell J.D., Peebles R.S, Dupont, W.D et al. (2023). Respiratory syncytial virus infection during infancy and asthma during childhood in the USA (INSPIRE): a population-based, prospective birth cohort study.*The Lancet*, 401(10389), 1669-1680.

47. Robinson C.P, Busl K.M. Neurologic Manifestations of Severe Respiratory Viral Contagions. *Critical Care Explorations*. 2020;2(4):e0107. doi:10.1097/cce.0000000000000107

48. Milas A, Shah A, Anand N, Saunders-Kurban M, Patel S. Respiratory Syncytial Virus Associated Myocarditis Requiring Venoarterial Extracorporeal Membrane Oxygenation. *Case Reports in Infectious Diseases*. May 08 2017;2017:7074508. doi:10.1155/2017/7074508

49. Ivey K.S, Edwards K.M, Talbot H.K. Respiratory Syncytial Virus and Associations With Cardiovascular Disease in Adults. *Journal of the American College of Cardiology*. Ap 10 2018;71(14):1574-1583. doi:10.1016/j.jacc.2018.02.013

50. Eisenhut M, Thorburn K. Hepatitis Associated with Severe Respiratory Syncytial Virus-positive Lower Respiratory Tract Infection. *Scandinavian Journal of Infectious Diseases*. Jan 1 2002;34(3):235-235. doi:10.1080/00365540110077191

51. Swissmedic. Beyfortus® (principe actif: nirsévimab). In: Public Summary SwissPAR, editor. 2024;https://www.swissmedic.ch/swissmedic/fr/home/notre-profil/publications/public-summary-swiss-par/public-summary-swiss-par-beyfortus.html Accessed 17.07.2024

52. Pediatric Infectious Disease Group of Switzerland. Publications, Recommendations, and Guidelines. 2024; https://pigs.ch/publications/ Accessed 30.07.2024

53. Federal Drug Administration. FDA Approves First Respiratory Syncytial Virus (RSV) Vaccine. 2023; https://www.fda.gov/news-events/press-announcements/fda-approves-first-respiratory-syncytial-virus-rsv-vaccine Accessed 17.07.2024

54. Shafagati N, Williams J. Human metapneumovirus - what we know now. *F1000Research*. 2018;7:135. doi:10.12688/f1000research.12625.1

55. Rafeek R.A., Divarathna V.M, Noordeen F. A review on disease burden and epidemiology of childhood parainfluenza virus infections in Asian countries. *Reviews in Medical Virology*. Mar 2021;31(2):e2164. doi:10.1002/rmv.2164

56. Pawełczyk M, Kowalski M.L. The Role of Human Parainfluenza Virus Infections in the Immunopathology of the Respiratory Tract. *Current Allergy and Asthma Reports.* 2017;17(3):16-16. doi:10.1007/s11882-017-0685-2

57. Russell E, Ison M.G. Parainfluenza Virus in the Hospitalized Adult. *Clinical Infectious Diseases*. 2017;65(9):1570-1576. doi:10.1093/cid/cix528

58. Frost H.M, Robinson C.C, Dominguez S.R. Epidemiology and Clinical Presentation of Parainfluenza Type 4 in Children: A 3-Year Comparative Study to Parainfluenza Types 1–3. *The Journal of Infectious Diseases*. 2013;209(5):695-702. doi:10.1093/infdis/jit552

59. Centers for Disease Control and Prevention. Human Parainfluenza viruses (HPIVs). 2022;https://www.cdc.gov/parainfluenza/seasons.html Accessed 25.08.2023

60. Christensen A, Kesti O, Elenius V, et al. Human bocaviruses and paediatric infections. *The Lancet Child & Adolescent Health*. 2019;3(6):418-426. doi:10.1016/s2352-4642(19)30057-4

61. Lee H.N, Koo H.J, Kim S.H, Choi S-H, Sung H, Do K-H. Human Bocavirus Infection in Adults: Clinical Features and Radiological Findings. *Korean Journal of Radiology*. 2019;20(7):1226-1235

62. Watanabe A.S.A, Luchs A, Leal É, et al. Complete Genome Sequences of Six Human Bocavirus Strains from Patients with Acute Gastroenteritis in the North Region of Brazil. *Genome Announcements*. 2018;6(17):e00235-18. doi:10.1128/genomeA.00235-18

63. Brebion A, Vanlieferinghen P, Déchelotte P, et al. Fatal Subacute Myocarditis Associated with Human Bocavirus 2 in a 13-Month-Old Child. *Journal of Clinical Microbiology*. 2014;52(3):1006-1008. doi:doi:10.1128/JCM.03013-13

64. Schildgen O, Schildgen V. The Role of the Human Bocavirus (HBoV) in Respiratory Infections. In: Tang Y-W, Stratton C.W, eds. *Advanced Techniques in Diagnostic Microbiology: Volume 2: Applications*. Springer International Publishing; 2018:281-301.

65. Greber U.F, Flatt J.W. Adenovirus Entry: From Infection to Immunity. *Annual Review of Virology*. 2019;6(1):177-197. doi:10.1146/annurev-virology-092818-015550

66. Radke J.R, Cook J.L. Human adenovirus infections: update and consideration of mechanisms of viral persistence. *Current Opinion in Infectious Diseases*. 2018;31(3):251-256. doi:10.1097/qco.0000000000000451

67. Lynch J.P, 3rd, Kajon A.E. Adenovirus: Epidemiology, Global Spread of Novel Serotypes, and Advances in Treatment and Prevention. *Seminars in Respiratory and Critical Care Medicine*. Aug 2016;37(4):586-602. doi:10.1055/s-0036-1584923

68. Hu W, Zhang M, Xu Z, Li J, Wang F-S, Li T. Severe Acute Hepatitis of Unknown Etiology in Children: Is It Caused by Pathogens or Non-infectious Factors? *Infectious Diseases & Immunity*. 2022;2(3):200-203. doi:10.1097/id9.0000000000000060

69. Reyne M.I, Allen D.M, Levickas A, et al. Detection of human adenovirus F41 in wastewater and its relationship to clinical cases of acute hepatitis of unknown aetiology. *Science of The Total Environment*. Jan 20 2023;857(Pt 2):159579. doi:10.1016/j.scitotenv.2022.159579

70. Tapparel C, Siegrist F, Petty T.J, Kaiser L. Picornavirus and enterovirus diversity with associated human diseases. *Infection, Genetics and Evolution*. 2013/03/01/ 2013;14:282-293. doi:10.1016/j.meegid.2012.10.016

71. Zell R. Picornaviridae—the ever-growing virus family. *Archives of Virology*. Feb 01 2018;163(2):299-317. doi:10.1007/s00705-017-3614-8

72. Monto A.S. The seasonality of rhinovirus infections and its implications for clinical recognition. *Clinical Therapeutics*. Dec 2002;24(12):1987-97. doi:10.1016/s0149-2918(02)80093-5

73. Worldwide Influenza Centre, WHO CC for Reference and Research on Influenza, The Francis Crick Institute; 2024 Report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2024/2025. 2024.

74. European Centre for Disease Prevention and Control. Influenza virus characterization - Summary report, Europe, January 2024. 2024 https://www.ecdc.europa.eu/en/publications-data/influenza-virus-characterization-summary-report-europe-january-2024 Accessed 17.07.2024

75. World Health Organization. Recommended composition of influenza virus vaccines for use in the 2024-2025 northern hemisphere influenza season. 2024;https://www.who.int/publications/m/item/recommended-composition-of-influenza-virus-vaccines-for-use-in-the-2024-2025-northern-hemisphere-influenza-season Accessed 07.03.2024

76. Omoto S, Speranzini V, Hashimoto T, et al. Characterization of influenza virus variants induced by treatment with the endonuclease inhibitor baloxavir marboxil. *Scientific Reports*. Jun 25 2018;8(1):9633. doi:10.1038/s41598-018-27890-4

77. Meijer A, Rebelo-de-Andrade H, Correia V, et al. Global update on the susceptibility of human influenza viruses to neuraminidase inhibitors, 2012-2013. *Antiviral Research*. Oct 2014;110:31-41. doi:10.1016/j.antiviral.2014.07.001

78. Zürcher T, Yates P.J, Daly J, et al. Mutations conferring zanamivir resistance in human influenza virus N2 neuraminidases compromise virus fitness and are not stably maintained in vitro. *Journal of Antimicrobial Chemotherapy*. Oct 2006;58(4):723-32. doi:10.1093/jac/dkl321

79. Takashita E, Meijer A, Lackenby A, et al. Global update on the susceptibility of human influenza viruses to neuraminidase inhibitors, 2013-2014. *Antiviral Research*. May 2015;117:27-38. doi:10.1016/j.antiviral.2015.02.003

80. van der Vries E, Stelma F.F, Boucher C.A.B. Emergence of a Multidrug-Resistant Pandemic Influenza A (H1N1) Virus. *New England Journal of Medicine*. 2010;363(14):1381-1382. doi:doi:10.1056/NEJMc1003749

81. Pizzorno A, Abed Y, Bouhy X, et al. Impact of mutations at residue I223 of the neuraminidase protein on the resistance profile, replication level, and virulence of the 2009 pandemic influenza virus. *Antimicrobial Agents and Chemotherapy*. Mar 2012;56(3):1208-14. doi:10.1128/aac.05994-11

82. Rambaut A, Holmes E.C, O'Toole Á, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nature Microbiology*. Nov 01 2020;5(11):1403-1407. doi:10.1038/s41564-020-0770-5

83. European Centre for Disease Control and Prevention. ECDC de-escalates BA.2, BA.4 and BA.5 from its list of variants of concern. 2023;https://www.ecdc.europa.eu/en/news-events/ecdc-de-escalates-ba2-ba4-and-ba5-its-list-variants-concern Accessed 03.04.2024

84. World Health Organization. FluNet Summary-Number of specimens positive for influenza by subtype. 2024;https://apps.who.int/flumart/Default?Hemisphere=Southern&ReportNo=5 Accessed 17.07.2024

85. European Centre for Disease Prevention and Control, World Health Organization European Region. Respiratory virus surveillance network webinar. 2024 Influenza updates\20240513_RegionalWebinar_EndOfSeason.pdf

86. Patel M.C, Nguyen H.T, Pascua P.N.Q, et al. Multicountry Spread of Influenza A(H1N1)pdm09 Viruses with Reduced Oseltamivir Inhibition, May 2023-February 2024. *Emerging Infectious Diseases*. Jul 2024;30(7):1410-1415. doi:10.3201/eid3007.240480

87. Centers for Disease Control and Prevention. Fluview interactive. Novel Influenza A Virus Infections. 2024;https://gis.cdc.gov/grasp/fluview/Novel_Influenza.html Access 16.07.2024

88. European Centre for Disease Prevention and Control. Communicable disease threats report, 31 March - 6 April 2024, week 14. 2024. Weekly Bulletin.https://www.ecdc.europa.eu/sites/default/files/documents/communicable-disease-threats-report-week-14-2024.pdf

89. Centers for Disease Control and Prevention. CDC Reports First U.S. Human Infection in 2024 with Variant Influenza Virus. 2024;https://www.cdc.gov/swine-flu/comm-resources/first_us_human_infection_avian_flu.html#:~:text=April%205%2C%202024%20%E2%80%94%20On%20March%2029%2C%202024%2C,direct%20contact%20with%20pigs%20prior%20to%20illness%20onset Accessed 29.07.2024

90. Centers for Disease Control and Prevention. CDC Reports Two Human Infections with Variant Influenza Viruses. 2024;https://www.cdc.gov/flu/spotlights/2023-2024/two-variant-flu-infections-reported-PA.html Accessed 29.07.2024

91. World Health Organization. Influenza A(H1N2) variant virus infection - United Kingdom of Great Britain and Northern Ireland. 2023. Disease Outbreak News. https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON496 Accessed 01.12.2023

92. Food and Agriculture Organization of the United Nations, World Health Organization, World Organisation for Animal Health. Joint FAO/WHO/WOAH preliminary assessment of recent influenza A(H5N1) viruses 23 April 2024. 2024 23.04.2024. https://cdn.who.int/media/docs/default-source/global-influenza-programme/2024_04_23_fao-woah-who_h5n1_assessment.pdf?sfvrsn=3ca3dba6_2&download=true Accessed 12.07.2024

93. World Health Organization. Cumulative number of confirmed human cases† for avian influenza A(H5N1) reported to WHO, 2003-2024. 2024;https://cdn.who.int/media/docs/default-source/influenza/h5n1-human-case-cumulative-table/2024_feb_tableh5n1.pdf?sfvrsn=bccd8c23_1&download=true Accessed 16.07.2024

94. Uyeki T.M, Milton S, Abdul Hamid C, et al. Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Dairy Farm Worker. *New England Journal of Medicine*. May 3 2024;doi:10.1056/NEJMc2405371

95. Centers for Disease Control and Prevention. CDC A(H5N1) Bird Flu Response Update July 26, 2024. 2024;https://www.cdc.gov/bird-flu/spotlights/h5n1-response-07262024.html Accessed 02.08.2024

96. European Centre for Disease Prevention and Control. Communicable Disease Threats Report- Week 21,18-24 May 2024. 2024. Weekly Bulletin. https://www.ecdc.europa.eu/sites/default/files/documents/Communicable-disease-threats-report-week-21-2024_0.pdf

97. European Centre for Disease Prevention and Control. Communicable disease threats report, 29 June−5 July 2024, week 27. 2024. Weekly Bulletin. https://www.ecdc.europa.eu/en/publications-data/communicable-disease-threats-report-29-june-5-july-2024-week-27

98. World Health Organization. Summary and risk assessment, from 29 March to 3 May 2024. 2024. Influenza at the human-animal interface. https://cdn.who.int/media/docs/default-source/influenza/human-animal-interface-risk-assessments/influenza-at-the-human-animal-interface-summary-and-assessment--from-29-march-to-3-may-2024.pdf?sfvrsn=e9ab83e2_3&download=true Accessed 16.07.2024

99. World Health Organization. Avian Influenza Weekly Update Number 954. 2024;https://cdn.who.int/media/docs/default-source/wpro---documents/emergency/surveillance/avian-influenza/ai_20240705.pdf?sfvrsn=5f006f99_137 Accessed 29.07.2024

100. World Health Organization. Avian Influenza A (H9N2)-India. Disease Outbreak News. 2024;https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON523 Accessed 29.07.2024

101. World Health Organization. Avian Influenza Weekly Update Number 947. 17.05.2024

102. World Health Organization. Avian Influenza A(H5N2)-Mexico. 2024. Disease Outbreak News. 5 June 2024;https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON520#:~:text=Influenza%20A(H5N2)%20viruses%20have,human%20cases%20are%20not%20unexpected. Accessed 10.06.2024

103. European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Fusaro A, et al. Avian influenza overview December 2023–March 2024. *EFSA Journal*. 2024;22(3):e8754

104. European Food Safety Authority, European Centre for Disease Prevention and Control, European Union Reference Laboratory for Avian Influenza, Fusaro A, et al. Avian influenza overview March-June 2024. *EFSA Journal*. Jul 2024;22(7):e8930.

105. Centers for Disease Control and Prevention. Highlights in the History of Avian Influenza (Bird Flu) Timeline – 2020-2024; https://www.cdc.gov/flu/avianflu/timeline/avian-timeline-2020s.htm Accessed 10.06.2024

106. Office of the State Veterinarian. Alaska Department of Environmental Conservation's Division of Environmental Health. Highly Pathogenic Avian Influenza (HPAI) Outbreaks and Biosecurity Toolkit from USDA APHIS. March 18 2024 https://dec.alaska.gov/eh/vet/announcements/avian-influenza-outbreaks/ Accessed 18.07.2024

107. The Poultry Site. Cambodia reports avian influenza outbreak near Vietnam border. https://www.thepoultrysite.com/news/2023/11/cambodia-reports-avian-influenza-outbreak-near-vietnamese-border Accessed 02.08.2024

108. World Organisation for Animal Health. United States of America - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Follow up report 52. 2024. https://wahis.woah.org/#/in-review/4451 Accessed 15.07.2024

109. Animal and Plant Health Inspection Service. U.S. Department of Agriculture. Highly Pathogenic Avian Influenza (HPAI) H5N1 Detections in Alpacas. 2024. https://www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/hpai-detections/mammals/highly-pathogenic-avian Accessed 15.07.2024

110. Agriculture Victoria. Avian influenza (bird flu)- Current situation.2024. https://agriculture.vic.gov.au/biosecurity/animal-diseases/poultry-diseases/avian-influenza-bird-flu?utm_source=agriculture-vic-gov-au&utm_medium=vanity-url-

301ssredirect&utm_content=avianinfluenza&utm_campaign=agriculture Accessed 05.06.2024

111. Office Fédéral de la Sécurité Alimentaire. Grippe aviaire chez l'animal.2024 https://www.blv.admin.ch/blv/fr/home/tiere/tierseuchen/uebersicht-seuchen/alle-tierseuchen/ai.html Accessed 05.06.2024

112. Vogelgrippe. Massnahmen gegen Vogelgrippe im Kanton Zürich aufgehoben. 2024.https://www.zh.ch/de/umwelt-tiere/tiere/tierseuchen/vogelgrippe-aviaere-influenza.html Accessed 05.06.2024

113. Guan L, Eisfeld A.J, Pattinson D, et al. Cow's Milk Containing Avian Influenza A(H5N1) Virus - Heat Inactivation and Infectivity in Mice. *New England Journal of Medicine*. Jul 4 2024;391(1):87-90. doi:10.1056/NEJMc2405495

114. Domínguez À, Soldevila N, Torner N, et al. Usefulness of Clinical Definitions of Influenza for Public Health Surveillance Purposes. *Viruses*. Jan 14 2020;12(1)doi:10.3390/v12010095

115. European Centre for Disease Prevention and Control. Seasonal influenza vaccination recommendations and coverage rates in EU/EEA Member States. 2023. https://www.ecdc.europa.eu/en/publications-data/seasonal-influenza-vaccination-recommendations-and-coverage-rates-eueea-member Accessed 26.08.2024

116. Maurel M, Howard J, Kissling E, et al. Interim 2023/24 influenza A vaccine effectiveness: VEBIS European primary care and hospital multicentre studies, September 2023 to January 2024. *Eurosurveillance*. 2024;29(8):2400089. doi:doi:https://doi.org/10.2807/1560-7917.ES.2024.29.8.2400089

117. European Centre for Disease Prevention and Control. Interim COVID-19 vaccination coverage in the EU/EEA during the 2023–24 season campaigns. 2024. https://www.ecdc.europa.eu/en/publications-data/interim-covid-19-vaccination-coverage-eueea-during-2023-24-season-campaigns Accessed 26.08.2024

118. Yum S, Hong K, Sohn S, Kim J, Chun B.C. Trends in Viral Respiratory Infections During COVID-19 Pandemic, South Korea. *Emerging Infectious Disease journal*. 2021;27(6):1685. doi:10.3201/eid2706.210135

119. Agha R, Avner J.R. Delayed seasonal RSV surge observed during the COVID-19 pandemic. *Pediatrics*. 2021;148(3)

120. Abu-Raya B, Viñeta Paramo M, Reicherz F, Lavoie P.M. Why has the epidemiology of RSV changed during the COVID-19 pandemic? *eClinicalMedicine*. Jul 2023;61:102089. doi:10.1016/j.eclinm.2023.102089

121. Duppenthaler A, Gorgievski-Hrisoho M, Frey U, Aebi C. Two-year periodicity of respiratory syncytial virus epidemics in Switzerland. *Infection*. Mar 2003;31(2):75-80. doi:10.1007/s15010-002-3124-8

122. Delestrain C, Danis K, Hau I, et al. Impact of COVID-19 social distancing on viral infection in France: A delayed outbreak of RSV. *Pediatric Pulmonology*. Dec 2021;56(12):3669-3673. doi:10.1002/ppul.25644

123. Foley D.A, Yeoh D.K, Minney-Smith C.A, et al. The Interseasonal Resurgence of Respiratory Syncytial Virus in Australian Children Following the Reduction of Coronavirus Disease 2019-Related Public Health Measures. *Clinical Infectious Diseases*. Nov 02 2021;doi:10.1093/cid/ciaa1906

124. Center for Preparedness and Response, Centers for Disease Control and Prevention. Increased Interseasonal Respiratory Syncytial Virus (RSV) Activity in Parts of the Southern United States. 06.07.2021. 2021;https://emergency.cdc.gov/han/2021/han00443.asp Accessed 25.08.2023

125. National Institute for Communicable Diseases. Increase in Respiratory syncitial virus (RSV) cases 2020. 2021;https://www.nicd.ac.za/increase-in-respiratory-syncytial-virus-rsv-cases-2020/ Accessed: 25.08.2023

126. Li Y, Wang X, Broberg EK, Campbell H, Nair H. Seasonality of respiratory syncytial virus and its association with meteorological factors in 13 European countries, week 40 2010 to week 39 2019. *Eurosurveillance*. Apr 2022;27(16)doi:10.2807/1560-7917.Es.2022.27.16.2100619

127. McMichael A.J, Woodruff R.E, Hales S. Climate change and human health: present and future risks. *Lancet*. Mar 11 2006;367(9513):859-69. doi:10.1016/s0140-6736(06)68079-3

128. van Summeren J, Meijer A, Aspelund G, et al. Low levels of respiratory syncytial virus activity in Europe during the 2020/21 season: what can we expect in the coming summer and autumn/winter? *Eurosurveillance*. Jul 2021;26(29)doi:10.2807/1560-7917.Es.2021.26.29.2100639

129. den Hartog G, van Kasteren P.B, Schepp R.M, Teirlinck A.C, van der Klis F.R.M, van Binnendijk R.S. Decline of RSV-specific antibodies during the COVID-19 pandemic. *The Lancet Infectious Diseases*. Jan 2023;23(1):23-25. doi:10.1016/s1473-3099(22)00763-0

130. Centers for Disease Control and Prevention. About Human Metapneumovirus. 2024;About Human Metapneumovirus | Human Metapneumovirus | CDC Accessed 05.06.2024

131. Heininger U, Kruker A.T, Bonhoeffer J, Schaad U.B. Human metapneumovirus infections—biannual epidemics and clinical findings in children in the region of Basel, Switzerland. *European Journal of Pediatrics*. Feb 24 2009;168(12):1455. doi:10.1007/s00431-009-0949-5

132. Zhu R, Guo C, Zhao L, et al. Epidemiological and genetic characteristics of human metapneumovirus in pediatric patients across six consecutive seasons in Beijing, China. *International Journal of Infectious Diseases*. Feb 01 2020;91:137-142. doi:10.1016/j.ijid.2019.11.012

133. Fratty I.S, Reznik-Balter S, Nemet I, et al. Outbreak of Influenza and Other Respiratory Viruses in Hospitalized Patients Alongside the SARS-CoV-2 Pandemic. *Frontiers in Microbiology*. 2022;13:902476. doi:10.3389/fmicb.2022.902476

134. Matera L, Manti S, Petrarca L, et al. An overview on viral interference during SARS-CoV-2 pandemic. *Frontiers in Pediatrics.* 2023;11:1308105. doi:10.3389/fped.2023.1308105

135. World Health Organization. WHO COVID-19 dashboard. https://data.who.int/dashboards/covid19/cases?n=c Accessed 26.08.2024

136. European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern as of 27 July 2023. 2023;https://www.ecdc.europa.eu/en/covid-19/variants-concern Accessed 05.06.2024

137. Global Initiative on Sharing Influenza Data. Overview of Variants in Countries. 2024;https://covariants.org/per-country?region=Switzerland Accessed: 20.05.2024

138. Global Initiative on Sharing Influenza Data. Detect and analyze variants of SARS-CoV-2.2024;https://cov-spectrum.org/explore/Switzerland/AllSamples/AllTimes Accessed 20.05.2024

139. Marshall N.C, Kariyawasam R.M, Zelyas N, Kanji J.N, Diggle M.A. Broad respiratory testing to identify SARS-CoV-2 viral co-circulation and inform diagnostic stewardship in the COVID-19 pandemic. *Virology Journal*. May 01 2021;18(1):93. doi:10.1186/s12985-021-01545-9

140. Zhang Y, Su L, Chen Y, et al. Etiology and clinical characteristics of SARS-CoV-2 and other human coronaviruses among children in Zhejiang Province, China 2017–2019. *Virology Journal*. Apr 30 2021;18(1):89. doi:10.1186/s12985-021-01562-8

141. De Groote N.P, Haynes A.K, Taylor C, et al. Human parainfluenza virus circulation, United States, 2011-2019. *Journal of Clinical Virology*. Mar 2020;124:104261. doi:10.1016/j.jcv.2020.104261

142. Greiff D.R.L, Patterson-Robert A, Blyth C.C, Glass K, Moore H.C. Epidemiology and seasonality of human parainfluenza serotypes 1-3 in Australian children. *Influenza and Other Respiratory Viruses*. Sep 2021;15(5):661-669. doi:10.1111/irv.12838

143. Polo D, Lema A, Gándara E, Romalde J.L. Prevalence of human bocavirus infections in Europe. A systematic review and meta-analysis. *Transboundary and Emerging Diseases*. Sep 2022;69(5):2451-2461. doi: 10.1111/tbed.14233

144. Guido M, Tumolo M.R, Verri T, et al. Human bocavirus: Current knowledge and future challenges. *World Journal of Gastroenterology*. 2016;22(39):8684-8697. doi:10.3748/wjg.v22.i39.8684

145. Peci A, Winter A-L, Gubbay J.B, et al. Community-acquired respiratory viruses and co-infection among patients of Ontario sentinel practices, April 2009 to February 2010. *Influenza and Other Respiratory Viruses*. 2013;7(4):559-566. doi:https://doi.org/10.1111/j.1750-2659.2012.00418.x

146. Lansbury L, Lim B, Baskaran V, Lim W.S. Co-infections in people with COVID-19: a systematic review and meta-analysis. *Journal of Infection*. 2020;81(2):266-275. doi:10.1016/j.jinf.2020.05.046

147. Eldesouki R.E, Uhteg K, Mostafa H.H. The circulation of Non-SARS-CoV-2 respiratory viruses and coinfections with SARS-CoV-2 during the surge of the Omicron variant. *Journal of Clinical Virology*. Aug 01 2022;153:105215. doi:https://doi.org/10.1016/j.jcv.2022.105215

148. European Centre for Disease Prevention and Control, World Health Organization European Region. Influenza virus characterization-Summary report,Europe, March 2024. 2024. https://www.ecdc.europa.eu/sites/default/files/documents/influenza-ECDC-WHO-Report-March-2024.pdf

149. Dhanasekaran V, Sullivan S, Edwards K.M, et al. Human seasonal influenza under COVID-19 and the potential consequences of influenza lineage elimination. *Nature Communications*. Mar 31 2022;13(1):1721. doi:10.1038/s41467-022-29402-5

150. Global Center for Health Security. Nearly 1.8 million chickens will be culled in the latest bird flu outbreak at a Colorado poultry farm 2024; https://www.unmc.edu/healthsecurity/transmission/2024/07/10/nearly-1-8-million-chickens-will-be-culled-in-the-latest-bird-flu-outbreak-at-a-colorado-poultry-farm/ Accessed 14.08.2024

151. Reuters. Chicken culling, disposal raise concern as bird flu spreads. 2024. https://www.reuters.com/business/healthcare-pharmaceuticals/chicken-culling-disposal-raise-concern-bird-flu-spreads-2024-07-18/ Accessed 14.08.2024

152. World Organization for Animal Health and Food Agricultural Organization of the United Nations Network of Expertise on Animal Influenza. Strategic challenges in the global control of high pathogenicity avian influenza. 90 GS. 2023; https://www.woah.org/app/uploads/2023/05/a-90sg-8.pdf

153. World Health Organization. (2022). Operational considerations for respiratory virus surveillance in Europe (No. WHO/EURO: 2022-5841-45606-65427). World Health Organization. Regional Office for Europe.

154. Henritzi D, Zhao N, Starick E, et al. Rapid detection and subtyping of European swine influenza viruses in porcine clinical samples by haemagglutinin- and neuraminidase-specific tetra- and triplex real-time RT-PCRs. *Influenza and Other Respiratory Viruses*. 2016;10(6):504-517. doi:10.1111/irv.1240

155. Shu B, Garten R, Emery S, et al. Genetic analysis and antigenic characterization of swine origin influenza viruses isolated from humans in the United States, 1990–2010. *Virology*. May 01 2012;422(1):151-160. doi:10.1016/j.virol.2011.10.016

156. Watzinger F, Suda M, Preuner S, et al. Real-time quantitative PCR assays for detection and monitoring of pathogenic human viruses in immunosuppressed pediatric patients. *Journal of Clinical Microbiology*. Nov 2004;42(11):5189-98. doi:10.1128/jcm.42.11.5189-5198.2004

157. Zhou B, Wentworth D.E. Influenza A virus molecular virology techniques. *Methods In Molecular Biology*. 2012;865:175-92. doi:10.1007/978-1-61779-621-0_11

158. Zhou B, Lin X, Wang W, et al. Universal Influenza B Virus Genomic Amplification Facilitates Sequencing, Diagnostics, and Reverse Genetics. *Journal of Clinical Microbiology*. 2014;52(5):1330-1337. doi:10.1128/JCM.03265-13

Geneva, August 29th 2024

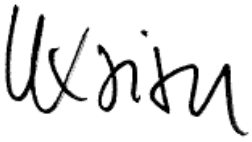
Mrs Tania Spedaliero

Dr Ana Rita Gonçalves Cabecinhas

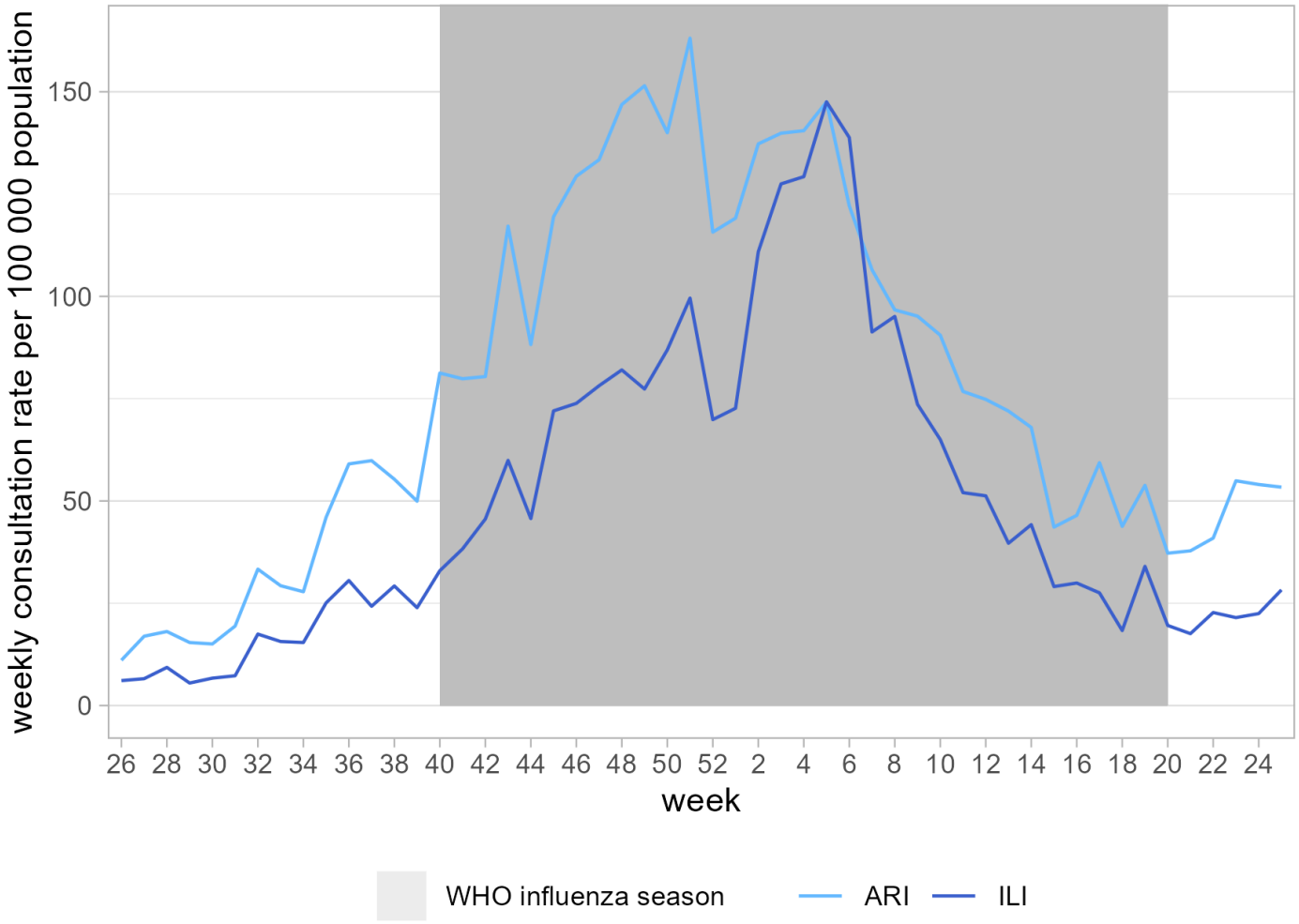
Mrs Patricia Suter-Boquete

Dr Manuel Schibler

Professor Laurent Kaiser



Appendix 1: Seasonal consultations due to an ILI and an ARI in Switzerland, FOPH



https://idd.bag.admin.ch/diseases/influenza/statistic

Appendix 2: Description of the co-detections (40/2023-16/2024)

Weeks	Co-detections									
40	RV-EV/SARS-CoV2	HPIV2-4/ RV-EV								2
41	HPIV2-4/ RV-EV	VRS/RV-EV								2
42	HPIV2-4/ SARS-CoV2	HCoVOC43/SARS-CoV2								2
43	RV-EV/SARS-CoV2	IA/SARS-CoV2								2
44	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2								2
45	RV-EV/HCoVOC43									1
46	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	RV-EV/IB							3
47	RV-EV/HAdV / IB	RV-EV/SARS-CoV2	RV-EV/HCoVOC43	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	HPIV2-4/ SARS-CoV2	HMPV/SARS-CoV2/HAdV			7
48	HCoVHKU1/VRS/SARS-CoV2	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	VRS/SARS-CoV2						4
49	VRS/SARS-CoV2	SARS-CoV2/ HAdV	HAdV /VRS	IA/SARS-CoV2	IA/SARS-CoV2/HCoVHKU1	HPIV2-4/ SARS-CoV2	IA/SARS-CoV2	RV-EV/SARS-CoV2	HCoVHKU1/VRS	9
50	IA/SARS-CoV2	VRS/SARS-CoV2	VRS/SARS-CoV2	IA/SARS-CoV2	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	IA/HCoVHKU1	VRS/SARS-CoV2	HPIV2-4/ VRS	9
51	SARS-CoV2/ HAdV	RV-EV/SARS-CoV2	RV-EV/IA	IA/SARS-CoV2						4
52	HAdV /VRS									1
1	HPIV2-4/ SARS-CoV2	VRS/RV-EV	HPIV1-3/HAdV							3
2	IA/HCoVOC43	RV-EV/IA	RV-EV/IA	IA/SARS-CoV2	IA/SARS-CoV2	IA/HCoVOC43	IA/SARS-CoV2			7
3	IA/SARS-CoV2	IA/SARS-CoV2	IB/VRS	VRS/SARS-CoV2	IA/SARS-CoV2					5
4	IA/SARS-CoV2	VRS/SARS-CoV2	HCoVOC43/HCoVHKU1/IA	RV-EV/IA	IA/HCoVOC43					5
5	IA/SARS-CoV2	HBoV/HCoVOC43/RV-EV	IA/HCoVHKU1	VRS/RV-EV	IA/HCoVHKU1					5
6	HPIV1-3/HCoVOC43	IA/HCoVHKU1	HBoV/HAdV	IA/SARS-CoV2	IA/SARS-CoV2	HPIV1-3/HCoVHKU1				6
7	HCoVHKU1/VRS	HCoVOC43/HAdV	IA/VRS							3
8	HCoVOC43/SARS-CoV2	RV-EV/IA	HMPV/HCoVHKU1	IA/HCoVHKU1	HMPV/HAdV	HMPV/HCoV229E	IA/SARS-CoV2			7
9	HPIV1-3/HAdV/RV-EV	IA/SARS-CoV2								2
10	HCoVOC43/VRS	RV-EV/HAdV	HCoVHKU1/VRS	HAdV/HCoV229E	RV-EV/HCoVOC43					5
11	HMPV/RV-EV	HPIV1-3/SARS-CoV2	HAdV/HCoV229E	HMPV/HCoV229E						4
12	RV-EV/HAdV	HPIV1-3/RV-EV								2
13										0
14	RV-EV/HAdV	RV-EV/HAdV	RV-EV/HAdV							3
15	HPIV1-3/RV-EV									1
16	IB/SARS-CoV2	HMPV/RV-EV								2
Total										99

Appendix 3: Lists of SARS-CoV-2 isolates submitted to GISAID (40/2023-16/2024)

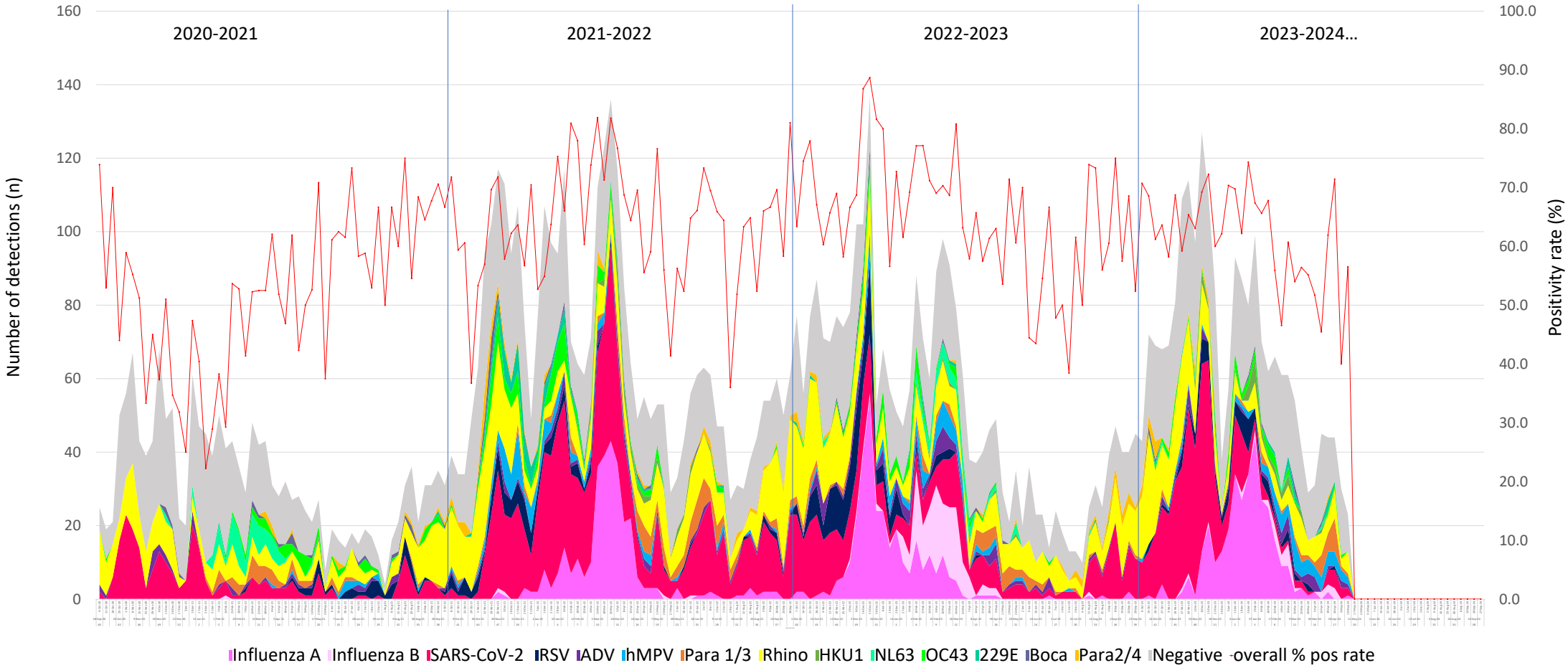
Isolate name	Pangolin clade	Collection date	GISAID_ID
hCoV-19/Switzerland/FR-SNRCI-HUG-42731205/2023	EG.5.1.3	20231003	EPI_ISL_18437867
hCoV-19/Switzerland/FR-SNRCI-HUG-42742178/2023	HK.3	20231003	EPI_ISL_18437868
hCoV-19/Switzerland/VS-SNRCI-HUG-42752266/2023	EG.5.1.1	20231005	EPI_ISL_18437869
hCoV-19/Switzerland/TI-SNRCI-HUG-42785189/2023	FL.1.5.1	20231006	EPI_ISL_18437910
hCoV-19/Switzerland/BE-SNRCI-HUG-42808170/2023	GK.1.1	20231009	EPI_ISL_18437915
hCoV-19/Switzerland/SO-SNRCI-HUG-42807741/2023	XBB.1.16.6	20231009	EPI_ISL_18437914
hCoV-19/Switzerland/TI-SNRCI-HUG-42784402/2023	EG.5.1.1	20231009	EPI_ISL_18437909
hCoV-19/Switzerland/LU-SNRCI-HUG-42784217/2023	XBB.1.16.6	20231009	EPI_ISL_18437908
hCoV-19/Switzerland/LU-SNRCI-HUG-42807307/2023	HV.1	20231010	EPI_ISL_18437913
hCoV-19/Switzerland/LU-SNRCI-HUG-42807230/2023	XBB.1.5	20231011	EPI_ISL_18437912
hCoV-19/Switzerland/VS-SNRCI-HUG-42808301/2023	FL.1.5	20231011	EPI_ISL_18437916
hCoV-19/Switzerland/TI-SNRCI-HUG-42808340/2023	EG.10.1	20231010	EPI_ISL_18437911
hCoV-19/Switzerland/BE-SNRCI-HUG-42850891/2023	EG.5.1.4	20231013	EPI_ISL_18437937
hCoV-19/Switzerland/BE-SNRCI-HUG-42851023/2023	HV.1	20231013	EPI_ISL_18437872
hCoV-19/Switzerland/LU-SNRCI-HUG-42849830/2023	EG.5.1.1	20231016	EPI_ISL_18437871
hCoV-19/Switzerland/ZH-SNRCI-HUG-42849870/2023	XBB.1.41.1	20231016	EPI_ISL_18437866
hCoV-19/Switzerland/VD-SNRCI-HUG-42851311/2023	FL.1.5.1	20231014	EPI_ISL_18437938
hCoV-19/Switzerland/TI-SNRCI-HUG-42872341/2023	EG.5.1	20231019	EPI_ISL_18485616
hCoV-19/Switzerland/AG-SNRCI-HUG-42872566/2023	HV.1	20231017	EPI_ISL_18485611
hCoV-19/Switzerland/BE-SNRCI-HUG-42872601/2023	FL.1.5.1	20231018	EPI_ISL_18485613
hCoV-19/Switzerland/BE-SNRCI-HUG-42872756/2023	GA.4	20231017	EPI_ISL_18485612
hCoV-19/Switzerland/BE-SNRCI-HUG-42873398/2023	XBB.1.16.11	20231017	EPI_ISL_18485614
hCoV-19/Switzerland/LU-SNRCI-HUG-42882887/2023	HK.3	20231019	EPI_ISL_18485617
hCoV-19/Switzerland/ZH-SNRCI-HUG-42882990/2023	BA.2.86	20231019	EPI_ISL_18485615
hCoV-19/Switzerland/BE-SNRCI-HUG-42901698/2023	EG.5.1.1	20231019	EPI_ISL_18485603
hCoV-19/Switzerland/SG-SNRCI-HUG-42914314/2023	EG.5.1.1	20231020	EPI_ISL_18485619
hCoV-19/Switzerland/BE-SNRCI-HUG-42913994/2023	EG.5.1.1	20231023	EPI_ISL_18485605
hCoV-19/Switzerland/AG-SNRCI-HUG-42914061/2023	HK.5	20231023	EPI_ISL_18485604
hCoV-19/Switzerland/AG-SNRCI-HUG-42922918/2023	EG.5.1	20231023	EPI_ISL_18485628
hCoV-19/Switzerland/BE-SNRCI-HUG-42922971/2023	HK.3	20231023	EPI_ISL_18485609
hCoV-19/Switzerland/VS-SNRCI-HUG-42924084/2023	HV.1	20231024	EPI_ISL_18485618

Isolate name	Pangolin clade	Collection date	GISAID_ID
hCoV-19/Switzerland/TI-SNRCI-HUG-42924741/2023	GK.1.3	20231024	EPI_ISL_18485622
hCoV-19/Switzerland/FR-SNRCI-HUG-42933292/2023	HK.3	20231025	EPI_ISL_18485610
hCoV-19/Switzerland/BE-SNRCI-HUG-42933355/2023	EG.5.1.4	20231025	EPI_ISL_18485607
hCoV-19/Switzerland/ZH-SNRCI-HUG-42933620/2023	EG.5.1.1	20231024	EPI_ISL_18485606
hCoV-19/Switzerland/BE-SNRCI-HUG-42943494/2023	EG.5.1.4	20231026	EPI_ISL_18485624
hCoV-19/Switzerland/AG-SNRCI-HUG-42943584/2023	HK.3	20231026	EPI_ISL_18485620
hCoV-19/Switzerland/TI-SNRCI-HUG-42943618/2023	EG.5.1.6	20231026	EPI_ISL_18485608
hCoV-19/Switzerland/BE-SNRCI-HUG-42961635/2023	HK.3	20231026	EPI_ISL_18485623
hCoV-19/Switzerland/BE-SNRCI-HUG-42961621/2023	EG.5.1.3	20231026	EPI_ISL_18485621
hCoV-19/Switzerland/BE-SNRCI-HUG-42961518/2023	HK.3	20231027	EPI_ISL_18485625
hCoV-19/Switzerland/BE-SNRCI-HUG-42975109/2023	XBB.1.16.11	20231026	EPI_ISL_18485627
hCoV-19/Switzerland/VS-SNRCI-HUG-42975046/2023	EG.6.1	20231030	EPI_ISL_18485626
hCoV-19/Switzerland/NE-SNRCI-HUG-42974801/2023	EG.5.1.1	20231030	EPI_ISL_18485629
hCoV-19/Switzerland/SG-SNRCI-HUG-43606814/2024	JN.1.3	20240108	EPI_ISL_18824173
hCoV-19/Switzerland/LU-SNRCI-HUG-43607285/2024	JN.1.1.1	20240108	EPI_ISL_18824172
hCoV-19/Switzerland/VS-SNRCI-HUG-43618929/2024	JN.1	20240109	EPI_ISL_18824171
hCoV-19/Switzerland/BE-SNRCI-HUG-43630567/2024	JN.1	20240109	EPI_ISL_18824174
hCoV-19/Switzerland/BL-SNRCI-HUG-43641834/2024	JN.1	20240109	EPI_ISL_18824176
hCoV-19/Switzerland/AG-SNRCI-HUG-43642065/2024	JN.1	20240111	EPI_ISL_18824175
hCoV-19/Switzerland/TI-SNRCI-HUG-43663083/2024	JN.1.4	20240110	EPI_ISL_18824177
hCoV-19/Switzerland/ZH-SNRCI-HUG-43663363/2024	JN.1	20240112	EPI_ISL_18824179
hCoV-19/Switzerland/VD-SNRCI-HUG-43663399/2024	JN.1	20240111	EPI_ISL_18824178
hCoV-19/Switzerland/LU-SNRCI-HUG-43675568/2024	JN.1	20240115	EPI_ISL_18876265
hCoV-19/Switzerland/ZH-SNRCI-HUG-43675746/2024	JN.1	20240115	EPI_ISL_18876267
hCoV-19/Switzerland/BE-SNRCI-HUG-43675976/2024	JN.1.3	20240113	EPI_ISL_18876256
hCoV-19/Switzerland/GR-SNRCI-HUG-43700488/2024	JN.1.4	20240117	EPI_ISL_18876264
hCoV-19/Switzerland/TI-SNRCI-HUG-43732408/2024	JN.1.7	20240119	EPI_ISL_18876266
hCoV-19/Switzerland/ZH-SNRCI-HUG-43868243/2024	JN.1	20240202	EPI_ISL_18931253
hCoV-19/Switzerland/TI-SNRCI-HUG-43904423/2024	JN.1.6	20240205	EPI_ISL_18931251
hCoV-19/Switzerland/VD-SNRCI-HUG-43937742/2024	JN.1	20240209	EPI_ISL_18931252
hCoV-19/Switzerland/AG-SNRCI-HUG-44015727/2024	JN.1.3	20240219	EPI_ISL_19002369
hCoV-19/Switzerland/LU-SNRCI-HUG-44080569/2024	JN.1	20240226	EPI_ISL_19002388
hCoV-19/Switzerland/SG-SNRCI-HUG-44171078/2024	JN.1.11	20240307	EPI_ISL_19002389
hCoV-19/Switzerland/BE-SNRCI-HUG-44279023/2024	JN.1.1	20240318	EPI_ISL_19059617

Appendix 4: Lists of influenza isolates submitted to GISAID and to ENA (2023/2024)

Collection date	GISAID Isolate-ID	ENA Isolate-ID	Isolate name	Originating Lab
2023-Oct-27	EPI_ISL_18860307	NA	A/Switzerland/43879/2023	Swiss National Reference Centre for Influenza
2023-Oct-28	EPI_ISL_18860308	NA	A/Switzerland/62589/2023	Swiss National Reference Centre for Influenza
2023-Nov-14	EPI_ISL_18860309	NA	A/Switzerland/28412/2023	Swiss National Reference Centre for Influenza
2023-Nov-24	EPI_ISL_18860310	NA	A/Switzerland/25668/2023	Swiss National Reference Centre for Influenza
2023-Dec-04	EPI_ISL_18860352	NA	A/Switzerland/03645/2023	Swiss National Reference Centre for Influenza
2023-Dec-04	EPI_ISL_18860312	NA	A/Switzerland/15143/2023	Swiss National Reference Centre for Influenza
2023-Dec-04	EPI_ISL_18860311	NA	A/Switzerland/05394/2023	Swiss National Reference Centre for Influenza
2023-Dec-05	EPI_ISL_18860316	NA	A/Switzerland/37119/2023	Swiss National Reference Centre for Influenza
2023-Dec-05	EPI_ISL_18860313	NA	A/Switzerland/26340/2023	Swiss National Reference Centre for Influenza
2023-Dec-06	EPI_ISL_18860315	NA	A/Switzerland/26882/2023	Swiss National Reference Centre for Influenza
2023-Dec-06	EPI_ISL_18860314	NA	A/Switzerland/26735/2023	Swiss National Reference Centre for Influenza
2023-Dec-07	EPI_ISL_18860319	NA	A/Switzerland/57527/2023	Swiss National Reference Centre for Influenza
2023-Dec-07	EPI_ISL_18860318	NA	A/Switzerland/38268/2023	Swiss National Reference Centre for Influenza
2023-Dec-07	EPI_ISL_18860317	NA	A/Switzerland/37623/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860325	NA	A/Switzerland/82550/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860324	NA	A/Switzerland/82133/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860323	NA	A/Switzerland/70913/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860322	NA	A/Switzerland/70704/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860321	NA	A/Switzerland/70673/2023	Swiss National Reference Centre for Influenza
2023-Dec-11	EPI_ISL_18860320	NA	A/Switzerland/70358/2023	Swiss National Reference Centre for Influenza
2023-Dec-12	EPI_ISL_18860326	NA	A/Switzerland/94675/2023	Swiss National Reference Centre for Influenza
2023-Dec-14	EPI_ISL_18860327	NA	A/Switzerland/05626/2023	Swiss National Reference Centre for Influenza
2023-Dec-15	EPI_ISL_18860353	NA	A/Switzerland/25664/2023	Swiss National Reference Centre for Influenza
2023-Dec-15	EPI_ISL_18860329	NA	A/Switzerland/26988/2023	Swiss National Reference Centre for Influenza
2023-Dec-15	EPI_ISL_18860328	NA	A/Switzerland/26600/2023	Swiss National Reference Centre for Influenza
2023-Dec-18	EPI_ISL_18860330	NA	A/Switzerland/51134/2023	Swiss National Reference Centre for Influenza
2023-Dec-19	EPI_ISL_18860331	NA	A/Switzerland/51316/2023	Swiss National Reference Centre for Influenza
2023-Dec-20	EPI_ISL_18860354	NA	A/Switzerland/61567/2023	Swiss National Reference Centre for Influenza
2023-Dec-20	EPI_ISL_18860332	NA	A/Switzerland/72782/2023	Swiss National Reference Centre for Influenza
2023-Dec-21	EPI_ISL_18860335	NA	A/Switzerland/96493/2023	Swiss National Reference Centre for Influenza
2023-Dec-21	EPI_ISL_18860334	NA	A/Switzerland/96485/2023	Swiss National Reference Centre for Influenza
2023-Dec-21	EPI_ISL_18860333	NA	A/Switzerland/96430/2023	Swiss National Reference Centre for Influenza
2023-Dec-23	EPI_ISL_18860336	NA	A/Switzerland/13218/2023	Swiss National Reference Centre for Influenza
2023-Dec-26	EPI_ISL_18860338	NA	A/Switzerland/20760/2023	Swiss National Reference Centre for Influenza
2023-Dec-28	EPI_ISL_18860345	NA	A/Switzerland/42569/2023	Swiss National Reference Centre for Influenza
2023-Dec-28	EPI_ISL_18860344	NA	A/Switzerland/42555/2023	Swiss National Reference Centre for Influenza
2023-Dec-28	EPI_ISL_18860343	NA	A/Switzerland/42546/2023	Swiss National Reference Centre for Influenza
2023-Dec-28	EPI_ISL_18860339	NA	A/Switzerland/20899/2023	Swiss National Reference Centre for Influenza
2023-Dec-29	EPI_ISL_18860342	NA	A/Switzerland/42537/2023	Swiss National Reference Centre for Influenza
2023-Dec-29	EPI_ISL_18860341	NA	A/Switzerland/42478/2023	Swiss National Reference Centre for Influenza
2023-Dec-29	EPI_ISL_18860340	NA	A/Switzerland/42469/2023	Swiss National Reference Centre for Influenza
2023-Dec-29	EPI_ISL_18860337	NA	A/Switzerland/20710/2023	Swiss National Reference Centre for Influenza
2024-Jan-01	EPI_ISL_18860346	NA	A/Switzerland/53039/2024	Swiss National Reference Centre for Influenza
2024-Jan-02	EPI_ISL_18860347	NA	A/Switzerland/63081/2024	Swiss National Reference Centre for Influenza
2024-Jan-03	EPI_ISL_18860348	NA	A/Switzerland/63193/2024	Swiss National Reference Centre for Influenza
2024-Jan-11	EPI_ISL_19359940	ERS20919067	A/Switzerland/63114/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359952	ERS20919030	A/Switzerland/75703/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359931	ERS20919041	A/Switzerland/11993/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359920	ERS20919081	A/Switzerland/88489/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359905	ERS20919028	A/Switzerland/75669/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359899	ERS20919080	A/Switzerland/88538/2024	Swiss National Reference Centre for Influenza
2024-Jan-15	EPI_ISL_19359894	ERS20919069	A/Switzerland/75843/2024	Swiss National Reference Centre for Influenza
2024-Jan-16	EPI_ISL_19359938	ERS20919033	A/Switzerland/512/2024	Swiss National Reference Centre for Influenza
2024-Jan-19	EPI_ISL_19359946	ERS20919094	A/Switzerland/32892/2024	Swiss National Reference Centre for Influenza
2024-Jan-19	EPI_ISL_19359937	ERS20919063	A/Switzerland/32523/2024	Swiss National Reference Centre for Influenza
2024-Jan-19	EPI_ISL_19359917	ERS20919037	A/Switzerland/32147/2024	Swiss National Reference Centre for Influenza
2024-Jan-19	EPI_ISL_19359910	ERS20919059	A/Switzerland/32378/2024	Swiss National Reference Centre for Influenza
2024-Jan-22	EPI_ISL_19359926	ERS20919066	A/Switzerland/45440/2024	Swiss National Reference Centre for Influenza
2024-Jan-22	EPI_ISL_19359896	ERS20919052	A/Switzerland/45466/2024	Swiss National Reference Centre for Influenza
2024-Jan-22	EPI_ISL_19361302	ERS20919057	A/Switzerland/45264/2024	Swiss National Reference Centre for Influenza
2024-Jan-23	EPI_ISL_19359907	ERS20919038	A/Switzerland/80122/2024	Swiss National Reference Centre for Influenza
2024-Jan-23	EPI_ISL_19361300	ERS20919040	A/Switzerland/69113/2024	Swiss National Reference Centre for Influenza
2024-Jan-24	EPI_ISL_19359915	ERS20919031	A/Switzerland/68813/2024	Swiss National Reference Centre for Influenza
2024-Jan-25	EPI_ISL_19359898	ERS20919070	A/Switzerland/99731/2024	Swiss National Reference Centre for Influenza
2024-Jan-25	EPI_ISL_19359890	ERS20919044	A/Switzerland/11906/2024	Swiss National Reference Centre for Influenza
2024-Jan-26	EPI_ISL_19359887	ERS20919036	A/Switzerland/00120/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19359950	ERS20919091	A/Switzerland/25065/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19359945	ERS20919032	A/Switzerland/12060/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19359936	ERS20919093	A/Switzerland/11990/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19359927	ERS20919046	A/Switzerland/12460/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19357696	ERS20919055	A/Switzerland/12617/2024	Swiss National Reference Centre for Influenza
2024-Jan-30	EPI_ISL_19359941	ERS20919078	A/Switzerland/12018/2024	Swiss National Reference Centre for Influenza
2024-Jan-30	EPI_ISL_19359935	ERS20919072	A/Switzerland/24351/2024	Swiss National Reference Centre for Influenza
2024-Jan-30	EPI_ISL_19359904	ERS20919029	A/Switzerland/24677/2024	Swiss National Reference Centre for Influenza
2024-Jan-31	EPI_ISL_19359901	ERS20919095	A/Switzerland/46021/2024	Swiss National Reference Centre for Influenza
2024-Jan-31	EPI_ISL_19359885	ERS20919058	A/Switzerland/34967/2024	Swiss National Reference Centre for Influenza
2024-Feb-02	EPI_ISL_19359930	ERS20919035	A/Switzerland/67627/2024	Swiss National Reference Centre for Influenza
2024-Feb-02	EPI_ISL_19359902	ERS20919051	A/Switzerland/67917/2024	Swiss National Reference Centre for Influenza
2024-Feb-05	EPI_ISL_19359942	ERS20919056	A/Switzerland/79656/2024	Swiss National Reference Centre for Influenza
2024-Feb-05	EPI_ISL_19359912	ERS20919096	A/Switzerland/79698/2024	Swiss National Reference Centre for Influenza
2024-Feb-05	EPI_ISL_19359895	ERS20919053	A/Switzerland/79393/2024	Swiss National Reference Centre for Influenza
2024-Feb-06	EPI_ISL_19359960	ERS20919050	A/Switzerland/91862/2024	Swiss National Reference Centre for Influenza
2024-Feb-12	EPI_ISL_19359956	ERS20919088	A/Switzerland/60608/2024	Swiss National Reference Centre for Influenza
2024-Feb-13	EPI_ISL_19359948	ERS20919045	A/Switzerland/60868/2024	Swiss National Reference Centre for Influenza
2024-Feb-13	EPI_ISL_19359933	ERS20919073	A/Switzerland/72288/2024	Swiss National Reference Centre for Influenza
2024-Feb-13	EPI_ISL_19359891	ERS20919068	A/Switzerland/72177/2024	Swiss National Reference Centre for Influenza
2024-Feb-14	EPI_ISL_19359949	ERS20919092	A/Switzerland/72309/2024	Swiss National Reference Centre for Influenza
2024-Feb-15	EPI_ISL_19361299	ERS20919060	A/Switzerland/83558/2024	Swiss National Reference Centre for Influenza
2024-Feb-16	EPI_ISL_19359924	ERS20919085	A/Switzerland/4294/2024	Swiss National Reference Centre for Influenza
2024-Feb-16	EPI_ISL_19359916	ERS20919083	A/Switzerland/04446/2024	Swiss National Reference Centre for Influenza
2024-Feb-19	EPI_ISL_19359919	ERS20919048	A/Switzerland/15810/2024	Swiss National Reference Centre for Influenza
2024-Feb-19	EPI_ISL_19361298	ERS20919049	A/Switzerland/15795/2024	Swiss National Reference Centre for Influenza
2024-Feb-20	EPI_ISL_19359939	ERS20919084	A/Switzerland/37739/2024	Swiss National Reference Centre for Influenza
2024-Feb-21	EPI_ISL_19359943	ERS20919101	A/Switzerland/37628/2024	Swiss National Reference Centre for Influenza
2024-Feb-21	EPI_ISL_19359906	ERS20919105	A/Switzerland/37388/2024	Swiss National Reference Centre for Influenza
2024-Feb-23	EPI_ISL_19359886	ERS20919064	A/Switzerland/68478/2024	Swiss National Reference Centre for Influenza
2024-Feb-23	EPI_ISL_19361303	ERS20919077	A/Switzerland/68826/2024	Swiss National Reference Centre for Influenza
2024-Feb-26	EPI_ISL_19359953	ERS20919034	A/Switzerland/80281/2024	Swiss National Reference Centre for Influenza
2024-Feb-26	EPI_ISL_19359925	ERS20919090	A/Switzerland/80342/2024	Swiss National Reference Centre for Influenza
2024-Feb-26	EPI_ISL_19359900	ERS20919042	A/Switzerland/80821/2024	Swiss National Reference Centre for Influenza
2024-Mar-01	EPI_ISL_19359923	ERS20919082	A/Switzerland/35699/2024	Swiss National Reference Centre for Influenza
2024-Mar-01	EPI_ISL_19359911	ERS20919089	A/Switzerland/34312/2024	Swiss National Reference Centre for Influenza
2024-Mar-04	EPI_ISL_19361301	ERS20919061	A/Switzerland/47775/2024	Swiss National Reference Centre for Influenza
2024-Mar-04	EPI_ISL_19357655	ERS20919074	A/Switzerland/48148/2024	Swiss National Reference Centre for Influenza
2024-Mar-11	EPI_ISL_19359932	ERS20919065	A/Switzerland/14227/2024	Swiss National Reference Centre for Influenza
2024-Mar-14	EPI_ISL_19359947	ERS20919104	A/Switzerland/47014/2024	Swiss National Reference Centre for Influenza
2024-Mar-18	EPI_ISL_19361297	ERS20919099	A/Switzerland/90958/2024	Swiss National Reference Centre for Influenza
2024-Mar-19	EPI_ISL_19359951	ERS20919043	A/Switzerland/02652/2024	Swiss National Reference Centre for Influenza
2024-Apr-02	EPI_ISL_19361304	ERS20919054	A/Switzerland/11744/2024	Swiss National Reference Centre for Influenza
2024-Apr-17	EPI_ISL_19359957	ERS20919103	A/Switzerland/51944/2024	Swiss National Reference Centre for Influenza
2024-Apr-17	EPI_ISL_19358832	ERS20919087	A/Switzerland/52333/2024	Swiss National Reference Centre for Influenza
2024-May-06	EPI_ISL_19359944	ERS20919079	A/Switzerland/16620/2024	Swiss National Reference Centre for Influenza
2023-Nov-15	EPI_ISL_18860349	NA	B/Switzerland/28459/2023	Swiss National Reference Centre for Influenza
2023-Dec-15	EPI_ISL_18860350	NA	B/Switzerland/26859/2023	Swiss National Reference Centre for Influenza
2024-Jan-16	EPI_ISL_19359934	ERS20919071	B/Switzerland/329/2024	Swiss National Reference Centre for Influenza
2024-Jan-29	EPI_ISL_19359909	ERS20919086	B/Switzerland/24894/2024	Swiss National Reference Centre for Influenza
2024-Feb-02	EPI_ISL_19359914	ERS20919047	B/Switzerland/67247/2024	Swiss National Reference Centre for Influenza
2024-Feb-13	EPI_ISL_19359921	ERS20919039	B/Switzerland/60849/2024	Swiss National Reference Centre for Influenza
2024-Feb-21	EPI_ISL_19359888	ERS20919076	B/Switzerland/48531/2024	Swiss National Reference Centre for Influenza
2024-Mar-01	EPI_ISL_19361305	ERS20919098	B/Switzerland/35634/2024	Swiss National Reference Centre for Influenza
2024-Mar-01	EPI_ISL_19359929	ERS20919102	B/Switzerland/35585/2024	Swiss National Reference Centre for Influenza
2024-Mar-13	EPI_ISL_19359958	ERS20919075	B/Switzerland/47323/2024	Swiss National Reference Centre for Influenza
2024-Mar-04	EPI_ISL_19359903	ERS20919100	B/Switzerland/48156/2024	Swiss National Reference Centre for Influenza
2024-Mar-04	EPI_ISL_19359889	ERS20919106	B/Switzerland/48223/2024	Swiss National Reference Centre for Influenza
2024-Apr-22	EPI_ISL_19361296	ERS20919097	B/Switzerland/93020/2024	Swiss National Reference Centre for Influenza
2024-Apr-15	EPI_ISL_19359913	ERS20919062	B/Switzerland/29051/2024	Swiss National Reference Centre for Influenza

Appendix 5: Detection of respiratory viruses in Sentinella since 2020



Appendix 6: Table of reference influenza HA sequences from GISAID used in phylogenetic analyses

Segment ID	Segment	Country	Collection date	Isolate-ID	Isolate name	Originating Lab	Submitting Lab	Authors
A(H1N1)pdm09 reference strains								
EPI1312566	HA	Australia	2018-Jan-04	EPI_ISL_330190	A/Brisbane/02/2018	WHO Collaborating Centre for Influenza Reference and Research on Influenza	Centers for Disease Control and Prevention	
EPI1641015	HA	Denmark	2019-Nov-10	EPI_ISL_400732	A/Denmark/3280/2019	Statens Serum Institute	Statens Serum Institute	Trebbien, R.
EPI1889244	HA	Ghana	2021-Jul-21	EPI_ISL_4005759	A/Ghana/1894/2021	University of Ghana	Crick Worldwide Influenza Centre	
EPI1716630	HA	China	2019-Jun-17	EPI_ISL_416759	A/Guangdong-Maonan/SWL1536/2019 CNIC-1909	Guangdong Provincial Center for Disease Control and Prevention	WHO Chinese National Influenza Center	
EPI1725283	HA	Ireland	2020-Jan-01	EPI_ISL_424676	A/Ireland/87733/2019	National Institute for Medical Research	Centers for Disease Control and Prevention	
EPI2250485	HA	United States	2022-Oct-29	EPI_ISL_16200618	A/Maine/10/2022	Maine Health and Environmental Testing Laboratory	Centers for Disease Control and Prevention	
EPI2286597	HA	Norway	2022-Jun-15	EPI_ISL_16465046	A/Norway/25089/2022	WHO National Influenza Centre	Crick Worldwide Influenza Centre	
EPI1098411	HA	France	2017-Oct-20	EPI_ISL_284660	A/Paris/1447/2017		Institut Pasteur	
EPI1274591	HA	Switzerland	2017-Dec-20	EPI_ISL_321313	A/Switzerland/3330/2017	National Institute for Medical Research	Centers for Disease Control and Prevention	
EPI1957293	HA	Australia	2021-Oct-16	EPI_ISL_8767089	A/Sydney/5/2021	Clinical Virology Unit, CDIM	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Iannello,P; Lau,H; Spirason,N; Moselen,J; Aziz,A; Komadina,N.
EPI1718610	HA	Australia	2019-Nov-22	EPI_ISL_417210	A/Victoria/2570/2019	Alfred Hospital	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Iannello,P; Lau,H; Todd,A; Spirason,N; Moselen,J; Komadina,N.
EPI2447516	HA	Australia	2022-Oct-02	EPI_ISL_17102775	A/Victoria/4897/2022	WHO Collaborating Centre for Reference and Research on Influenza	Centers for Disease Control and Prevention	
EPI2437457	HA	Australia	2022-Oct-02	EPI_ISL_17072386	A/Victoria/4897/2022 (22/316)	WHO Collaborating Centre for Reference and Research on Influenza	National Institute for Biological Standards and Control (NIBSC)	Nicolson, Carolyn
EPI2224978	HA	United States	2022-Oct-25	EPI_ISL_15928563	A/Wisconsin/67/2022	Wisconsin State Laboratory of Hygiene	Centers for Disease Control and Prevention	
A(H3N2) reference strains								
EPI1843689	HA	Bangladesh	2020-Oct-04	EPI_ISL_959654	A/Bangladesh/4005/2020	Centers for Disease Control and Prevention	Crick Worldwide Influenza Centre	
EPI1838942	HA	Cambodia	2020-Sep-25	EPI_ISL_732333	A/Cambodia/925256/2020	Institut Pasteur du Cambodia	Crick Worldwide Influenza Centre	
EPI1841492	HA	Cambodia	2020-Jul-16	EPI_ISL_806547	A/Cambodia/e0826360/2020	Institute Pasteur du Cambodia	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Iannello,P; Lau,H; Spirason,N; Moselen,J; Aziz,A; Komadina,N.
EPI2238870	HA	Spain	2022-Sep-14	EPI_ISL_16043979	A/Catalonia/NSVH161512067/2022	Hospital Universitari Vall d'Hebron	Crick Worldwide Influenza Centre	
EPI1885402	HA	Australia	2021-Mar-16	EPI_ISL_3534319	A/Darwin/6/2021	WHO Collaborating Centre for Reference and Research on Influenza	Centers for Disease Control and Prevention	
EPI1888006	HA	Australia	2021-Apr-17	EPI_ISL_3801278	A/Darwin/9/2021	Royal Darwin Hospital	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Iannello,P; Lau,H; Spirason,N; Moselen,J; Aziz,A; Komadina,N.
EPI1641083	HA	Denmark	2019-Oct-25	EPI_ISL_400748	A/Denmark/3264/2019	Statens Serum Institute	Statens Serum Institute	Trebbien, R.
EPI2736719	HA	Finland	2023-Aug-01	EPI_ISL_18237981	A/Finland/402/2023	Finnish Institute for Health and Welfare, THL	Finnish Institute for Health and Welfare, THL	Ikonen, Niina; Lindh, Erika; Tervo, Niko
EPI1719960	HA	China	2019-Jun-17	EPI_ISL_419005	A/Hong Kong/2671/2019 (19/292)	Centers for Disease Control and Prevention	National Institute for Biological Standards and Control (NIBSC)	Nicolson, Carolyn
EPI1318832	HA	United States	2017-Dec-14	EPI_ISL_331213	A/Kansas/14/2017	Centers for Disease Control and Prevention	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Iannello,P; Lau,H; Kaye,M; Todd,A; Spirason,N; Komadina,N
EPI1995889	HA	Norway	2021-Nov-25	EPI_ISL_11140795	A/Norway/29511/2021	WHO National Influenza Centre	Crick Worldwide Influenza Centre	
EPI2047241	HA	Slovenia	2022-Feb-10	EPI_ISL_12943148	A/Slovenia/8720/2022	Laboratory for Virology, National Institute of Public Health	Crick Worldwide Influenza Centre	
EPI1884889	HA	Sweden	2021-Apr-16	EPI_ISL_3315857	A/Stockholm/5/2021	Public Health Agency of Sweden	Crick Worldwide Influenza Centre	
EPI2235788	HA	Australia	2022-May-29	EPI_ISL_16003445	A/Sydney/732/2022	Childrens Hospital Westmead	WHO Collaborating Centre for Reference and Research on Influenza	Deng,Y-M; Barr,I; Aziz,A
EPI2996923	HA	Australia	2023-Sep-12	EPI_ISL_18864920	A/Sydney/856/2023	WHO Collaborating Centre for Reference and Research on Influenza	Crick Worldwide Influenza Centre	
EPI2996987	HA	Australia	2023-Oct-02	EPI_ISL_18864928	A/Sydney/878/2023	WHO Collaborating Centre for Reference and Research on Influenza	Crick Worldwide Influenza Centre	
EPI2236266	HA	Thailand	2022-Jul-11	EPI_ISL_16014504	A/Thailand/8/2022	WHO National Influenza Centre, National Institute of Medical Research (NIMR)	WHO Collaborating Centre for Reference and Research on Influenza	Okada,P; Yuigun,S; Kala,S; Deng,Y-M; Barr,I; Aziz,A
EPI2087583	HA	Germany	2022-Apr-01	EPI_ISL_13704107	A/Thuringen/10/2022	Robert Koch Institute Nationales Referenzzentrum für Influenza	Crick Worldwide Influenza Centre	
B/Victoria lineage refrence strains								
EPI1845793	HA	Austria	2021-Jan-09	EPI_ISL_983345	B/Austria/1359417/2021	University of Vienna	Crick Worldwide Influenza Centre	
EPI2690180	HA	Spain	2023-Jan-03	EPI_ISL_18109004	B/Catalonia/2279261NS/2023	National Institute for Medical Research	Centers for Disease Control and Prevention	
EPI1001931	HA	United States	2017-Feb-25	EPI_ISL_264099	B/Colorado/06/2017	Colorado Department of Health Lab	Centers for Disease Control and Prevention	
EPI2411732	HA	United States	2021-Jul-17	EPI_ISL_16947021	B/Connecticut/01/2021	Connecticut Department. of Public Health	Centers for Disease Control and Prevention	
EPI1807427	HA	Cote d'Ivoire	2020-May-28	EPI_ISL_609945	B/Cote d'Ivoire/948/2020	Pasteur Institut of Côte d'Ivoire	Crick Worldwide Influenza Centre	
EPI2739235	HA	Norway	2023-Aug-21	EPI_ISL_18244146	B/Norway/08717/2023	Stavanger Universitetssykehus, Avd. for Medisinsk Mikrobiologi	Norwegian Institute of Public Health	Bragstad, K; Hungnes, O; Madsen, MP;Rohringer, A;Riis, R
EPI2690397	HA	Paraguay	2023-Jun-21	EPI_ISL_18109031	B/Paraguay/2102/2023	Central Laboratory of Public Health	Centers for Disease Control and Prevention	
EPI2639346	HA	Slovenia	2023-Mar-22	EPI_ISL_18007306	B/Slovenia/924/2023	Laboratory for Virology, National Institute of Public Health	Crick Worldwide Influenza Centre	
EPI2100743	HA	Sweden	2022-Mar-22	EPI_ISL_13983278	B/Stockholm/3/2022	Public Health Agency of Sweden	Crick Worldwide Influenza Centre	
EPI1482046	HA	United States	2019-Jan-19	EPI_ISL_362540	B/Washington/02/2019	Washington State Public Health Laboratory	Centers for Disease Control and Prevention	