Virological Surveillance of Influenza in Belgium

Season 2019-2020

VIRAL DISEASES
National Influenza Centre (WHO-recognized)

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EPIDEMIOLOGY OF INFECTIOUS DISEASES
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A. Abstract

The 2019-2020 winter season was characterized by the occurrence after the flu epidemic of the COVID-19 pandemic. The Influenza epidemic in Belgium lasted 6 weeks and was a flu season of moderate intensity characterized by the co-circulation of A(H1N1)pdm09 and A(H3N2), with the predominance of A(H1N1). The epidemic threshold was crossed at week 4-2020 (January 13 to January 19, 2020 with an incidence of 245 consultations /100.000 inhabitants and the peak was reached in week 5 with 550 consultations/100.000 inhabitants. After week 5- 2020, the incidence of ILI consultations decreased but remained above the threshold for several weeks likely due to the COVID-19 epidemic with a new ILI peak at week 13 exceeding the influenza peak seen in week 5 (Fig. 1). The emergence of COVID-19, spreading through respiratory transmission, required the implementation of physical distancing measures likely contributed to an abrupt decline of the influenza season.
The majority of the H1N1 viruses fell in the 6B.1A5A subgroup represented by the reference strain A/Norway/3433/2018.

About half of the sequenced A(H3N2) viruses belonged to the clade 3C.2a1 and the remaining belonged to the clade 3C.3a close the vaccine strain for the northern hemisphere A/Kansas/14/2017.

Most of the seqenced influenza B-Victoria viruses were triple-deletion variants similar to B/Washington/02/2019.
Respiratory samples were also analysed for other respiratory viruses. In the ILI population, 70 % of the patients were positive for at least one respiratory virus (including Influenza and co-infections). In the SARI population, 52% of the patients were positive for at least one respiratory viruses (including influenza, SARS-COV-2, other respiratory viruses or different combination of co-infection). From week 10 , the first SARS-CoV-2 patient were diagnosed.
These patients were mostly adults and children above 14 years old.
Severity was moderate in comparison to the previous season and comparable to previous seasons.

None of the analyzed strains presented mutations known to be associated to resistance to antivirals neuraminidase inhibitors (Oseltamivir et Zanamivir).

B. Background

Influenza virus is a leading cause of human morbidity and mortality worldwide. On average, influenza viruses infect 5 to 15% of the global population, resulting in ~500,000 deaths annually (1). Each year, a flu epidemic occurs usually during the winter period, and three or four times per century a new influenza virus emerges. The type of influenza virus circulating and the vulnerability of the population determine the severity of the epidemic or pandemic.
The major objectives of the surveillance are to monitor influenza activity (intensity, duration, severity, …) all over the year, to determine the type and subtypes of circulating strains and their antigenic and genetic characterization, to contribute to the annual determination of influenza vaccine content, to assess the overall vaccine effectiveness, to monitor resistance to antivirals and to detect new potentially pathogenic influenza viruses.
Since 2011, the surveillance has been extended to Severe Acute Respiratory Infection (SARI) cases as a tool to monitor severe diseases caused by influenza to complement surveillance of outpatient monitoring of influenza-like illness (ILI). The main objectives are to measure

incidence, risk factors, clinical spectrum and outcomes of SARI caused by influenza virus and other respiratory pathogens and to monitor indicators of severity, season after season.
Furthermore, there is always a risk of emergence of new pathogenic viruses, as it was the case this season with the emergence of the SARS-CoV-2 virus.
This report is mainly focusing on the virological results.

C. Methods

C.1.1. Sentinel Surveillance of ILI

Network of Sentinel General Practices

In Belgium, the influenza surveillance is performed by the National Influenza Centre (NIC), in collaboration with the Unit of Health Services Research and the Unit of Epidemiology of Infectious Diseases of Sciensano in Brussels. A network of sentinel general practices (SGPs) has been involved since 2007 in the clinical and virological influenza surveillance (2). The main purposes of the surveillance are the early detection of an influenza epidemic, the study of the intensity and duration of the epidemic, the identification and characterisation of circulating viruses and the participation to the selection of next-season influenza vaccine strains. The development of capability to detect new emerging viruses, the estimation of vaccine effectiveness and the monitoring of the antiviral susceptibility are also important tasks

Clinical surveillance

The SGPs network is geographically representative of all GPs in Belgium. Besides the number of acute respiratory infections by age group, the GPs reported weekly, on a standardised form, every patient with an influenza-like illness (ILI). The general criteria for ILI are: sudden onset of symptoms, high fever, respiratory (i.e. cough, sore throat) and systemic symptoms (headache, muscular pain). For every patient, age group (<5, 5-14, 15-64, 65-84, 85+), hospitalisation, antiviral treatment, and vaccination status were recorded (3).

Virological surveillance

These GPs are also involved in the virological surveillance and are invited to collect 2 nasopharyngeal swabs/week (each week, the first two patients presenting for ILI belonging to different households).
Sampling kits are sent to all physicians. Each kit contained the materials required to collect nasopharyngeal swabs (2 nostrils + 1 throat) in patients with influenza-like illness. The material consisted of tubes containing 3 ml of transport medium [UTM (COPAN)], swabs [flocked Swabs (COPAN)] and patient registration forms. Samples and forms are returned to the National influenza Centre by mail (postage paid) and new kits are regularly sent depending on the shipment of samples. Patients information, clinical and epidemiological data and laboratory results are encoded in the LIMS system. The lab results of each patient were sent to the physician, after scientific and medical validation.
With the occurrence of the COVI19 pandemic, the surveillance system has been disrupted since march when physicians could not have physical examination of their patient.

C.1.2. Sentinel Surveillance of SARI

Network of sentinel hospitals

Following the A(H1N1)2009 pandemic, the WHO and the European Centre for Disease Prevention and Control (ECDC) recommended hospital-based surveillance of severe acute respiratory infections (SARI) as a tool to monitor severe disease caused by influenza to complement outpatient surveillance of influenza like illness (ILI) or acute respiratory illness (ARI) to cover the full spectrum of influenza-related disease. As a result, the Belgian NIC has extended, since 2011, its surveillance to SARI cases. The main objectives were 1) to build a clinical and virological database of hospital cases permitting to rate the severity across seasons and pandemics; 2) to detect signals of severity during the course of an epidemic or a pandemic; 3) to describe genotypic and phenotypic characteristics of influenza viruses associated with severe forms of infection; 4) to test clinical samples for other respiratory viruses.

During the 2019-2020 influenza season, six hospitals located in the three regions of the country participated to the surveillance. The SARI case definition (adapted from the SARI case definition from WHO) is: an acute respiratory illness with onset within the last ten days, fever of ≥ 38°C (or history of fever), cough or dyspnoea, and that required hospitalisation (for 24h or more). As we are mostly interested in severe influenza cases, the surveillance is carried out only during the epidemic period of seasonal influenza. Pediatric and adult units collected both clinical data and nasopharyngeal swabs from patients who corresponded to the case definition.

Sampling kits contained the materials required to collect 2 nasopharyngeal swabs (nostrils and throat) per patient responding to the SARI case definition. The material consisted of tubes containing 3 ml of transport medium [UTM (COPAN)], swabs [flocked Swabs (COPAN)] and patient registration forms. Samples and forms are returned to the NIC by mail (postage paid) and new kits are sent regularly to hospitals depending on the shipment of samples.

Patients information, clinical and epidemiological data and laboratory results are encoded in the LIMS system. All the results of one patient are sent to the hospital, after scientific and medical validation, once the results for influenza typing and subtyping and the results for the other respiratory viruses are available.

The following hospitals participated in the SARI surveillance during season 2019-2020:

- Cliniques Universitaires UCL, Mont-Godinne, Belgium
- Centre Hospitalier Universitaire St-Pierre, Brussels, Belgium
- Department of Laboratory Medicine, Medical Microbiology, Algemeen Ziekenhuis Sint-Jan, Brugge, Belgium
- Internal Medicine-Infectious Diseases, Universitair Ziekenhuis Brussel, Brussels, Belgium
- Clinical Laboratory, Jessa Ziekenhuis, Hasselt, Belgium
- Infectiology, Grand Hôpital de Charleroi, Charleroi, Belgium

C.1.3. Non-Sentinel Surveillance

Hospitals and laboratories across the country are encouraged to collect samples from patients presenting with severe acute respiratory diseases in particular specific conditions: ARDS (acute respiratory distress syndrome), ECMO (extracorporeal membrane oxygenation), death, suspicion of antiviral resistance, returning from abroad. Monitoring of

clusters of Influenza cases is also an important task. This surveillance is carried out throughout the year.

C.1.4. Suspected cases of Avian Influenza H5N1 and H7N9

Influenza A (H5N1)

Since 2003, Belgian NIC at Sciensano was appointed as reference laboratory for testing of the H5N1 suspected cases, which are mainly cases returning from affected countries.

Influenza A (H7N9)

The Belgian NIC has developed molecular tests for the detection of A(H7N9) virus in suspected cases. The same surveillance strategy applies as for human infections with highly pathogenic avian influenza A(H5N1) virus.

C.1.5. Suspected Cases of MERS CoV

In Belgium, the National Reference Centre for MERS-CoV is the Microbiology and Immunology Department of UZ Leuven (NRC Respiratory Pathogens). However, the National Influenza Centre has developed real time PCR testing to analyse respiratory samples from suspected cases in the context of differential diagnosis with Influenza. So far there have not been any confirmed cases of MERS-CoV in Belgium.

C.1.6. Suspected Cases of SARS-CoV-2

In Belgium, the National Reference Centre for coronaviruses is the Microbiology and Immunology Department of UZ Leuven (NRC Respiratory Pathogens). However, since the begin of the COVID 19 pandemic the National Influenza Centre has developed different qRT Real Time PCR tests to analyse respiratory samples from patient from the networks of influenza surveillance for SARS-CoV-2.

C.1.7. Surveillance of other respiratory viruses

In addition to flu viruses, several other respiratory viruses can also circulate during the flu season and can cause symptoms and illness similar to those seen with flu infection. Respiratory infections are very common. They may be associated with significant morbidity and even mortality in young children and elderly patients. In about 30-60% of cases with influenza-like symptoms, no influenza virus can be detected, and in at least 20% of influenza-negative ILI cases, other respiratory viruses (such as RSV, rhinovirus, parainfluenza viruses, …) seem to be involved (10). Furthermore, severe influenza cases often seem to be complicated by co-infections with other respiratory viruses (11). We have developed 4 quadriplex Real time PCRs for the detection of 15 different respiratory viruses: respiratory syncytial virus (RSVA and RSVB), parainfluenza viruses (PIV1,2,3, 4), rhinoviruses/enterovirus (HRV/ENV), specific enterovirus D-68 (EV-D68), human metapneumoviruses (hMPV), paraechoviruses (HPeV), bocaviruses (HBoV), adenoviruses (ADV) and different coronaviruses (CoOC43, CONL63, Co229E).

C.2. Laboratory tests

C.2.1. Real-time RT-PCR Influenza

Nasopharyngeal swabs received at the NIC are tested with different real-time RT-PCRs: A/B typing followed by subtyping (for influenza A) or determination of the lineage (for influenza B). The sequence of tests is presented in Figure 1.

Typing A/B

A triplex Real-time qRT-PCR Influenza A/B/RP: adapted protocols (12,13); primers and probes for the matrix gene (influenza A) and hemagglutinin gene (influenza B). The RNaseP (RP) primers and probe target the human RNase P gene, which serves as an internal positive control for human nucleic acid.

Subtyping A (H1, H3, N1, N2)

For all influenza A positive samples, the subtype is determined.

- Real-time qRT-PCR Influenza A/H1 sw: adapted protocol from CDC (12); primers and probes are chosen in the hemagglutinine gene.
- Real-time qRT-PCR A/H3: adapted protocol from RIVM (14); primers and probes in the hemagglutinine gene.

For a subset of samples:

- Real-time qRT-PCR N1: adapted protocol from RIVM (14); primers and probes in the neuraminidase gene.
- Real-time qRT-PCR N2: adapted protocol from Pasteur Institute Paris (15); primers and probes in the neuraminidase gene.

A duplex Real Time PCR H1N2 has been validated and used for the subtyping of influenza A viruses during this season. This method permits to monitor the Hemagglutinin and neuraminidase at the same time, and to identify potential recombinant H1N2 .

Lineage B (Yamagata, Victoria)

For influenza B positive, the lineage (Yamagata or Victoria) is determined.

- Duplex Real-time qRT-PCR B YAM-VIC: adapted protocol from Olav Hungnes (16).

In case of un-subtypable influenza A, if the Ct value is < 36, primers and probe specific for the Nucleoprotein of animal influenza (SWA) are used (protocol CDC)(12): This test allows to determine if the influenza strain is of animal origin and to continue with complementary tests.

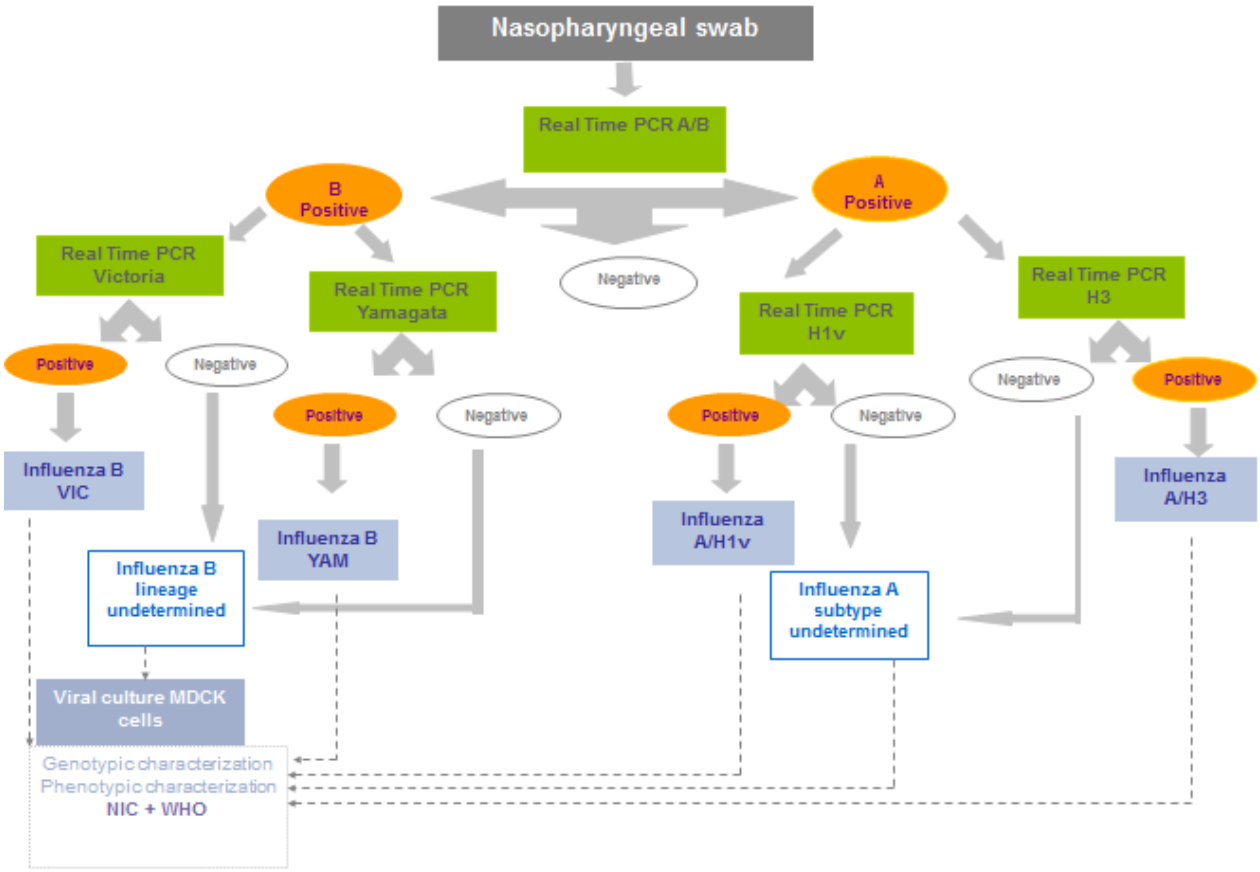


Figure 1. Sequence of the Real time PCR tests used during the 2019-2020 season.

Subtyping (H5, H7, …)

Samples from suspected cases of avian influenza are submitted to real-time RT-PCR A/B for typing and, in case of positivity, to different real-time RT-PCR for subtyping depending on the epidemiological and clinical context.

RT-PCR H5N1

Different sets of primers and probes H5 are used following different protocols: adapted protocol from Spackman et al. 2002 (17), adapted protocol from the Health Protection Agency, 2006 (18) and from Pasteur Institute (18b).

RT-PCR H7N9

Protocol adapted from WHO (19).

C.2.2 PCR tests for MERS CoV

Samples from suspected cases for MERS-CoV are submitted to specific real-time RT-PCRs for MERS-CoV (screening and confirmation); protocol from Corman *et al.2012* (20).

C.2.3 PCR tests for SARS-CoV-2

Different RT qPCR were developed for the detection of SARS-CoV-2.

- SARS -CoV-2 Real Time PCR (Duplex E Gene), adapted from Corman et al. 2019 (21)
- SARS-CoV-2 Real Time PCR (Triplex RdRP), adapted from Pasteur Institute 2020 (22)
- FLU SARS-CoV-2 Real Time PCR (Quadriplex A/B/RP/COV) in house qRTPCR (23)

Respiratory samples from the ILI and SARI surveillance were tested for SARS-CoV-2.

C.2.4 PCR tests for other respiratory viruses

Respiratory samples from the different surveillance networks (ILI, SARI, Hospital non-sentinel) were additionally submitted to 4 quadriplex Real-time RT-PCRs detecting 15 other respiratory viruses (Respiratory syncytial virus (RSVA and RSVB), parainfluenza viruses (PIV 1, 2, 3, 4), rhinoviruses/enterovirus (HRV/ENV), human metapneumoviruses (hMPV), paraechoviruses (HPeV), bocaviruses (HBoV), adenoviruses (ADV) and different coronaviruses (CoOC43, CONL63, Co229E)(24). For this season, a new test was included to detect Enterovirus D-68 (EV-D68) (Table 1).

MIX 1		MIX 2		MIX 3		MIX 4	
RSV A	HEX	PIV 1	ROX	Co 229E	ROX	Boca	Cy5
RSV B	ROX	PIV 2	HEX	Co OC43	HEX	PIV 4	HEX
hMPV	Cy5	PIV 3	FAM	Co NL63	Cy5	Paraecho	ROX
EV	FAM	Adéno	Cy5	Rhino	FAM	EV-D68	FAM

Table 1. Multiplex RT PCR tests for respiratory viruses

The protocols have been adapted from those of the Statens Serum institute (21) with some modifications (primers for rhinoviruses as described by Hombrouck et al. (10). Rhinoviruses and enteroviruses were considered together as rhinovirus/enterovirus (HRV/ENV). EV-D68 was tested separately (25).

C.2.5. Genetic characterisation

Since previous season, NGS has been introduced for the routine analysis of circulating strains. Amplification of the 8 segments of Influenza A and B were adapted from published protocols (26, 27). The sequencing of the amplicon was performed with MiSeq Illumina.
Sequence comparison, alignments and phylogenetic trees are realized using MEGA 7 program. Influenza sequences are compared to reference strains and vaccine strains. Based on evolutionary models, influenza strains can be classified in clades characterised by common and specific mutations.

C.2.6. Resistance to antivirals

The most commonly used antivirals are neuraminidase inhibitors [oseltamivir (Tamiflu ®) and zanamivir (Relenza ®)]. Influenza strains may develop resistance to these antivirals, and thus become less susceptible to their inhibitory activity. Resistant strains can be detected by phenotypic tests based on the use of MUNANA and IC50 measurement following the protocol recommended by the WHO reference laboratory (WHO-CC) in London, UK (22). Phenotypic resistance is often associated with mutations, causing reduced binding to the antiviral. For example, the Y275H mutation in N1 is associated with resistance to Oseltamivir. Other mutations associated with resistance to antivirals are also described for A(H3N2) and influenza B. Genotypic tests are based primarily on sequencing of Na gene to highlight potential mutations compared to reference sequences.

C.2.7. Sending of strains to London WHO CC

Each year, representative Belgian strains are sent to the WHO Collaborating Centre for Reference and Research on Influenza, Crick Worldwide Influenza Centre in London to undergo additional tests: antigenic and genetic characterization and monitoring of antiviral resistance. The characterization of circulating strains in Belgium contributes to the determination by WHO of the strains to be included in flu vaccines for the next season.

D. Results

D.1 Sentinel Influenza Surveillance of ILI

D.1.1 Clinical Surveillance

The 2019-2020 season the Influenza epidemic in Belgium lasted 8 weeks. The epidemic threshold was crossed on week 4-2020 (January 20 to January 26, 2020) (Fig. 2).
The intensity of the epidemic was moderate. After week 3-2020, the incidence of GP visits for influenza-like illness (ILI) rapidly increased to reach 550 GP consultations per 100.000 inhabitants in week 5-2020. From week 5- 2020, the incidence of ILI consultations decreased but remained above the threshold for several weeks likely due to the COVID-19 epidemic . In March 2020, the COVID-19 epidemic resulted in a new ILI peak in week 13-2020, exceeding the influenza peak observed in week 5. An update of the situation was published weekly (3).

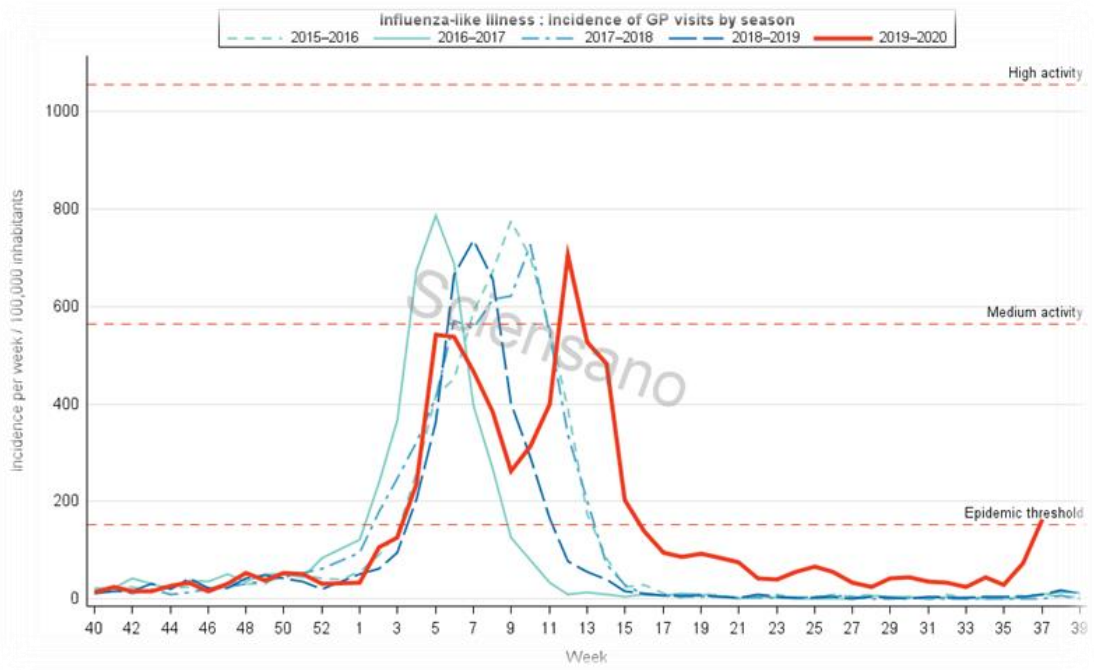


Figure 2a. Weekly incidence of influenza-like illness (ILI), 2019-2020 season, Belgium (Source: Sentinel general practices)

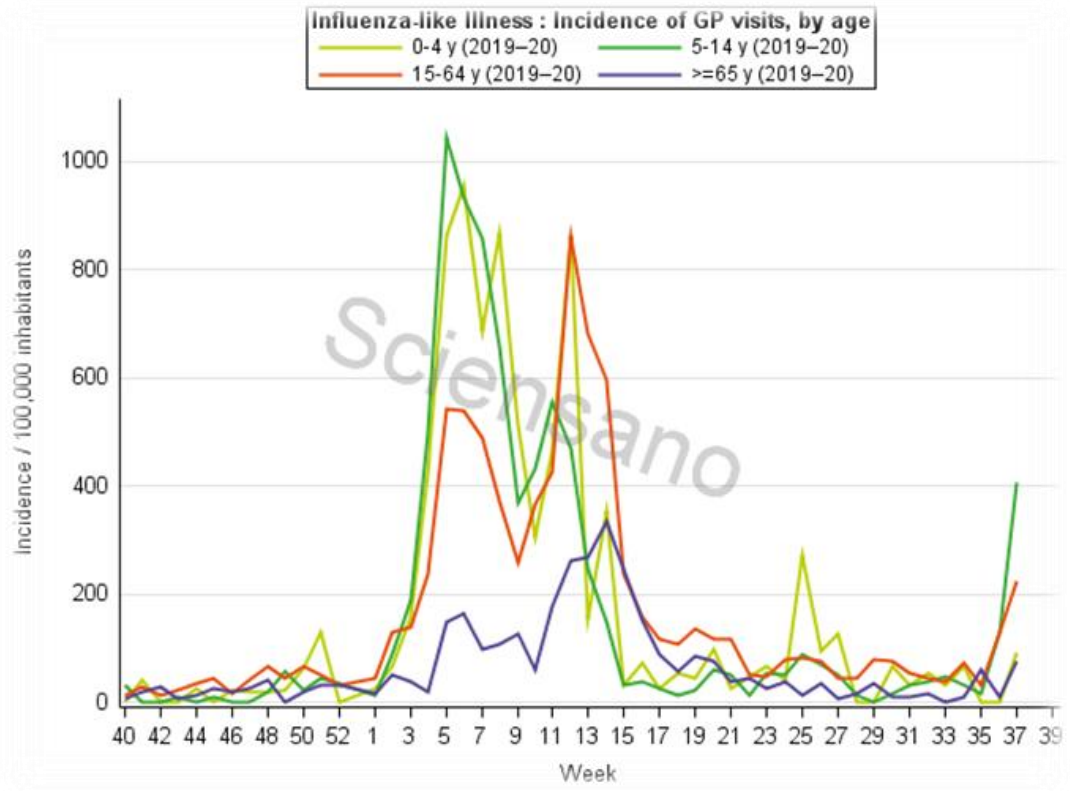


Figure 2b. Weekly incidence of influenza-like illness (ILI) by age groups, 2019-2020 season, Belgium (Source: Sentinel general practices).

D.1.2 Virological Influenza Surveillance

The influenza surveillance period started in week 40-2019 and continued to week 27-2020 .

Origin of samples

A total of 68 general practices (41 for Flanders, 22 for Wallonia and 5 for Brussels) took part in the virological surveillance and sent 698 nasopharyngeal swabs to the NIC.

Number of nasopharyngeal swabs

Flanders :	429
Wallonia :	225
Brussels :	44
Total :	**698**

From these samples **675** were suitable for analyses (sampling date available).

Influenza Typing and subtyping results

The first positive sample was diagnosed in week 45-2019 and increasingly large numbers of positive influenza cases were detected from week 1-2020 onwards, reaching a proportion of 73,5% in week 4-2020. These were mainly A(H1N1)pdm09 and A(H3N2) viruses with a predominance of A(H1N1). The circulation of influenza B was low .

From week 40-2019 to week 20-2020, 675 respiratory samples were sent by the sentinel GPs network and analysed at the National Influenza Centre. Of these samples, 311 (46%) were positive for influenza with 287 (42,5%) positive for influenza A and 24 (3,6 %) positive for influenza B.
Among the influenza A samples that were subtyped, 58,2% (167/287) were A(H1N1)pdm2009, 40,1 % (115/287) were A(H3N2) and 1,7% (5/287) could not be subtyped due to low viral load. All influenza B samples belonged to the Victoria lineage (table 2) and (fig.3).

		FLU detection/typing			FLU A subtyping			FLU B lineage		
		Negative	A	B	A H1	A H3	A NT	YAM	VIC	B NL
Total for season	Number of samples with given result	364	287	24	167	115	5	0	24	0
	Number of tested samples	675	675	675	287	287	287	24	24	24
	Percentage (%)	53,9	42,5	3,6	58,2	40,1	1,7	0,0	100,0	0,0

Table 2. Numbers and proportion of the different types and subtypes analysed during the 2019-2020 season

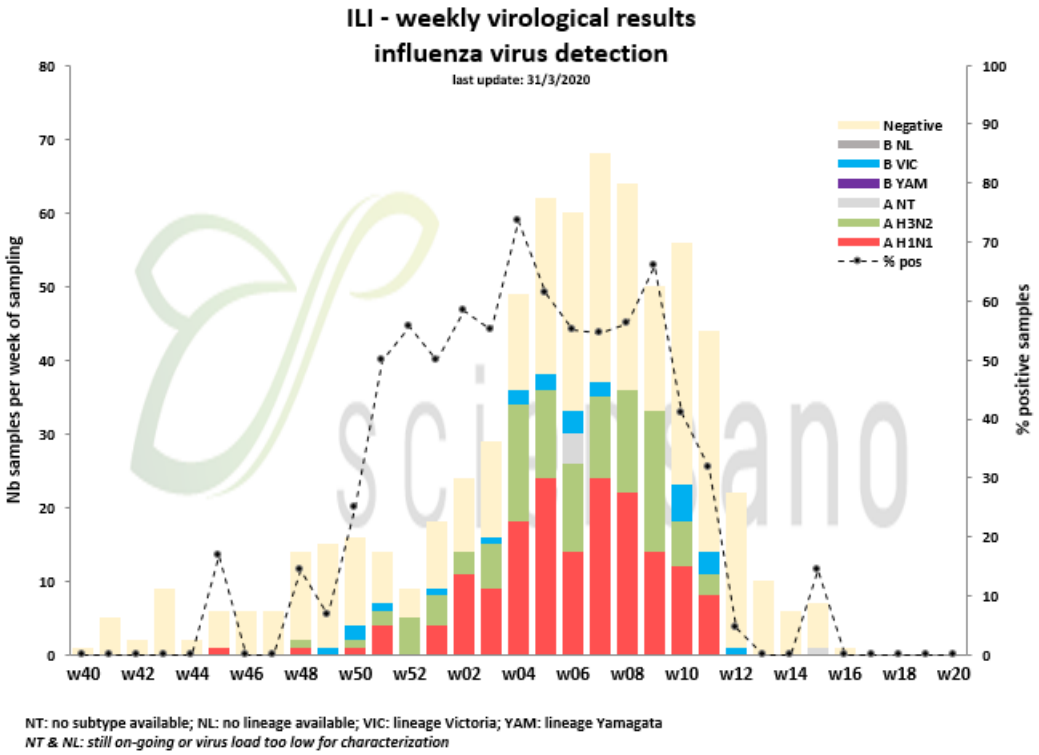


Figure 3. Weekly detection of influenza viruses in Belgium from week 40-2019 to week 20-2020 in the network of sentinel GPs.

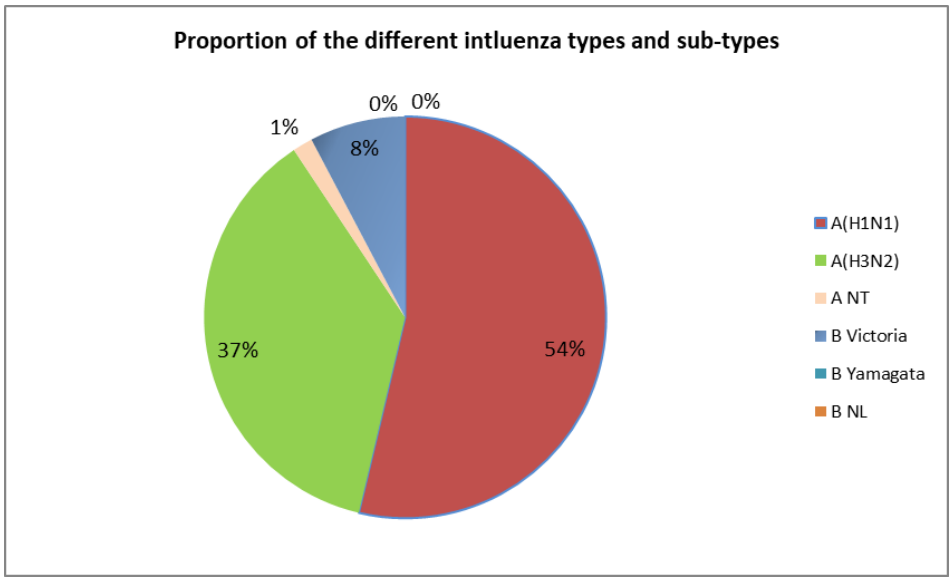


Figure 4. Repartition of the different types and subtypes during the influenza season 2019-2020 (ILI surveillance) .

Influenza viruses according to age group

The age was known for 670 patients. The NIC received a higher number of samples from the age group 15-44 and 45-64 years old. The rate of positivity was higher in the group 15-44 years old (Figure 5). Very few samples were collected from the age group < 5 years old and > 85 years old.

The distribution of influenza types (and subtypes) varied with age. A(H1N1) was the predominant virus in all age groups except in the age group of 5-14 where A(H3N2) was predominant.

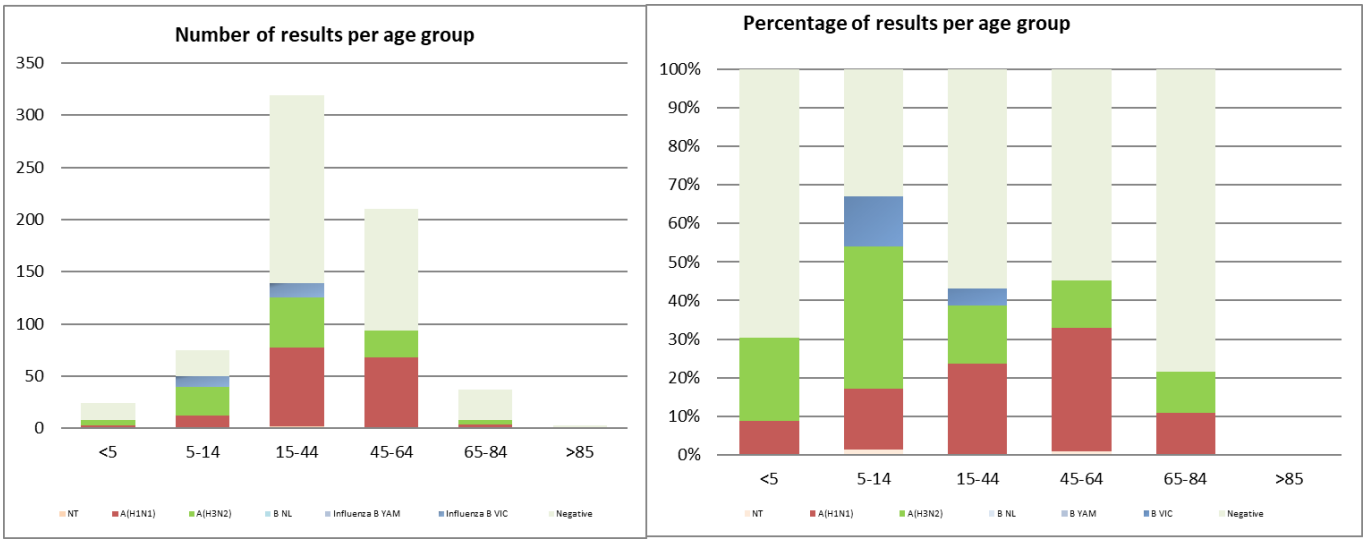


Figure 5. Influenza virus types and subtypes according to age group (NT= non subtyped) (numbers and percentages) influenza season 2019-2020 ILI surveillance .

D.2 Sentinel Influenza Surveillance of SARI

D.2.1 Virological Influenza Surveillance

Origin of samples

The SARI Surveillance started on week 1-2020 and ended on week 17-2020.
A total of 2166 SARI patients were registered in the database. From these patients, 1932 were tested for influenza viruses. The samples from the remaining 215 patients were only tested for SARS-CoV-2.
The age was known for 1913 patients and those were taken into account for the analyses of age groups.

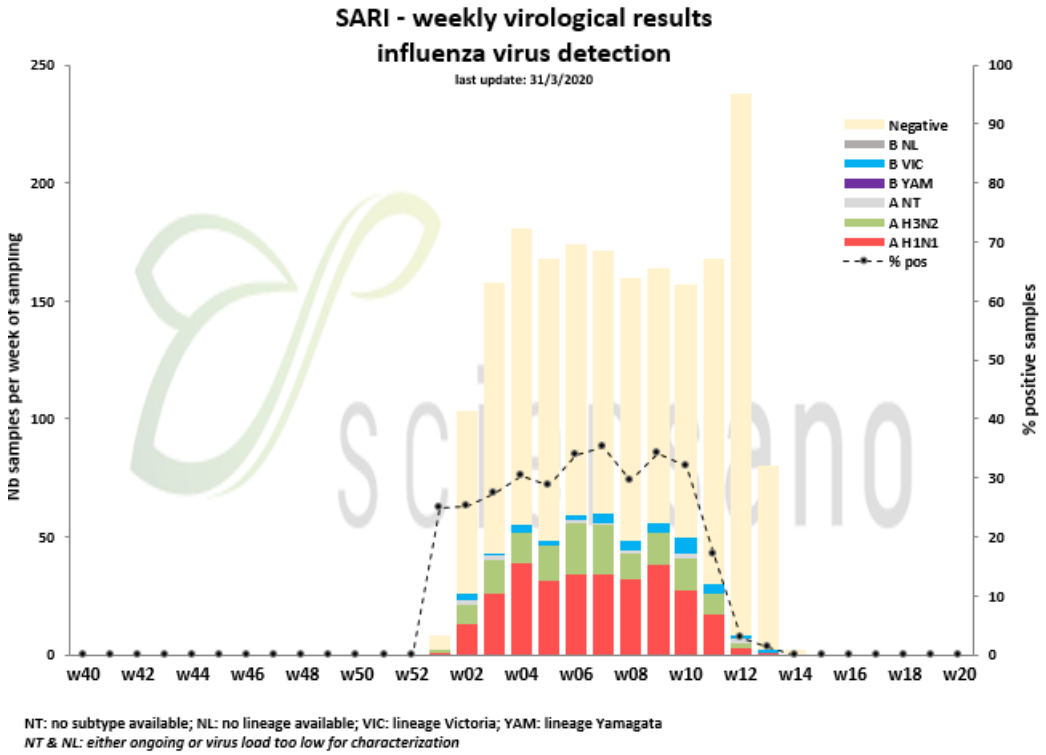
Influenza Typing and subtyping results

From week 1-2020 to week 17-2020, 1932 SARI (Severe Acute Respiratory Infections) respiratory specimens were tested for influenza by the National Influenza Center. Of these samples, 487 (25,2%) were positive for influenza viruses, of which most 451(23,3%) were positive for influenza A viruses and 36 (1,9%)for influenza B viruses (Table 3 and fig.6).

Of the subtyped influenza A samples, 65,6% (296/451) were A(H1N1)pdm09 viruses, 31,9% (144/451) were A(H3N2) viruses and 2.4% could not be subtyped due to low viral load. All the 36 influenza B viruses belonged to the the Victoria lineage (Table 3 and fig.7).

		FLU detection/typing			FLU A subtyping			FLU B lineage		
		Negative	A	B	A H1	A H3	A NT	YAM	VIC	B NL
Total for season	Number of samples with given result	1445	451	36	296	144	11	0	36	0
	Number of tested samples	1932	1932	1932	451	451	451	36	36	36
	Percentage (%)	74,8	23,3	1,9	65,6	31,9	2,4	0,0	100,0	0,0

Table 3. Repartition of the different types and subtypes during the influenza season 2019-2020 (SARI surveillance).



NT: no subtype available; NL: no lineage available; VIC: lineage Victoria; YAM: lineage Yamagata
NT & NL: either ongoing or virus load too low for characterization

Figure 6. Weekly detection of influenza viruses in Belgium in the SARI surveillance from week 1-2020 to week 20-2020 .

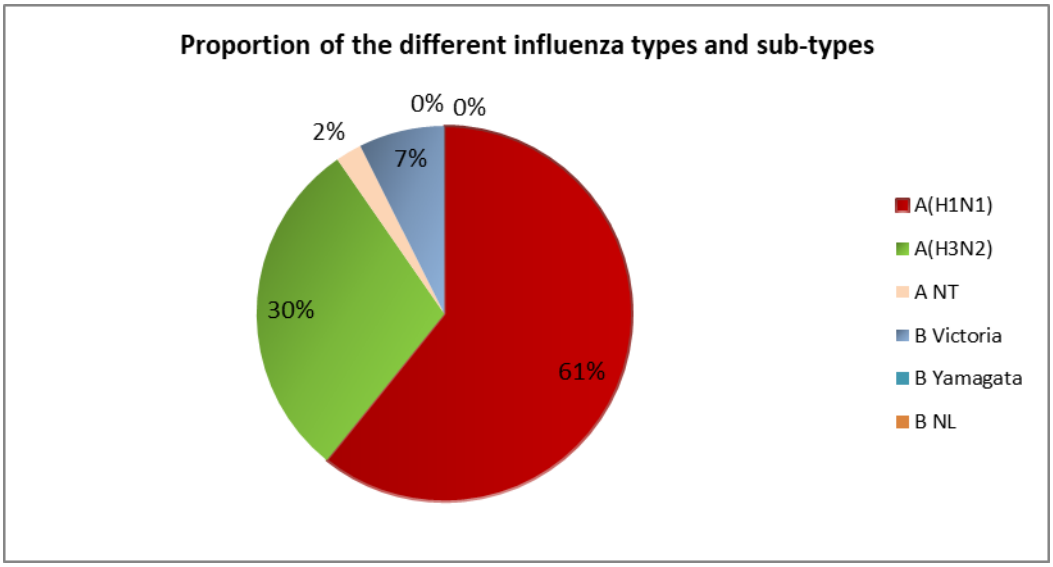


Figure 7. Repartition of the different types and subtypes during the influenza season 2019-2020 (SARI surveillance).

Age distribution of influenza viruses by types and subtypes

The age was known for 1913 patients. A higher number of samples was collected from children below 5 years old and adults of the 65-84 age group. The percentage of positivity for influenza viruses was lower in children below 5 years. The distribution of influenza types (and subtypes) varied with age with higher percentage of A(H3N2) in children (5-14 years old) (Figure 8).

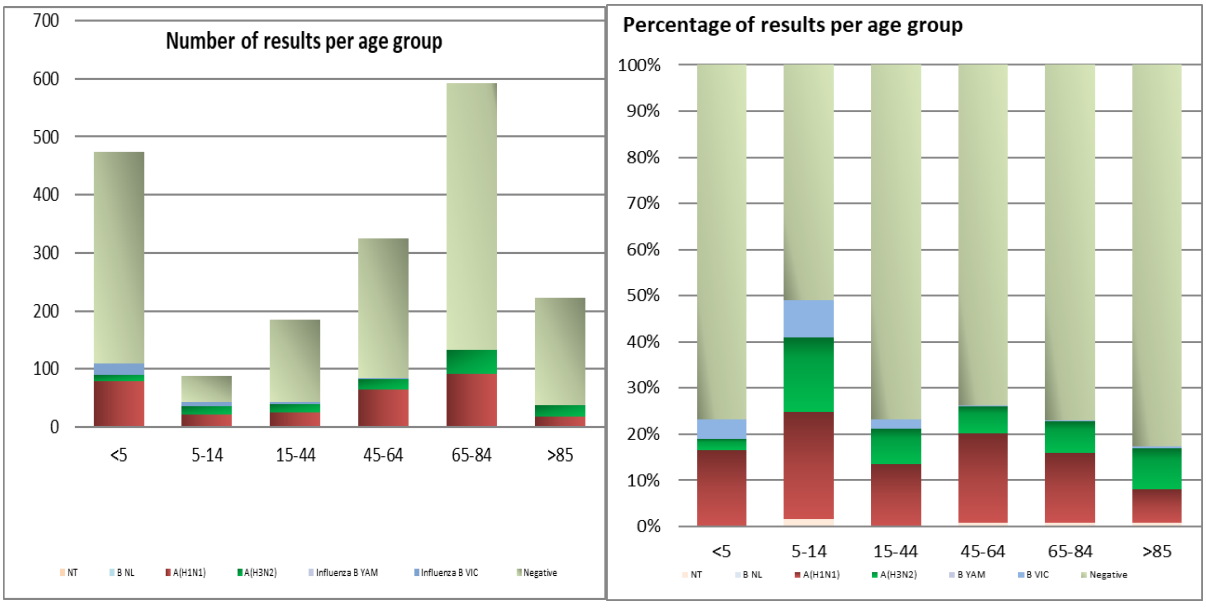


Figure 8. Influenza viruses according to age group SARI surveillance season 2019-2020 (numbers and percentages).

Positivity and subtype distribution of influenza viruses by surveillance scheme ILI/SARI

During this period, Influenza A(H1N1)pdm09 and A(H3N2) circulated in both surveillances.
The rate of positivity was higher in the ILI surveillance (46%) than in the SARI surveillance (25%). A(H1N1) was predominant in both surveillance.
There was no significant difference between both surveillances in the ratio of influenza A(H1N1)pdm09 to A(H3N2) infections among confirmed influenza A patients.

D.3 Non Sentinel surveillance

Thirty-seven respiratory samples from patients with severe influenza were sent from hospitals around the country during the 2019-2020 season and were analysed at the NIC for confirmation and subtyping. Thirteen were A(H1N1)pdm09, 6 were A(H3N2).

D.4 Suspected cases of Avian Influenza

No sample was sent to the NIC for diagnosis of Avian influenza during this season.

D.5 Suspected cases of MERS CoV

No sample was sent to the NIC for diagnosis of MERS CoV during this season.

D.6 Surveillance of SARS-CoV-2

D.6.1 ILI surveillance SARS-CoV-2

Since the begin of march 2020, all samples from the ILI surveillance were tested for SARS-CoV-2 using different qRT Real time PCR.
It should be noted that from that moment on, it was very difficult for the sentinel GP to send samples because due to the restrictions and precautions due to COVID, there were not allowed anymore to see their patients and furthermore suspected patients should be tests for SARS-COV-2 by the official way. Overall, 10% (20/182 samples) were positive for SARS-COV-2, the first positive samples were notice from week 10-2020 (Fig.9).

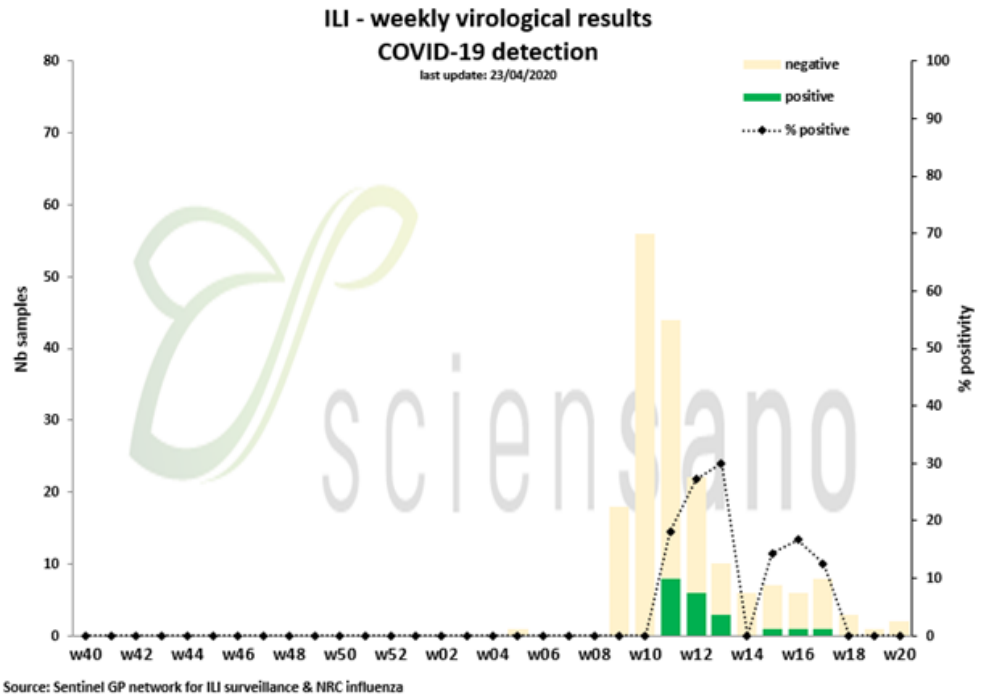


Figure 9. Weekly detection of SARS-CoV-2 in Belgium in the ILI surveillance from week 9-2020 to week 20-2020 .

D.6.1 SARI surveillance SARS-CoV-2

From the first of march, all SARI samples were systematically tested for SARS-CoV-2, and samples from mid-February were tested retrospectively. Overall, 1357 samples were tested and 268 were positive . The first positive samples were noticed since week 10-2020 with an increasing number of positive to reach a peak at week 11-2020 with a positivity rate of 80% (Fig.10).

As already mentioned for the ILI surveillance, the SARI surveillance was also heavily impacted by the pandemic, with a huge work for the hospitals.

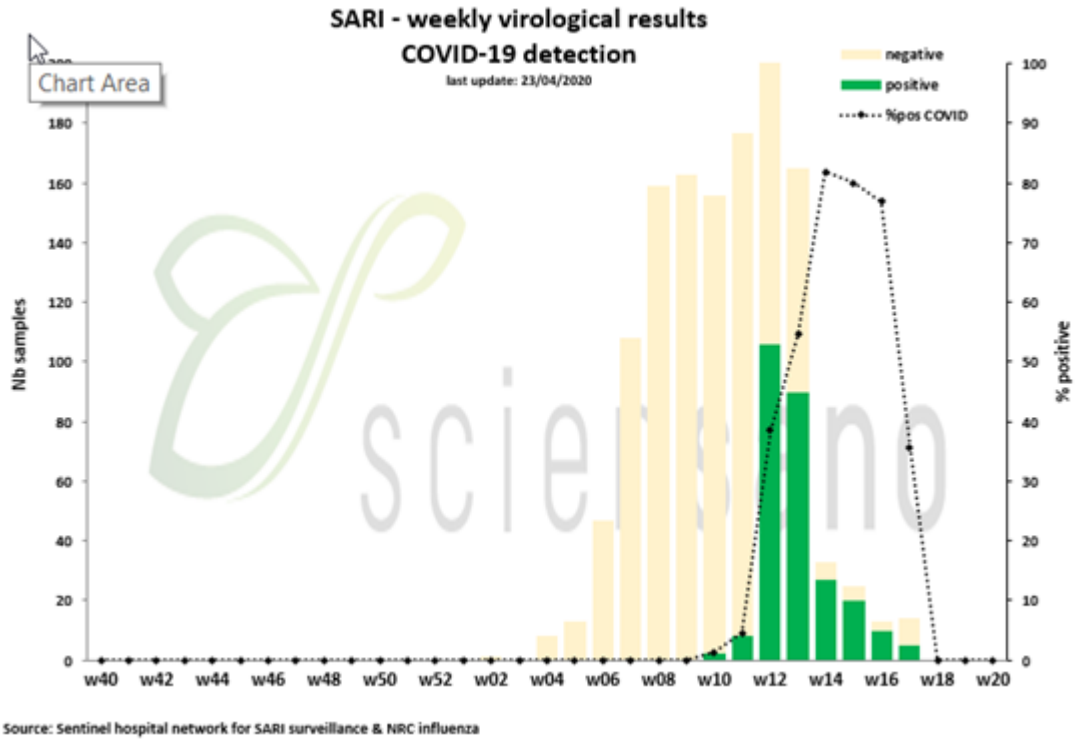


Figure 10.Weekly detection of respiratory viruses in Belgium in the SARI surveillance from week 4-2020 to week 20-2020 .

D.7 Other Respiratory viruses

All respiratory samples submitted to influenza diagnosis were also analysed for 16 other respiratory viruses: RSV-A and -B, PIV 1-2-3-4, HRV/ENV, EV-D68, hMPV, HPeV, HBoV, ADV and different Coronaviruses (Co229E, CoOC43, CoNL63).

D.7.1 ILI surveillance

Between weeks 40-2019 and 10-2020, 580 respiratory samples analysed for influenza were tested for other respiratory viruses. After week 10 the priority was focused on SARS-CoV-2 detection, so the samples were not tested systematically for other respiratory viruses. Overall, the positivity rate for influenza in the ILI surveillance was 47 %, which means that 53% of the samples were negative for influenza viruses. The analyses of positive and negative samples for the other respiratory viruses showed that, during the flu epidemic season, other respiratory viruses were also circulating in varying proportions. Overall, 70 % of the patients were positive for at least one respiratory virus (including Influenza and co-infections). Among the samples negative for influenza viruses, 83/258 (32%) were positive for one or more other respiratory viruses. The most prevalent other respiratory viruses were HRV/ENV (7%), hMPV (3%), RSV (3 %), CoOC43 (2,59%). For the other viruses, the percentages were lower (Figure 12).

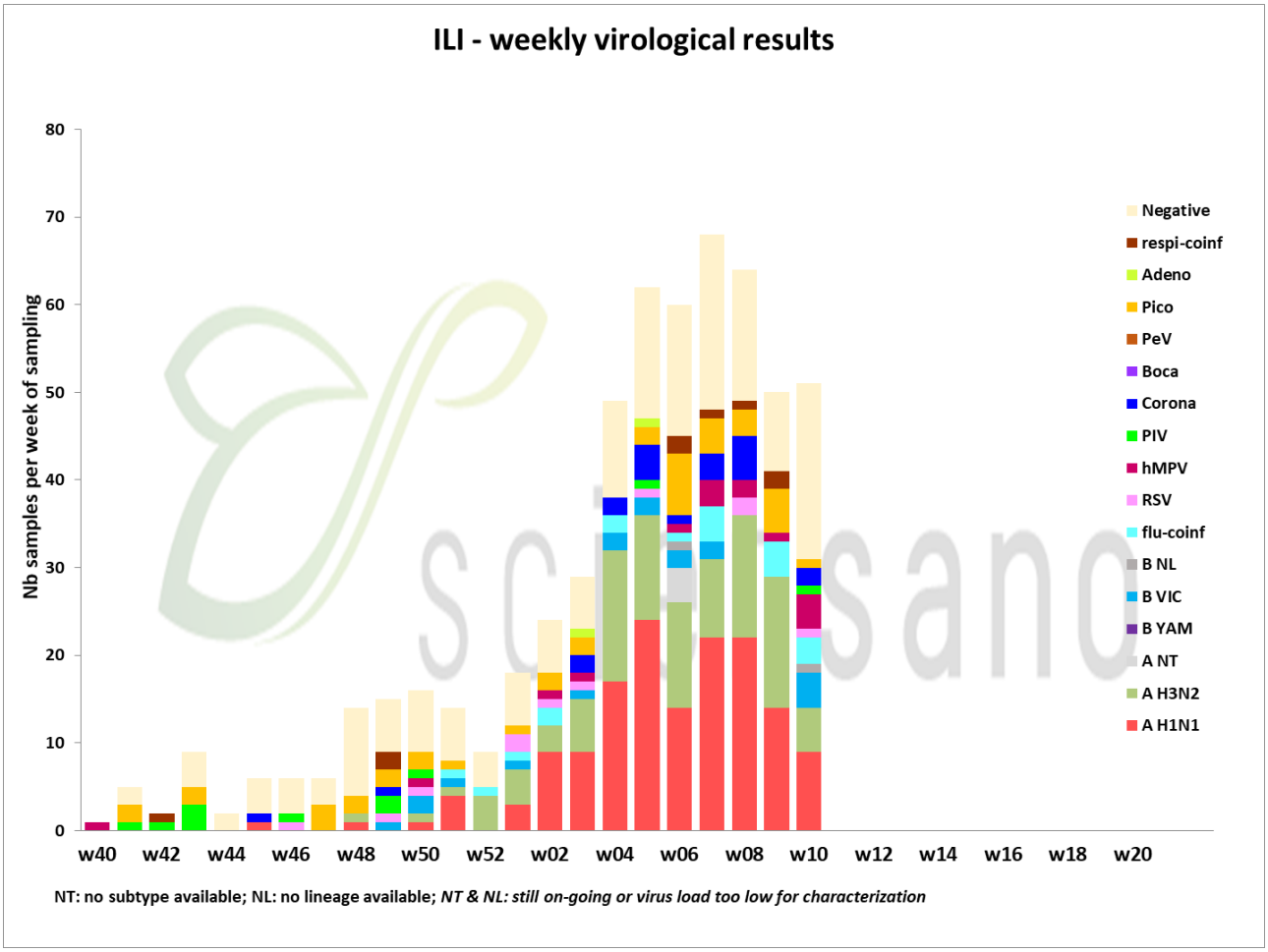


Figure 11. Weekly detection of respiratory viruses in Belgium in the SARI surveillance from week 1-2020 to week 14-2020 .

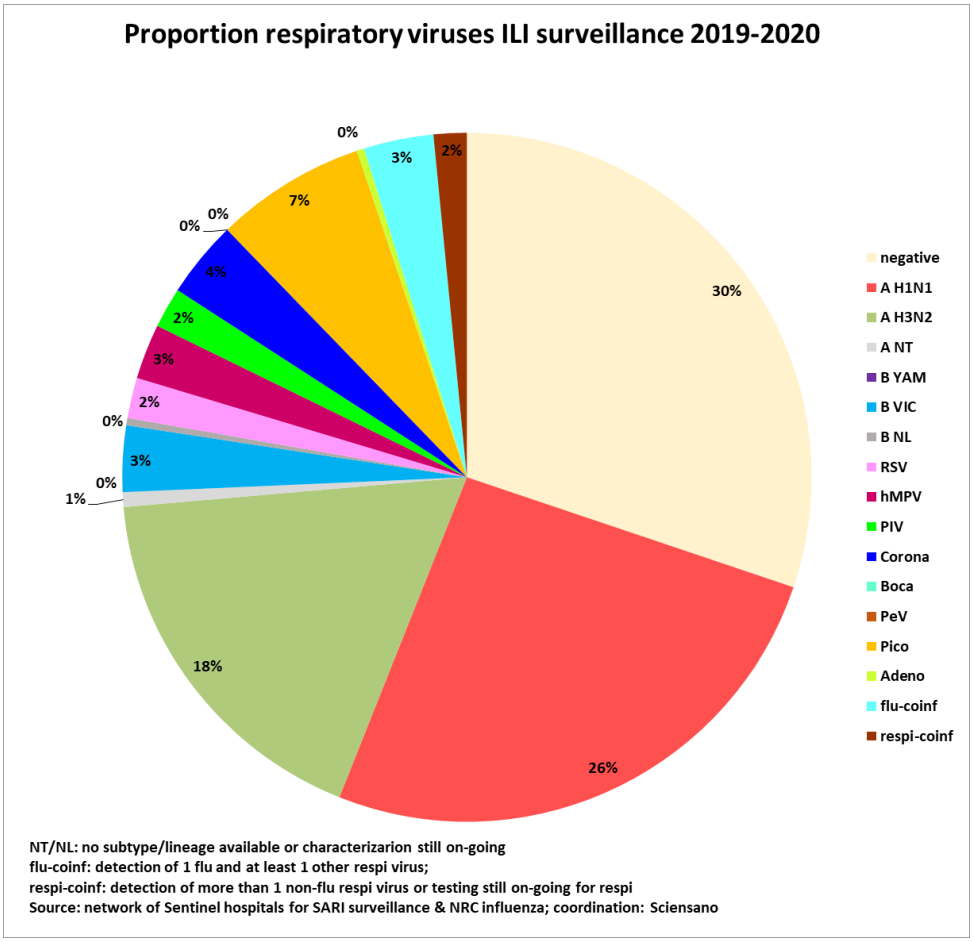


Figure 12. Proportion of the different respiratory viruses in the ILI surveillance in Belgium season 2019-2020

Proportion of the different respiratory viruses according to age group

The age group was known for 466 patients. The analyses were performed on these samples. The prevalence of the different respiratory viruses varies by age group with a higher percentage of other respiratory viruses in patients below the age of 5 years old. However, the numbers were very low in this age group (Figure 13a, 13b).

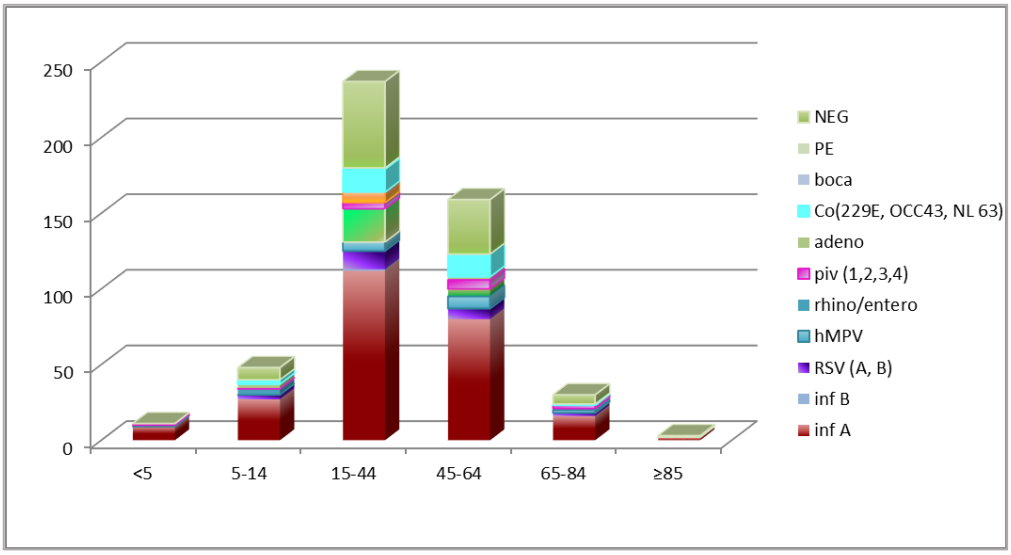


Figure 13a. Proportion of the different respiratory viruses in the ILI surveillance season 2019-2020 age group (Numbers).

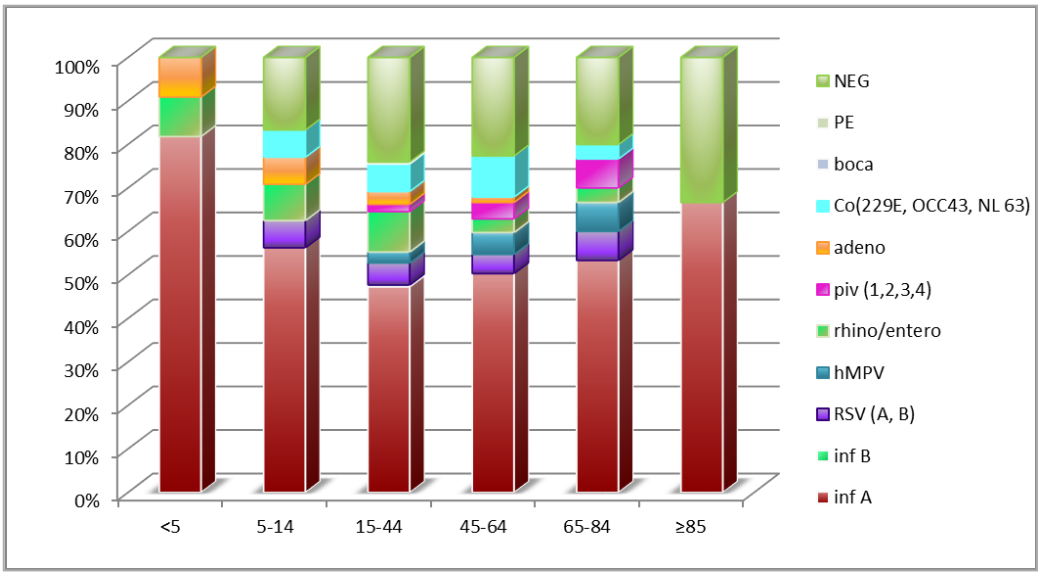


Figure 13b. Proportion of the different respiratory viruses in the ILI surveillance season 2018-2019 by age group (Percentages)

Co-infections

The percentage of co-infection was 6.5 % (32/493). Among influenza positive samples, co-infection with other viruses was observed in 21/258 samples (4.6%). Regarding co-infection of respiratory viruses other than influenza, the percentage of co-infection was 2.2% (11/493) and no particular combination of viruses was dominant.

D.7.2 SARI surveillance

From week 1-2020 to week 14-2020, a large proportion of SARI samples were also submitted to the diagnosis for other respiratory viruses. The number of tested samples was 1932. For 931/1932 (48 %) patients no respiratory viruses were detected and (52%) of the patients were positive for at least one respiratory viruses (including influenza, SARS-COV-2, other respiratory viruses or different combination of co-infection). The most prevalent respiratory viruses were Influenza A (22%), HRV/ENV viruses (12,2%), hMPV (7,5%), RSV (5,3%). Since week 12-2020, SARS-CoV-2 reached 6,2%. For the other viruses, the percentages were lower (Fig. 14 and fig.15).

Weekly evolution

Figure 14 shows the weekly proportion of respiratory viruses that were laboratory-confirmed during the 2019-2020 SARI surveillance period.
Influenza virus A(H1N1) and A(H3N2) were present from week 2 to week 11 and the proportion of influenza positive decreased since week 12.
From week 10 , the first SARS-CoV-2 patient were diagnosed.
As previously explained, these patients were mostly adults and children above 14 years old.

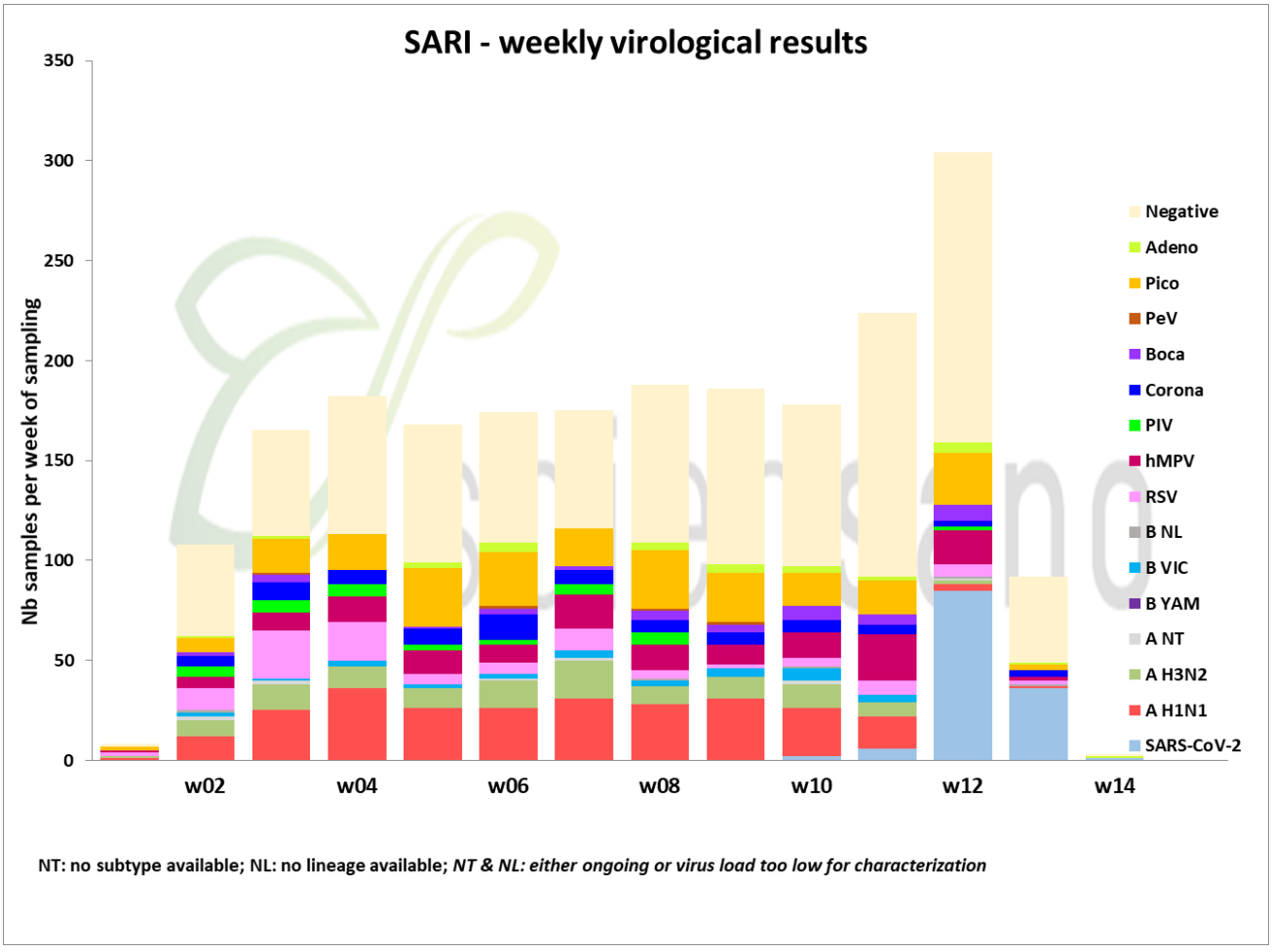


Figure 14. Weekly detection of respiratory viruses in Belgium in the SARI surveillance from week 1-2020 to week 14-2020 .

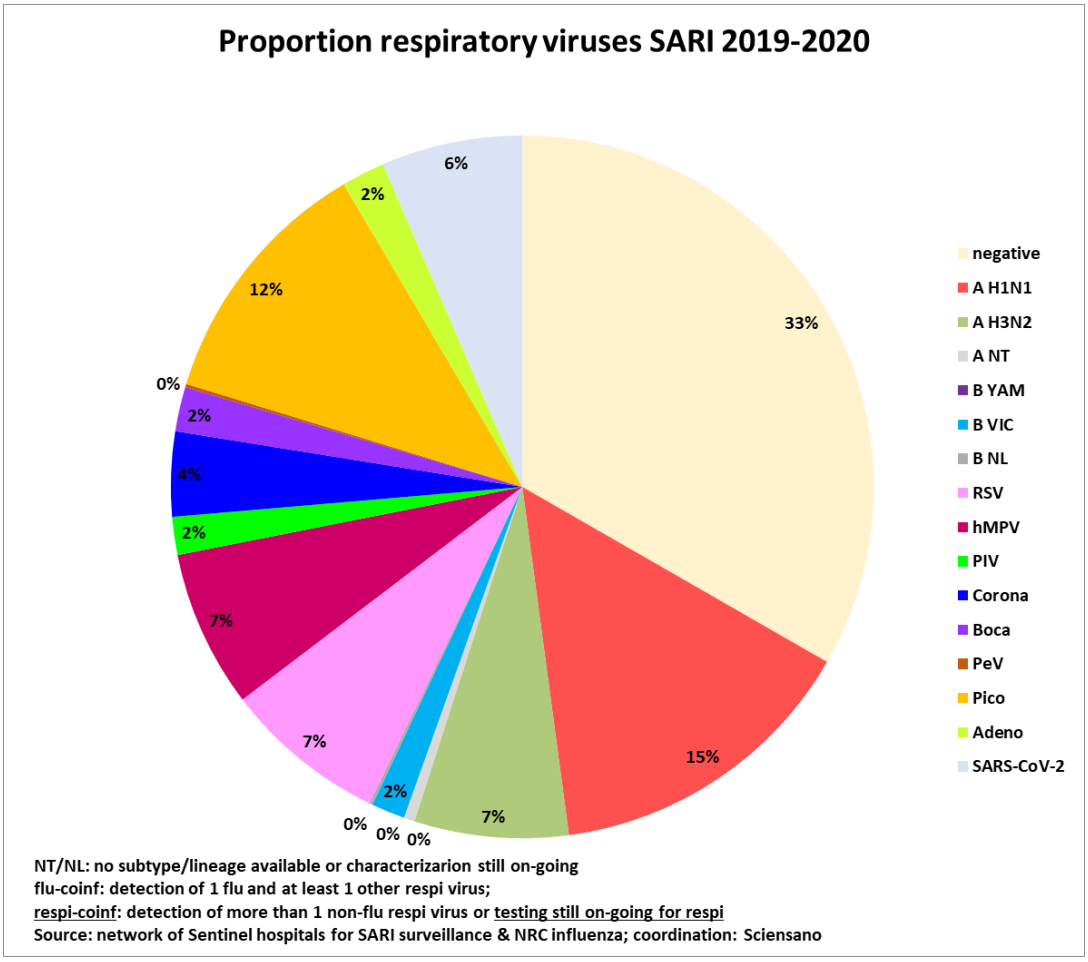


Figure 15. Proportion of the different respiratory viruses in Belgium in the SARI surveillance from week 1-2020 to week 14-2020 .

Proportion of the different respiratory viruses according to age group

The age group was known for 1913 patients and the analyses were performed on those samples The proportion of the different viruses varied between age groups.

In children below the age of 5 years old, the percentage of positivity for at least one respiratory virus reached 66%, with the most prevalent virus being influenza A (23,5%), rhino/enterovirus (18,7.8%), RSV (12%), adenovirus (7%). Influenza A was detected in all age group. SARS-CoV-2 virus was detected from week 10-2020, but in very few patients below the age of 14 years. Influenza A was detected in all age group. All tested respiratory viruses were detected in this age group with the most prevalent virus being RSV (41.2%), rhino/enterovirus (22.8%), adenovirus (16.6%), influenza A (13%) and hMPV (8.9%). In patients aged more than 85 years old, influenza A was far the most prevalent (43.7%), followed by RSV (11.5%) (Figure 16a and 16b).

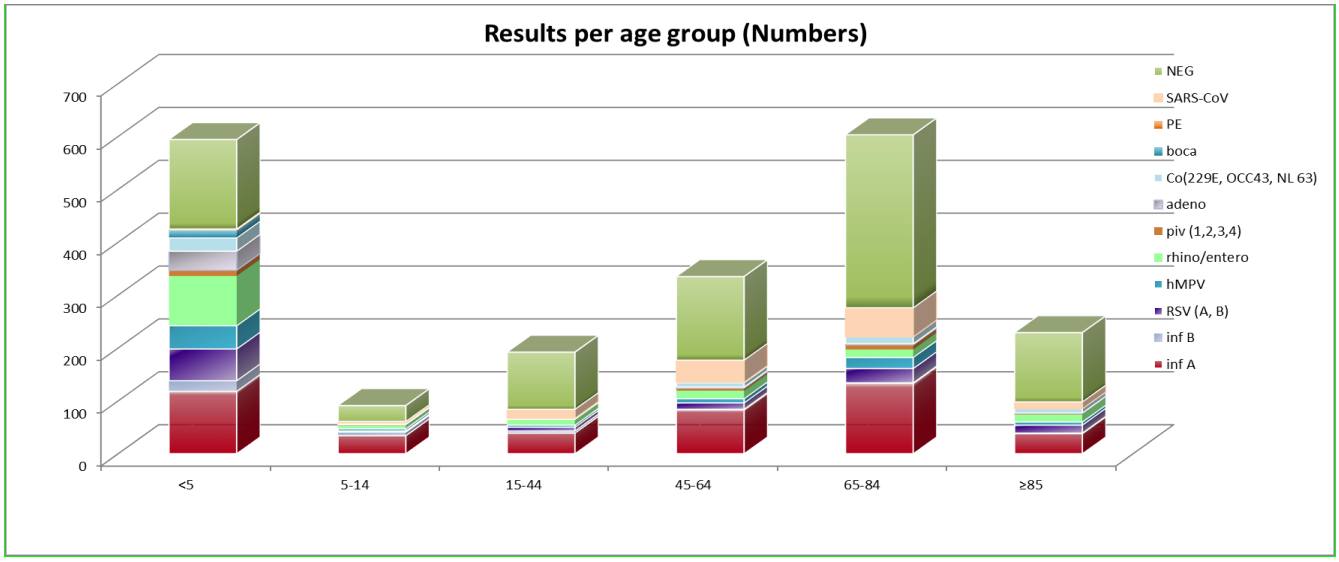


Figure 16a. Proportion of the different respiratory viruses in the SARI surveillance season 2019-2020 by age group (numbers)

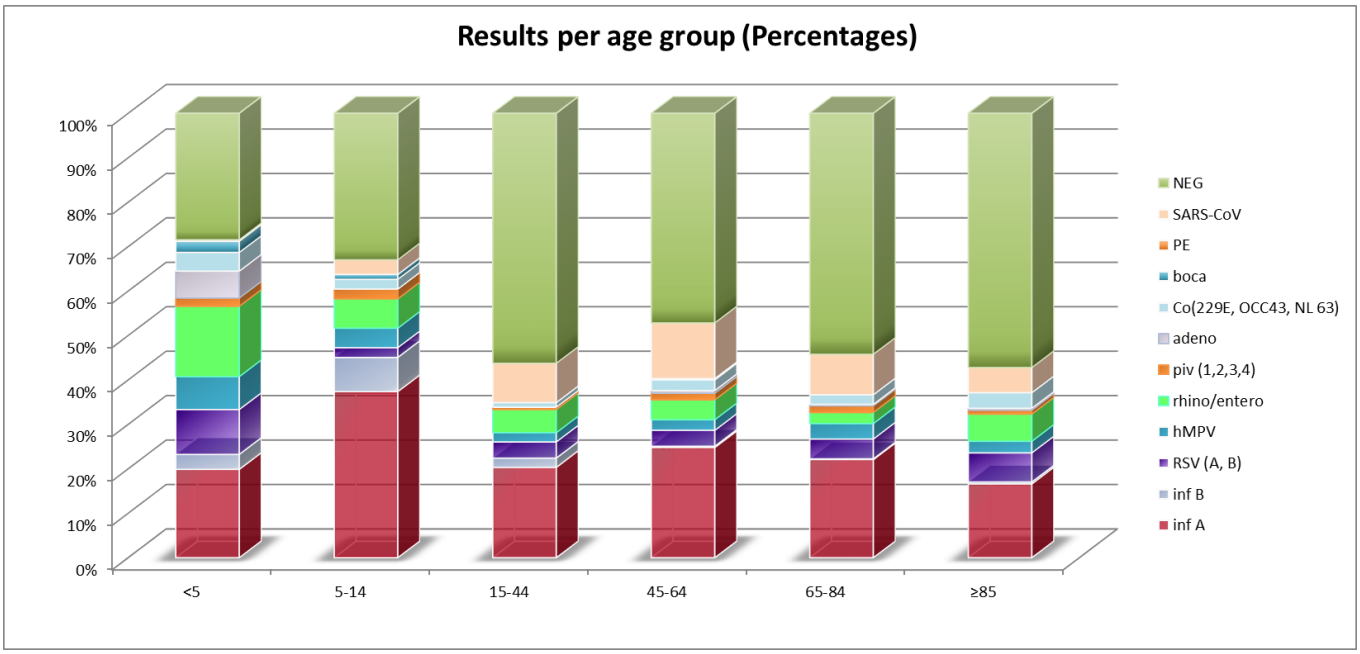


Figure 16b. Proportion of the different Respiratory viruses in the SARI surveillance season 2019-2020 by age group (percentages)

Coinfections

Overall, the percentage of co-infection (two to 4 viruses) was 6%, (122/1913). In patients below the age of 5 years old this percentage reached 15% (92/587). Among influenza A positive samples, co-infection with other viruses were observed in 47/445 (10%) with the most frequent associations being Influenza/HRV found in 16/47 (34%). Regarding co-infections by respiratory viruses other than influenza, the percentage was 5.2% (76/1913) with the most common viral co-infections being with HRV/ENV 56% (43/76). In patients positive for SARS-CoV-2, no coinfection was noticed, neither with influenza other respiratory viruses.

D.8. Characterisation of the influenza viruses

D.8.1 A(H1N1)pdm2009

Genetic characterisation

Genetic characteristics by whole-genome sequencing (WGS) of 43 A(H1N1)pdm09 were analyzed and some of them are presented in figure 17. All the HA genes fell into clade 6B.1A5. About 60% of the strains had the substitution D187A and Q189E. All these sequences have been submitted to GISAID.

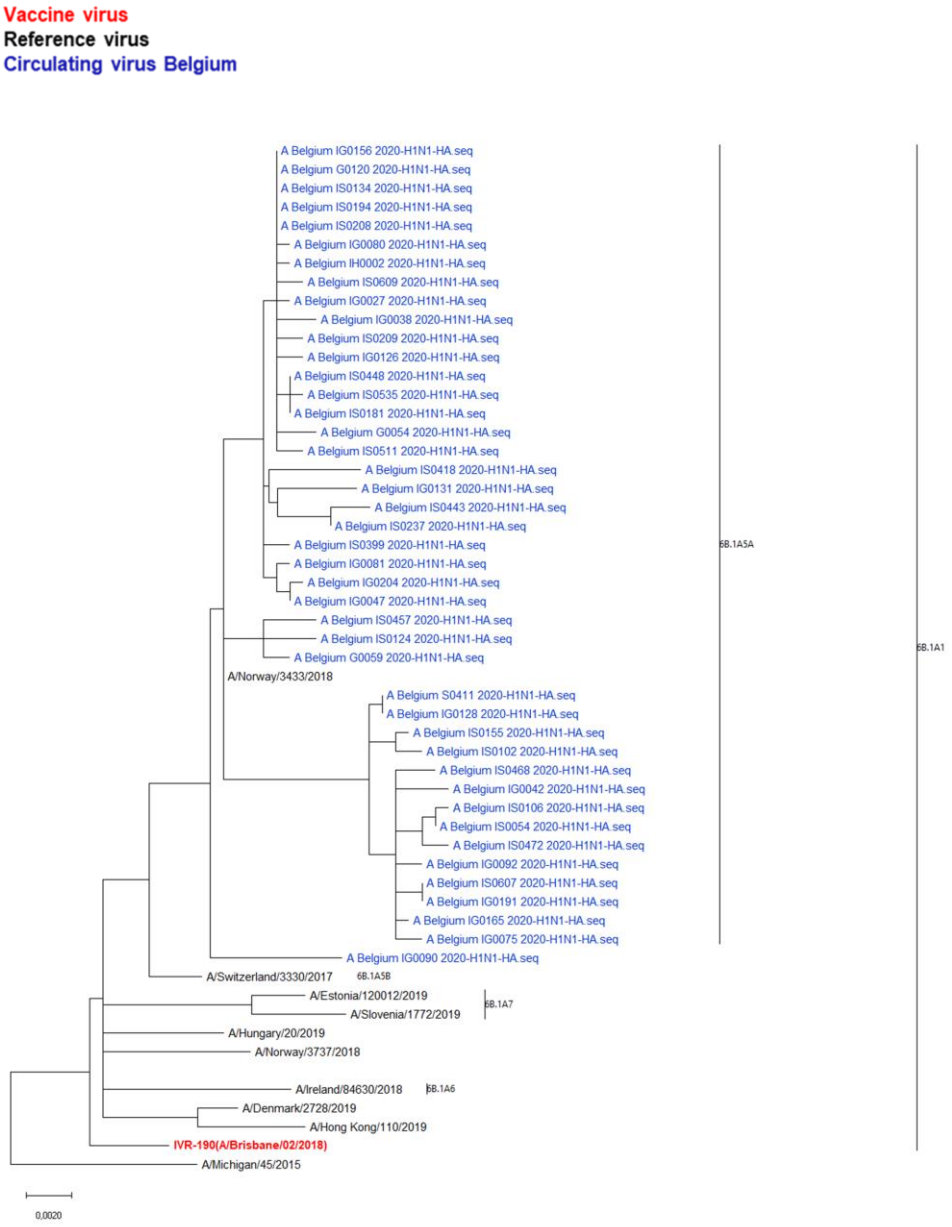


Figure 17. Phylogenetic analysis of influenza A(H1N1)pdm09 strains in Belgium, season 2019-2020

Antigenic characterisation

Four H1N1pdm09 viruses were recovered successfully. Two of them were poorly recognized by the panel of antisera whilst the remaining two were recognised generally well by the panel of antisera, including the antisera raised against the recent vaccine viruses egg-propagated A/Michigan/45/2015 and A/Brisbane/02/2018. (Table 4)

Table X-Y. Antigenic analyses of influenza A(H1N1)pdm09 viruses (2020-02-04)

Viruses	Other information	Passage history / Ferret number / Genetic group	Collection date	Passage history	Haemagglutination inhibition titre, Post-infection ferret antisera: A/Mich 45/15 Egg F31/16 +1 6B.1	A/Bayern 69/09 MDCK F09/15 +1	A/Lviv N6/09 MDCK F13/18 +1	A/Slov 2903/2015 Egg NIB F48/16 +1 6B.1	A/Paris 1447/17 MDCK F03/18 +2 6B.1A	A/Swit 2656/17 Egg F20/18 +1 6B.1A	A/Swit 3330/17 Egg F23/18 +1 6B.1A5	A/Norway 3433/18 MDCK F04/19 +1 6B.1A5	A/Ire 84630/18 MDCK F08/19 +1 6B.1A6	A/Bris 02/18 Egg F09/19 +1 6B.1A1	A/HK 110/19 MDCK F28/19
REFERENCE VIRUSES															
A/Michigan/45/2015		6B.1	2015-09-07	E3/E3	640	320	160	640	1280	1280	640	1280	640	640	ND
A/Bayern/69/2009	G155E		2009-07-01	MDCK5/MDCK1	80	640	160	<	160	160	80	160	40	80	ND
A/Lviv/N6/2009	G155E, D222G		2009-10-27	MDCK4/SIAT1/MDCK3	320	640	640	160	640	320	320	640	160	320	ND
A/Slovenia/2903/2015	clone 37	6B.1	2015-10-26	E4/E2	1280	320	320	1280	1280	1280	640	1280	1280	640	ND
A/Paris/1447/2017		6B.1A	2017-10-20	MDCK1/MDCK3	1280	320	80	1280	1280	1280	640	2560	1280	1280	ND
A/Switzerland/2656/2017		6B.1A	2017-12-21	E5/E3	1280	640	640	1280	2560	1280	1280	2560	1280	1280	ND
A/Switzerland/3330/2017	clone 35	6B.1A5B	2017-12-20	E6/E2	640	320	160	1280	1280	1280	1280	2560	1280	640	ND
A/Norway/3433/2018		6B.1A5A	2018-10-30	MDCK3	640	160	80	640	640	640	640	1280	640	640	ND
A/Ireland/84630/2018		6B.1A6	2018-11-28	MDCK1/MDCK3	1280	320	160	1280	1280	1280	640	1280	1280	640	ND
A/Brisbane/02/2018		6B.1A1	2018-01-04	E3/E1	1280	320	320	1280	2560	1280	1280	2560	1280	1280	40
A/Hong Kong/110/2019		6B.1A2	2019-01-01		ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	2560
TEST VIRUSES															
A/Belgium/G0001/2020		6B.1A5A	2019-12-19	MDCK1	640	320	160	640	1280	640	640	2560	640	640	ND
A/Belgium/G0537/2019		6B.1A5A	2019-12-18	MDCK1	40	80	40	<	<	40	40	80	<	<	640
A/Belgium/G0526/2019		6B.1A5A	2019-12-17	MDCK1	640	160	160	640	640	640	320	1280	640	320	ND
A/Belgium/G0460/2019		6B.1A5A	2019-11-05	MDCK1	80	80	80	40	80	80	80	640	<	80	160

Table 4. Antigenic analyses of influenza A(H1N1) viruses from Belgium 2029-2020 (WHO CC-London)

D.8.2 A(H3N2)

Genetic characterisation

In Belgium, about 40% of the positive influenza viruses were A(H3N2). Twenty two A(H3N2) were completely sequenced by next-generation sequencing (NGS) and are presented in figure 18. About half (10/22) of the sequenced viruses belonged to the subclade 3C.2a1. among which 5 had HA genes in subclade 3C.2a1b. The remaining 12 viruses belonged to the subclade 3C.3a. represented by the reference strain (A/England/538/2018). This group viruses, characterized by the amino acid substitutions T128A, R142G, A138S, F159S and N225D in the HA, is closed to the and the vaccine strain A/Kansas/14201(Fig. 18). All of these sequences have been submitted to GISAID.

As noticed during previous seasons, A(H3N2) viruses are evolving rapidly with emergence of several virus clusters defined by additional amino acid substitutions in the hemagglutinin, thereby emphasizing the need for continued monitoring of antigenic characteristics.

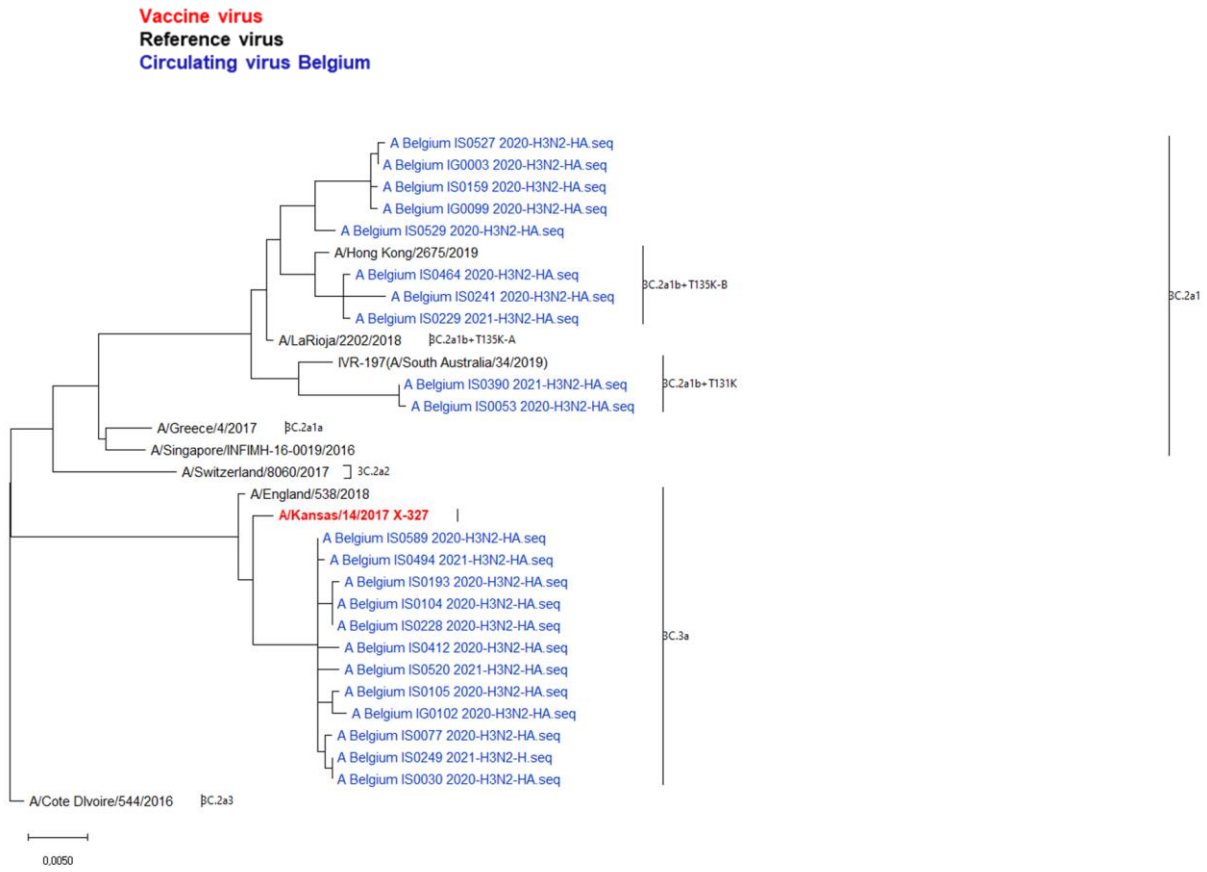


Figure 18. Phylogenetic analysis of the HA sequences of the A(H3N2) viruses analysed from Belgium and other European countries during the 2019-2020 season in comparison with the vaccine strain and the reference strains.

Antigenic characterisation

Antigenic characterisation of A(H3N2) viruses was always difficult by HI assay due to variable agglutination of red blood cells. The viruses belonging to goup 3C.3a were recognised well by antisera raised against the cell culture-propagated A/Kansas/14/2017 and cell culture-propagated A/England/538/2019, at titres equal to the homologous titres or higher for some assessed with the the A/Kansas/14/2017 antiserum. The only analyzed vius from the 3C.2a1b was poorly recognized by the antisera raised against 3C.3a viruses, but well recognized by antisera raised against cell culture-propagated A/La Rioja/2202/2018 and A/Norway/3275/2018, having HA genes in subclades 3C.2a1b+T135K-A and 3C.2a1b+T131K, respectively (table 5).

Table X-Y. Antigenic analyses of influenza A(H3N2) viruses (Guinea Pig RBC with 20nM Oseltamivir) 2020-01-24

Viruses	Other information	Collection date	Passage history	Haemagglutination inhibition titre: Post-infection ferret antisera										
	Passage history			A/HK 5738/14 MDCK	A/Bretagne 1413/17 SIAT	A/Singapore 0019/16 Egg 10^{-4}	A/La Rioja 2202/18 SIAT	A/Eng 538/18 SIAT	A/Norway 3275/18 SIAT	NYMC X-327 A/Kansas/14 Egg	A/Kansas 14/17 SIAT	A/Sth Aus 34/19 Egg	A/HK 2671/19 Egg	A/HK 2669/19 SIAT
	Ferret number			St Judes F60/17^{+1}	F01/18^{+1}	F13/19^{+1}	F26/18^{+1}	F31/18^{+1}	F03/19^{+1}	F16/19^{+1}	F17/19^{+1}	F45/19^{+1}	F44/19	F04/20^{+1}
	Genetic group			3C.2a	3C.2a2	3C.2a1	3C.2a1b	3C.3a	3C.2a1b	3C.3a	3C.3a	3C.2a1b	3C.2a1b	3C.2a1b+T135K-B
REFERENCE VIRUSES														
A/Hong Kong/5738/2014	3C.2a	2014-04-30	MDCK1/MDCK3/SIAT2	160	80	160	80	160	160	160	80	160	<	40
A/Bretagne/1413/2017	3C.2a2	2017-10-09	MDCK1/SIAT4	160	640	320	80	160	160	160	80	160	<	
A/Singapore/INFIMH-16-0019/2016	3C.2a1	2016-04-14	E5/E2	160	40	320	160	40	40	40	<	40	40	80
A/England/538/2018	3C.3a	2018-02-26	MDCK1/SIAT4	40	40	40	<	640	<	160	320	<	<	<
NYMC X-327 (A/Kansas/14/17)	3C.3a	2017-12-14	ExE1	40	<	40	<	320	<	1280	320	40	160	<
A/Kansas/14/2017	3C.3a	2017-12-14	SIAT3/SIAT2	40	40	40	<	320	40	160	160	<	<	<
A/South Australia/34/2019	3C.2a1b		E6/E1	160	640	320	80	80	640	40	40	1280	80	<
A/Hong Kong/2671/2019	3C.2a1b	2019-06-17	E8/E1	<	<	80	40	160	<	320	80	40	320	160
A/Hong Kong/2669/2019	3C.2a1b+T135K-B	2019-06-18	MDCK1/SIAT5	160	ND	160	160	160	320	80	160	160	160	320
TEST VIRUSES														
A/Belgium/G0004/2020	3C.3a	2019-12-30	SIAT1	40	80	80	40	640	40	160	320	40	<	ND
A/Belgium/G0003/2020	3C.2a1b+T135K-A	2019-12-26	SIAT1	160	80	160	160	160	320	80	80	160	40	ND
A/Belgium/G0540/2019	3C.3a	2019-12-24	SIAT1	40	80	80	40	640	40	160	320	40	<	ND
A/Belgium/G0538/2019	3C.3a	2019-12-24	SIAT1	40	80	40	<	640	40	160	320	40	<	ND
A/Belgium/G0539/2019	3C.3a	2019-12-23	SIAT1	160	80	160	80	640	80	320	320	80	<	ND
A/Belgium/G0506/2019	3C.3a	2019-11-28	SIAT2	80	ND	160	40	640	40	320	640	40	40	<
A/Belgium/G0514/2019	3C.3a	2019-12-10	SIAT1	40	ND	80	<	640	<	320	320	<	40	<
A/Belgium/G0528/2019	3C.3a	2019-12-19	SIAT1	80	ND	160	40	640	<	160	320	40	40	<
A/Belgium/G0542/2019	3C.3a	2019-12-23	SIAT1	40	ND	160	40	640	<	320	640	40	40	<

Table 5. Antigenic analyses of influenza A(H3N2) viruses from Belgium 2019-2020 (WHO CC-London)

D.8.3 B Yamagata

No influenza B Yamagata circulated during this season, none of them were sequenced nor submitted to antigenic characterisation

D.8.4 B Victoria

Genetic characterisation

In Belgium, this season, a small percentage of the detected influenza viruses were influenza B and all of them were from the Victoria lineage. Among the 8 sequenced viruses, 7 belonged to the subclade delta 162-164, with three amino acid deletions in the HA gene at positions 162 and 164 (Fig. 19, Fig. 20). All had the triple deletion (Δ162-164) with the substitution K136E, along with for some of them a G133R HA1 substitution. This deletion in the HA resulted in these viruses being antigenically different from the vaccine virus B/Colorado/06/2017 a (Δ 162-163) virus. The sequences have been submitted to GISAID.

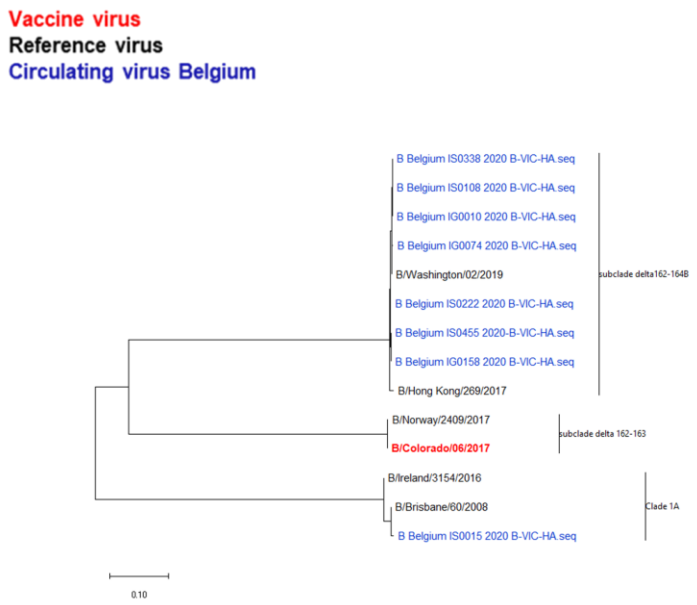


Figure 19. Phylogenetic analysis of circulating influenza B/Victoria viruses detected in Belgium during the 2019-2020 season.

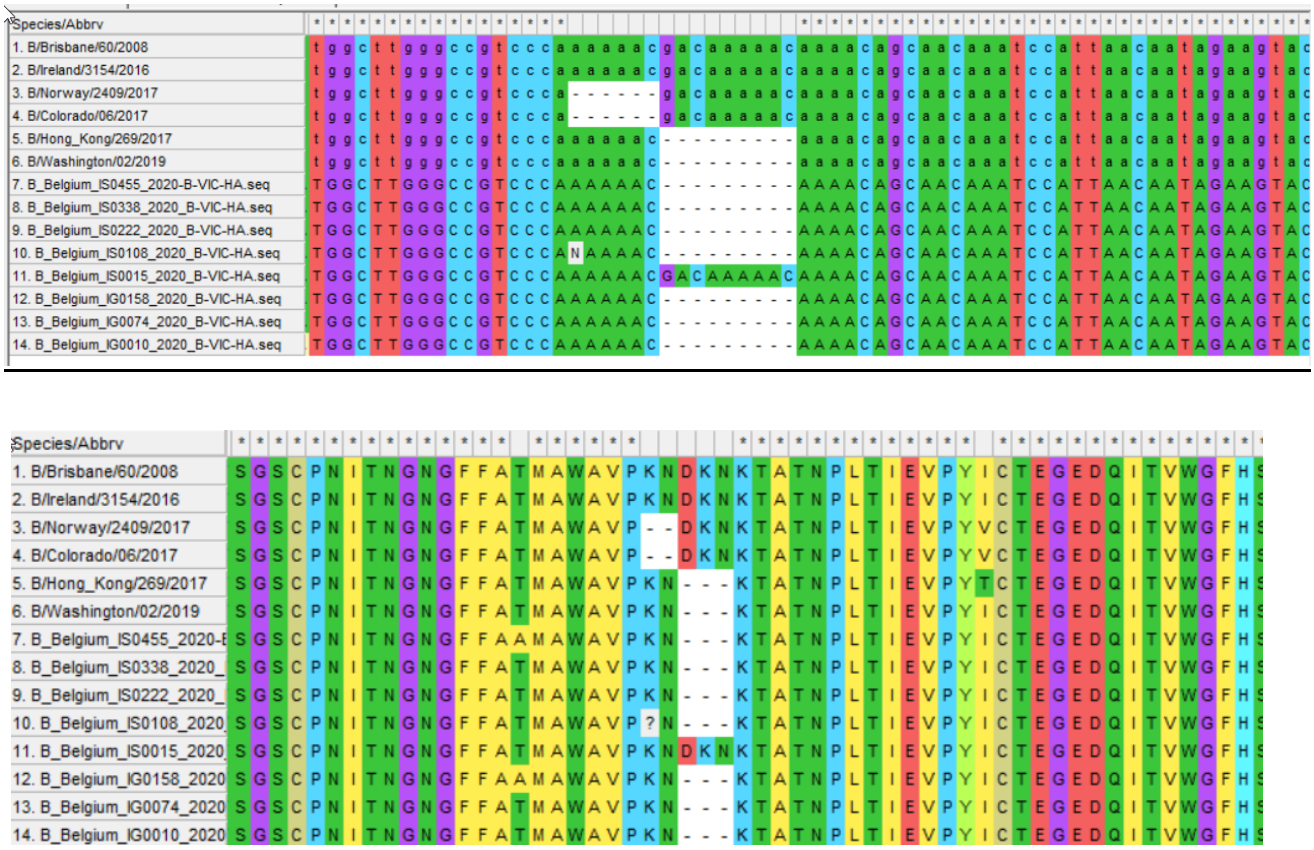


Figure 20. Part of the alignment of circulating influenza B/Victoria viruses detected in Belgium during the 2019-2020 season.

Antigenic characterisation

The antisera raised against the egg-propagated and the cell-propagated vaccine strain B/Colorado/06/2017 and against B/Norway/2409/2017, also a (Δ162-163) virus, recognised the test viruses poorly.

Table X-Y. Antigenic analyses of influenza B viruses (Victoria lineage) 2020-02-05

Viruses	Other information	Passage history	Collection date	Passage history	Haemagglutination inhibition titre: Post-infection ferret antisera									
					B/Bris 60/08 Egg	B/Bris 60/08 Egg	B/Sth Aus 81/12 Egg	B/Ireland 3154/16 MDCK	B/Nord-West 1/16 MDCK	B/Norway 2409/17 MDCK	B/Colorado 06/17 MDCK	B/Colorado 06/17 Egg	B/Wash'ton 02/19 MDCK	B/Wash'ton 02/19 Egg
		Ferret number			Sh 539, 540, 543, 544, 570, 571, 574 [+3]	F44/17 [*2]	F25/16 [*2]	F15/16 [*2]	F38/17 [*2]	F40/17 [*2]	F21/18 [*4]	F11/18 [*4]	F37/19 [*4]	F38/19 [*4]
		Genetic group			1A	1A	1A	1A	1A	1A(Δ2)	1A(Δ2)	1A(Δ2)	1A(Δ3)	1A(Δ3)
REFERENCE VIRUSES														
B/Brisbane/60/2008		1A	2008-08-04	E4/E4	1280	640	320	40	80	<	<	40	<	80
B/South Australia/81/2012		1A	2012-11-28	E4/E2	2560	1280	640	80	160	<	<	80	<	160
B/Ireland/3154/2016		1A	2016-01-14	MDCK1/MDCK4	2560	160	80	80	320	<	<	<	<	<
B/Nordrhein-Westfalen/1/2016		1A	2016-01-04	C2/MDCK2	2560	160	80	80	160	<	<	<	<	<
B/Norway/2409/2017		1A(Δ2)	2017-04-27	MDCK1/MDCK3	160	20	20	<	<	80	20	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	MDCK1/MDCK2	160	40	20	<	<	80	40	80	<	<
B/Colorado/06/2017		1A(Δ2)	2017-02-05	E5/E2	640	160	40	<	<	40	20	160	<	80
B/Washington/02/2019		1A(Δ3) B	2019-01-19	C2/MDCK2	640	80	40	<	<	<	<	80	40	320
B/Washington/02/2019		1A(Δ3) B	2019-01-19	E3/E2	1280	160	80	<	<	<	<	160	40	320
TEST VIRUSES														
B/Belgium/G0533/2019		1A(Δ3) B	2019-12-20	MDCK1	80	40	10	<	<	<	<	<	40	320
B/Belgium/G0513/2019		1A(Δ3) B	2019-12-09	MDCK1	160	80	20	<	<	<	<	<	80	320
B/Belgium/G0496/2019		1A(Δ3) B	2019-12-05	MDCK1	160	40	20	<	<	<	<	<	20	320

Table 6. Antigenic analyses of influenza B Victoria viruses from Belgium 2019-2020 (WHO CC-London)

D.9. Antiviral monitoring

All the strains analysed phenotypically, were sensitive to neuraminidase inhibitors: Oseltamivir and Zanamivir.

D.10. Composition of influenza virus vaccines

It is recommended that quadrivalent vaccines for use in the 2020-2021 northern hemisphere influenza season contain the following strains:

Egg-based Vaccines
- an A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus;
- an A/Hong Kong/2671/2019 (H3N2)-like virus;
- a B/Washington/02/2019 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Cell- or recombinant-based Vaccines
- an A/Hawaii/70/2019 (H1N1)pdm09-like virus;
- an A/Hong Kong/45/2019 (H3N2)-like virus;
- a B/Washington/02/2019 (B/Victoria lineage)-like virus; and
- a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus.

Saison	A/H1N1	A/H3N2	B	Quadrivalent
2000-2001	A/New Caledonia/20/99	A/Panama/2007/99)	B/Yamanashi/166/98	
2001-2002	"	"	B/Sichuan/379/2000	
2002-2003	"	"	B/Hong Kong/330/2001	
2003-2004	"	"	"	
2004-2005	"	A/Fujian/411/2002	B/Shanghai/361/2002	
2005-2006	"	A/California/7/2004	"	
2006-2007	"	A/Wisconsin/67/2005	B/Malaysia/2506/2004 VIC	
2007-2008	A/Solomon Islands/3/2006	"	"	
2008-2009	A/Brisbane/59/2007	A/Brisbane/10/2007	B/Florida/4/2006 YAM	
2009-2010	"	"	B/Brisbane/60/2008 VIC	
2010-2011	A/California/7/2009	A/Perth/16/2009	"	
2011-2012	"	"	"	
2012-2013	"	A/Victoria/361/2011	B/Wisconsin/1/2010 YAM	
2013-2014	"	A/Texas/50/2012	B/Massachusetts/2/2012 YAM	
2014-2015	"	"	"	
2015-2016	"	A/Switzerland/971529/2013	B/Phuket/3073/2013 YAM	B/Brisbane/60/2008 VIC
2016-2017	"	A/Hong-Kong/4801/2017	B/Brisbane/60/2008 VIC	B/Phuket/3073/2013 YAM
2017-2018	A/Michigan/45/2015	"	"	*
2018-2019	"	A/Singapore/INFIMH-16-0019/2016	B/Colorado/06/2017-like virus VIC	*
2019-2020	A/Brisbane/02/2018	A/Kansas/14/2017	"	*
2020-2021	A/Guangdong-Maonan/SWL1536/2019	A/Hong Kong/2671/2019	B/Washington/02/2019	*

Figure 21. Evolution of the composition of the trivalent influenza vaccine 2000 – 2021

D.11. Vaccine effectiveness

The results of the virological surveillance were used with the epidemiological data to estimate vaccine effectiveness against infection and against hospitalisation. The detailed results are presented in the Epidemiological Report prepared by the service Epidemiology of Infectious Diseases.

Overall, rates of vaccine effectiveness were comparable to those obtained the previous seasons.

D.12. Severity

The severity during the 2019-2020 was moderate for influenza viruses. However the season was marked by the beginning of the COVID-19 pandemic.

D13. Surveillance of all-cause mortality (BE-MOMO : Belgian Mortality Monitoring)

No significant all-cause mortality was observed during the influenza epidemic this season (28) (see https://epistat.wiv-isp.be/momo/)

E. Conclusion

The 2019–2020 influenza epidemic was of medium intensity and lasted 6 weeks. During the epidemic peak, a total number of 550 ILI consultations per 100.000 inhabitants was reached. The season was characterized by the mixed circulation of A(H1N1)pdm09 and A(H3N2) with a predominance of A(H1N1)pdm2009).

After week 5- 2020, the incidence of ILI consultations decreased but remained above the threshold for several weeks likely due to the COVID-19 epidemic with a new ILI peak at week 13 exceeding the influenza peak seen in week 5 -2020

Nearly all sequenced **A(H1N1)pdm2009** belonged to 6B.1A5A subgroup represented by the reference strain A/Norway/3433/2018.

About half of the sequenced A(H3N2) viruses belonged to the clade 3C.2a1 and the remaining belonged to the clade 3C.3a close the vaccine strain for the northern hemisphere A/Kansas/14/2017.

Most of the characterised influenza B-Victoria viruses were triple-deletion variants similar to B/Washington/02/2019.

Respiratory samples were also analysed for other respiratory viruses. In the ILI population, 70 % of the patients were positive for at least one respiratory virus (including Influenza and co-infections). In the SARI population, 52% of the patients were positive for at least one respiratory viruses (including influenza, SARS-COV-2, other respiratory viruses or different combination of co-infection). From week 10 , the first SARS-CoV-2 patient were diagnosed.

Influenza surveillance systems were severely disrupted with the COVID19 pandemic (difficulty for doctors to see their patients and to collect samples and send them to us for analysis, difficulty for hospitals to face additional demands, …)

It is essential to remain vigilant for the emergence of zoonotic and seasonal influenza viruses with pandemic potential and prepare for the next surveillance influenza seasons, in the context of the ongoing COVID-19 pandemic. Influenza surveillance systems can contribute not only to the monitoring of influenza viruses, but also to the monitoring of epidemiological trends, the geographical spread of CoV-2-SARS virus and the understanding of the co-circulation of CoV-2-SARS virus, influenza and other respiratory viruses.

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