VIROLOGICAL SURVEILLANCE 2023-2024 ANNUAL REPORT BELGIUM

National influenza centre

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For this, Sciensano builds on the more than 100 years of scientific expertise.

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Infectious diseases in humans - Viral diseases

Respiratory Viruses

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TABLE OF CONTENTS

BACKGROUND 7
KEY FACTS 8
SENTINEL SURVEILLANCE 9

1. Influenza-like illness 9

1.1 Clinical data..... 9
1.2 Influenza virus..... 9
1.3 Other respiratory viruses..... 10

2. Nursing home-ILI..... 11

1.1 Clinical data..... 11
1.2 Influenza virus..... 11
1.3 Other respiratory viruses..... 11

3. Severe Acute Respiratory infections (SARI)..... 11

1.1 Clinical data..... 11
1.2 Influenza virus..... 12
1.3 Other respiratory viruses..... 13

NON-SENTINEL SURVEILLANCE 14

1. Hospital laboratories (HOSPI)..... 14

1.1 Clinical data..... 14
1.2 Influenza virus..... 14
1.3 Other respiratory viruses..... 14

2. Zoonotic influenza..... 14

2.1. Active surveillance to monitor zoonotic influenza transmission events: ZOOIS..... 14

CHARACTERIZATION 15

1. Virus isolation..... 15
2. Antigenic characterization..... 16
3. Sequencing..... 16

3.1 Influenza viruses..... 17
3.2 SARS COV-2 Cornaviruses..... 20

QUALITY MANAGEMENT..... 22

1. Quality system..... 22
2. External Quality Assessment..... 22

2.1 Influenza viruses..... 22
2.2 SARS-CoV-2 coronaviruses..... 22
2.3 Other respiratory viruses..... 22

ACKNOWLEDGEMENTS 23

BACKGROUND

Influenza viruses cause acute respiratory disease, also known as flu. Annually, the virus causes epidemics, which has a huge impact on the health care systems and the economic.
Surveillance of influenza viruses is coordinated at a global level by WHO (World Health Organisation) through the GISRS network implemented in 1952. The network is organised with reference national laboratories in each country (National Influenza Centres), regional supranational organisations (such as ECDC, European Centre for Disease Control and prevention, in the European Union) and WHO Collaborating Centres, all working together to exchange information and virus isolates. The main objectives of the surveillance are (a) to monitor the influenza activity (start, intensity, duration) over the whole year, (b) to determine the type and subtype/lineage of influenza viruses circulating, (c) to characterise the viruses at the antigenic and genetic level, (d) to contribute to the decision process on the yearly influenza vaccine content, (e) to assess the overall vaccine effectiveness, (f) to monitor the susceptibility to antivirals of the circulating viruses, and (g) to detect the appearance of new (non-seasonal) influenza viruses in the human population.

Traditionally, an “influenza” season was defined by the period running from week 40 of one year to week 20 of the following year in the Northern Hemisphere. The other part of the year was defined as the interseasonal period.
Since the COVID-19 pandemic, the surveillance in Belgium is officially running all year round. From 2024 on, ECDC chose the season cut off for respiratory infections to be week 25, because historically the activity has been the lowest during these months (ECDC, personal communications). Therefore, this report includes data from week 40-2023 till the end of week 24-2024.

The surveillance relies on different systems. In Belgium, sentinel surveillance included networks of general practitioners (ILI: influenza-like illness), nursing homes (NH-ILI) and hospitals (SARI: severe acute respiratory infection). All other types of surveillance are designated as ‘non sentinel’ and cover the collection of data from different partners.

For the ILI surveillance (mild cases), several case definitions are available.
- WHO-ILI: An acute respiratory infection with measured fever of ≥ 38 C°, cough and with onset within the last 10 days.
- ECDC-ARI: sudden onset of symptoms with at least one of the following: cough, sore throat, shortness of breath, coryza and a clinician's judgement that the illness is due to an infection
- ECDC-ILI: sudden onset of symptoms with at least one general symptom among fever or feverishness, malaise, headache or myalgia, and at least one respiratory symptom among cough, sore throat or shortness of breath.

For the SARI surveillance (hospitalised cases) the Belgian case definition for patient recruitment was broadened from season 2023-2024 on, in order to identify respiratory infections other than influenza and infections in different age groups in a more sensitive way.

KEY FACTS

Based on the sentinel surveillance networks for influenza-like illness (ILI) and severe acute respiratory infections (SARI), the 2023-2024 season was characterized by the circulation of several respiratory viruses with epidemic waves overlapping each other. Respiratory syncytial virus was responsible for an epidemic wave in September-December 2023. Influenza viruses were responsible for a first epidemic wave at the end of December 2023, coinciding with a small wave of SARS-CoV-2, which was followed by a second wave of influenza viruses in January-February 2024, coinciding with a small peak of human metapneumovirus.

Seasonal influenza A viruses of the H1N1pdm09 and H3N2 subtypes, and influenza B virus of the Victoria lineage co-circulated with a dominance of H1N1pdm09 viruses. Remarkably, there was a low circulation of influenza B viruses during the 2023-2024 season.

SENTINEL SURVEILLANCE

1. Influenza-like illness (ILI)

1.1. CLINICAL DATA

Belgian general practitioners (GPs) can take part in an active virological surveillance for influenza viruses and other respiratory viruses, organised by Sciensano. The GPs are requested to take a nasopharyngeal swab from the first 3 ILI and first 2 acute respiratory infection (ARI) cases of the week belonging to different households. The NRC influenza provides the sampling kits (nasopharyngeal swab and UTM universal transport medium) and the packaging for sending the samples (prepaid envelops). All the samples are sent to the NRC influenza for testing.
During the 2023-2024 season, **35 general practitioners** took part in the virological ILI surveillance. This represents a drop by about 50% compared to the last pre-COVID19 season 2019-2020 (69 GPs).
A total of **853 samples**, mainly nasal swabs, were collected during the 2023-2024 season. Regarding the administrative region of origin, 384 samples were derived from participating GPs in Flanders, 394 samples from participating GPs in Wallonia and 75 samples from participating GPs in Brussels.
The received samples fell in 5 age groups: 120 samples were from patients between 0-19 years old (14%), 317 samples from patients between 20-39 years old (37%), 235 samples from patients between 40-59 years old (28%), 132 samples from patients between 60-79 years old (15%) and 14 samples from patients that were older than 80 (2%). For 35 samples the age was not reported (4%). All clinical data are summarized in Figure 1.

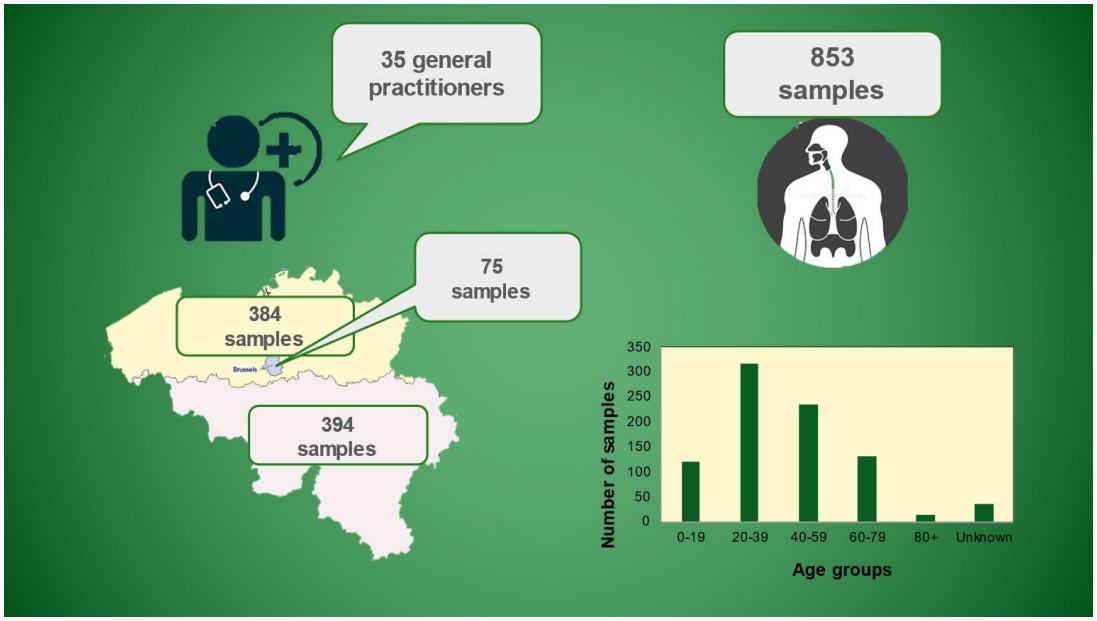

Figure 1. Overview on ILI clinical data.

1.2. INFLUENZA VIRUS

Out of the 853 received samples, 160 samples tested positive for influenza. The first positive sample was detected in week 46-2023 and the last positive sample in week 17-2024. The highest proportion of positive samples was reached in week 4-2024.
Overall the percentage of samples positive for the influenza virus typing for the season 2023-2024 was 19%, all samples were positive for influenza type A, except for one sample that was positive for influenza type B.
Among the 159 influenza A positive samples, the subtype could be determined for 157 samples. The H3N2 subtype was identified for 54 influenza positive samples, the H1N1dpm09 subtype was for 103

influenza positive samples. For 2 influenza A positive samples, the viral load was too low to allow subtype determination. Similarly, the lineage of the influenza B positive sample could not be determined due to a too low viral load. All data are summarized in Figure 2.

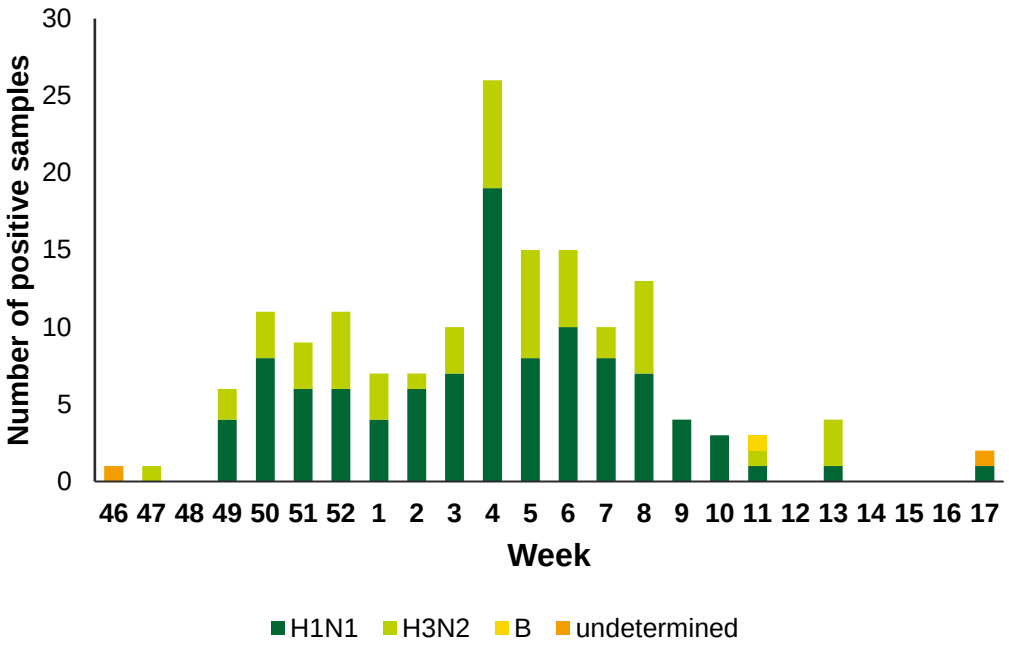

Figure 2. Weekly distribution of influenza viruses per type and subtype among ILI samples.

1.3. OTHER RESPIRATORY VIRUSES

Besides influenza, other respiratory viruses were monitored within the ILI network. Out of the 853 samples, 92 samples tested positive for SARS-CoV-2 (11%), the second most prevalent detected pathogen with 79 positive samples were the entero-/rhinoviruses (9%), and with 31 positive samples RSV was prevalent in 4% of the samples. Other respiratory viruses that were sporadically detected were human metapneumovirus (HMPV, #25; 3%), parainfluenza-3 (PIV3, #19; 2%) and coronavirus 229E (#16; 2%). Adenovirus (#2), PIV1 (#2), PIV2 (#2), PIV4 (#4) and bocavirus (#1) were very rarely detected. Coronavirus NL63 and paraechovirus were not detected (Figure 3). Out of the 853 samples, 420 samples tested negative for influenza and the above mentioned respiratory pathogens (Figure 3).

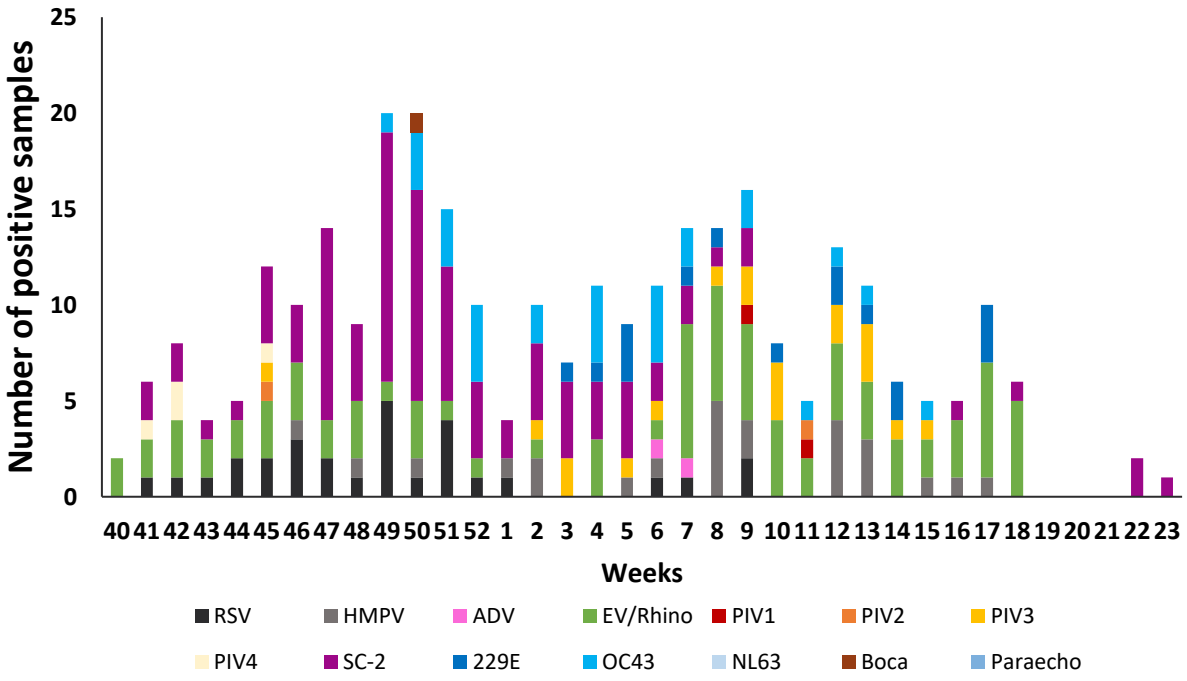

Figure 3. Weekly distribution of detected viruses among ILI samples.

2. Nursing home - ILI

2.1. CLINICAL DATA

The surveillance of influenza-like illness (ILI) in nursing homes (NH) started end of 2022. For virological follow-up, NHs were requested to take a nasopharyngeal swab from the first 2 ILI cases of the week. The NRC influenza provided the sampling kits (nasopharyngeal swab and UTM transport medium) and the packaging for sending the samples (prepaid envelops). All the samples were sent to the NRC influenza for testing.
During the 2023-2024 season **22 NHs participated**, 1 NH was located in the Brussels region, 7 NHs were located in the Walloon region and 14 NHs were located in Flanders. Overall, **102 samples** were tested.

2.2. INFLUENZA VIRUS

Out of the 102 received samples, 8 samples tested positive for influenza. The first positive sample was detected in week 49-2023 and the last positive sample in week 08-2024. The percentage of samples positive for the influenza virus typing for the season 2023-2024 was 8%, all samples were positive for influenza type A. Among the 8 influenza A positive samples, the H3N2 subtype was identified for 2 influenza positive samples, the H1N1dpm09 subtype was identified for 6 influenza positive samples.

2.3. OTHER RESPIRATORY VIRUSES

Out of the 102 samples, 12 samples tested positive for SARS-CoV-2 (12%), 15 samples tested positive for entero-/rhinoviruses (15%) and 7 samples tested positive for RSV (7%). Other respiratory viruses that were sporadically detected were human metapneumovirus (HMPV, #4; 4%), coronavirus OC43 (#3, 3%) and PIV4 (#3, 3%). PIV3 and bocavirus were only detected once (1%). For 102 samples no respiratory virus could be identified.

3. Severe Acute Respiratory Infections (SARI)

3.1. CLINICAL DATA

The surveillance of severe acute respiratory infections (SARI) is organised through a network of Belgian hospitals. The network was implemented in 2012, following the recommendations of WHO after the 2009 H1N1 pandemic to reinforce the surveillance of severe cases. More information on the network can be found on Sciensano's website[a]. Since 2012 the network included 6 hospitals, but since 2023 it is extended to **9 Belgian hospitals**. Four are located in Flanders, 2 in Brussels and 3 in Wallonia. The hospitals are requested to recruit all cases matching the case definition and to take a nasopharyngeal swab. All the samples were sent to the NRC influenza for testing.

A total of **6042 samples**, including swabs, bronchoalveolar lavages and aspirates, were collected during the 2023-2024 season. Regarding the administrative region of origin, 3039 samples were derived from participating hospitals in Flanders, 1546 samples from participating hospitals in Wallonia and 1457 samples from participating hospitals in Brussels.
The received samples fell in 5 age groups: 1522 samples were from patients between 0-19 years old (25%), 282 samples from patients between 20-39 years old (5%), 592 samples from patients between 40-59 years old (10%), 1952 samples from patients between 60-79 years old (32%) and 1369 samples from patients that were older than 80 (23%). For 325 samples the age was not reported (5%). All clinical data are summarized in Figure 4.

[a] https://www.sciensano.be/en/projects/severe-acute-respiratory-infection-surveillance-a-sentinel-network-hospitals

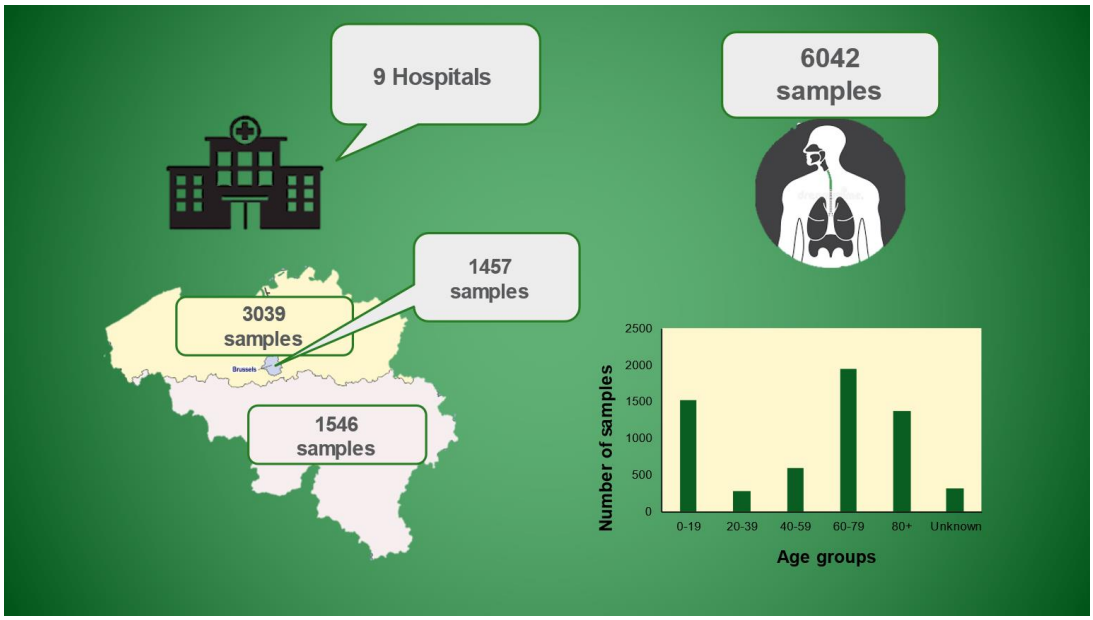

Figure 4. Overview on SARI clinical data.

3.2. INFLUENZA VIRUS

Out of the 6042 received samples, 730 samples tested positive for influenza. The first positive sample was detected in week 43-2023 and the last positive sample in week 23-2024. The highest proportion of positive samples was reached in week 5-2024.

Overall the percentage of samples positive for the influenza virus typing for the season 2023-2024 was 12%, except for 5 samples that were positive for influenza type B, all samples were positive for influenza type A.

Among the 725 influenza A positive samples, the subtypes could be determined for 709 samples. The H3N2 subtype was identified for 213 influenza positive samples, the H1N1dpm09 subtype was for 496 influenza positive samples. For 16 influenza A positive samples, the viral load was too low to allow subtype determination. All 5 influenza B positive samples belonged to the Victoria lineage. All data are summarized in Figure 5.

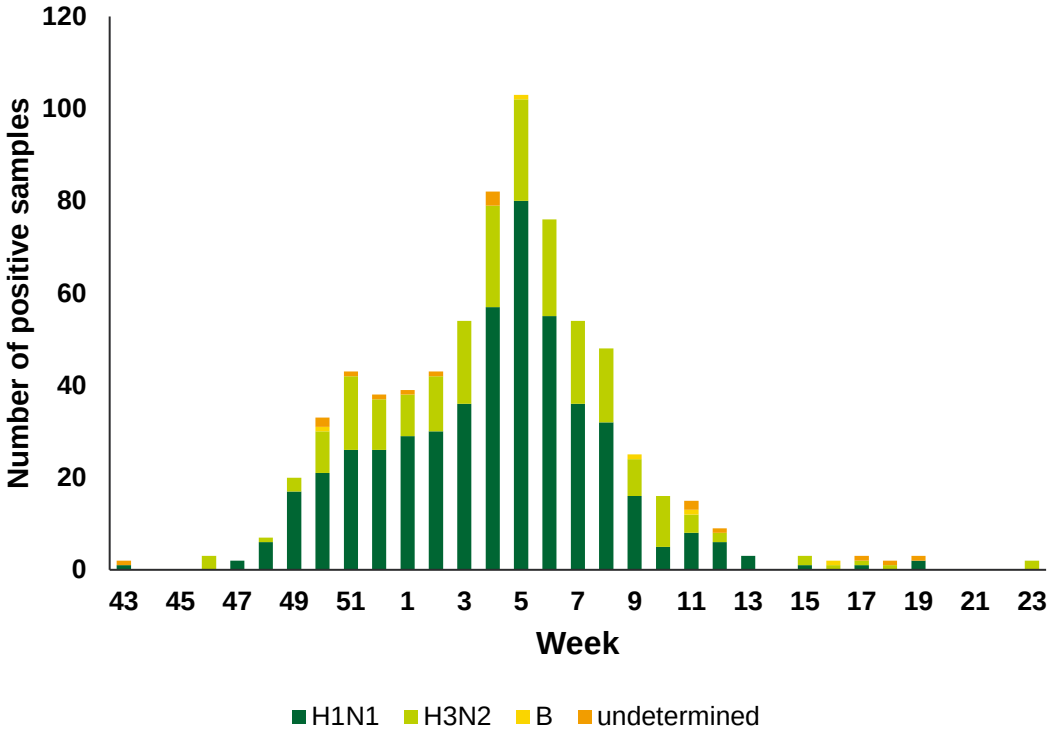

Figure 5. Weekly distribution of influenza viruses per type and subtype among SARI samples.

3.3. OTHER RESPIRATORY VIRUSES

Besides influenza, other respiratory viruses were monitored within the SARI network. Out of the 6042 samples, 440 samples tested positive for entero-/rhinoviruses (7%), the second most prevalent detected pathogen, with 384 positive samples, was HMPV (6%). SARS-CoV-2 (#370) and RSV (#384) were prevalent in 6% of the samples. Other respiratory viruses that were present, included parainfluenza-3 (PIV3, #189; 3%), coronavirus OC43 (#181, 3%), adenovirus (#157, 2.5%) and bocavirus (#104, 2%). coronavirus 229E (#55), PIV2 (#13), NL63 (#10), PIV1 and PIV4 (#9), and paraechovirus (#8) were rarely detected. Out of the 6042 samples, 2109 samples tested negative for influenza and the above mentioned respiratory pathogens (Figure 6).

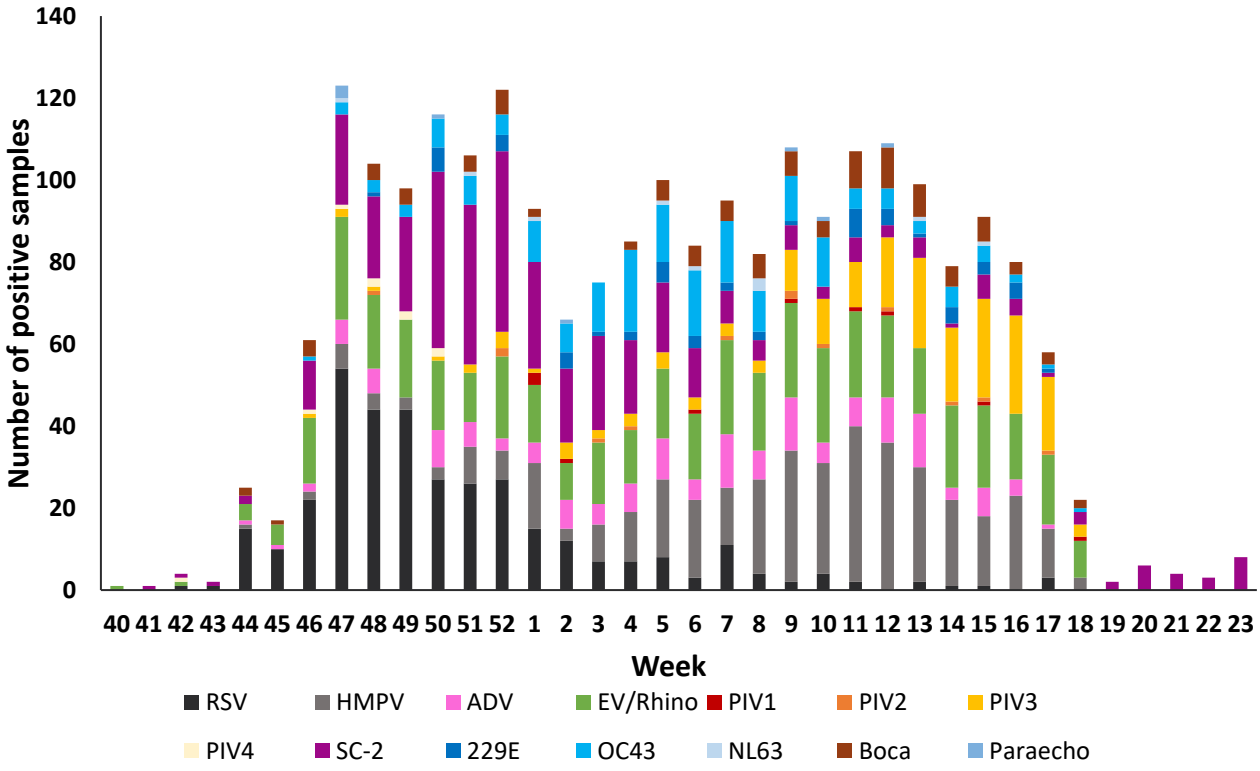

Figure 6. Weekly distribution of detected respiratory viruses among SARI samples.

NON-SENTINEL SURVEILLANCE

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1. Hospital laboratories (HOSPI)

1.1. CLINICAL DATA

Laboratories and hospitals from all over Belgium can send samples to the NRC influenza for confirmation of influenza positive cases or for the determination of the (zoonotic; cfr §2) subtype (influenza A) or the lineage (influenza B) or for a differential diagnostic with other respiratory viruses.

During the 2023-2024 season **11 hospitals** submitted samples, 2 hospitals were located in the Brussels region, 7 hospitals were located in Flanders and 2 hospitals were located in Wallonia. Overall, **272 samples** were tested.

1.2. INFLUENZA VIRUS

Out of the 272 received samples, 211 samples tested positive for influenza. The first positive sample was detected in week 37-2023 and the last positive sample in week 19-2024. The percentage of samples positive for the influenza virus typing for the season 2023-2024 was 78%, 210 samples were positive for influenza type A, 1 sample was positive for influenza type B. Among the 210 influenza A positive samples, the H3N2 subtype was identified for 65 influenza positive samples, the H1N1dpm09 subtype was identified for 142 influenza positive samples. For 3 influenza A positive samples, the viral load was too low to allow subtype determination.

1.3. OTHER RESPIRATORY VIRUSES

Out of the 272 samples, 11 samples tested positive for entero-/rhinoviruses (4%), 10 samples tested positive for RSV (4%) and 8 samples tested positive for SC-2 or adenoviruses (3%). Other respiratory viruses that were sporadically detected were bocavirus (#3, 3%) and HMPV, coronavirus OC43 and PIV4 (#2; 1%). Paraechovirus and PIV2 and PIV3 were only detected once. For 40 samples no respiratory virus could be identified.

2. Zoonotic influenza

The Belgian NRC influenza did not detect any positive samples of a human case of infection with a non-seasonal influenza virus (infection with an influenza virus of animal origin). However, as part of vigilance and based on the recommendation of the European Centre for Disease Prevention and Control (ECDC) and the WHO institution, before summer time, the NRC Influenza sent out a recommendation letter to all Belgian laboratories and hospitals to submit influenza A positive samples from patients admitted to the hospital for respiratory symptoms that were in (in)direct contact in the two (2) weeks prior to admission with birds (wild or poultry), wild animals (live or dead), pigs, ruminants, sick cats/dogs. Furthermore, hospitals should consider to test all cases of viral encephalitis or meningoencephalitis, for which no etiologic agent has been identified, for influenza viruses.

2.1. ACTIVE SURVEILLANCE TO MONITOR ZOONOTIC INFLUENZA TRANSMISSION EVENTS: ZOOIS

2.1.1. Background

ZOOIS is a study, that was launched on the 15th of December 2022 to build on an active surveillance system to evaluate the potential transmission of influenza viruses of animal origin to humans. The study is funded by Departement Zorg and is foreseen for 2 years, end date 31/12/2024.

The study can be divided in 2 major parts: **ZOOIS-sentinel** and **ZOOIS-outbreak**.

For **ZOOIS-sentinel** the objectives were to build networks for targeted people working with swine and birds. In total, after amendments in the original study protocol, 4 sentinel populations were included: (i) poultry farmers, (ii) bird rehabilitation centres, veterinarians working in the (iii) poultry or (iv) swine industry. Within each sentinel site, voluntary participants were recruited and information on the participant and its activities was collected. Virological follow-up of the participants was done by collection of a nasopharyngeal swab every 2 weeks that was analysed in RT-qPCR.

For **ZOOIS-outbreak** the objectives were to recruit people involved in the management of an outbreak of avian influenza on a poultry farm. Information on the participant and its activities was collected and virological follow-up was done by collection of a nasopharyngeal swab every 2 days over a period of 2 weeks. Swabs were analysed in RT-qPCR. In addition, for those willing to, a serological follow-up of participants could be done through the collection of a capillary blood sample on filter paper at enrolment and approximatively 4 weeks later, which could be tested in hemagglutination inhibition assay.

2.1.2. Results

In April 2024 an interim report on ZOOIS was prepared, below a summary on the virological results.

2.1.2.1. ZOOIS sentinel

In total 44 people participated. This included, over a total of 5 bird rehabilitation centres, 24 participants; and over a total of 5 swine veterinary practices, participants. No poultry farmers were willing to participate, yet starting from end of April/May 15 poultry veterinarians were willing to join the project.

From the end of September 2023 till the end of April 2024 we received 302 samples, 189 were derived from people working at bird rehabilitation centres, 113 from swine veterinarians. Two samples, derived from swine veterinarians, tested positive for influenza, one for type A and one for type B. Further subtyping revealed that the type A belonged to the human seasonal H1N1pdm09 subtype, and the type B belonged to lineage Victoria.
Out of the 302 samples, 8 samples tested positive for SC-2.

Since the study was launched in September 2023, 2 out of the 24 participants, working at a bird rehabilitation centre, decided to end their participation, for the swine veterinarians this was the case for 1 out of 20 participants.

2.1.2.2. ZOOIS outbreak

Since the project was launched (15/12/2022), 4 outbreaks were reported in Flanders, a summary is depicted in Table 1 below.

Table 1. Summary avian influenza outbreaks and their participation in ZOOIS outbreak

Location	Participation	Date
Diksmuide	No	01DEC23
Diksmuide	No	08DEC23
Alveringem	Yes	26DEC23
Veurne	Yes	29DEC23

End of December, an outbreak was reported in Alveringem. Since the people involved, reported Flu-like symptoms, they were tested for influenza and closely monitored, but outside the scope of the ZOOIS study. The 4th outbreak was originated in Veurne, both the farmer and his wife participated. No samples tested positive for Influenza A, B or SC-2.

CHARACTERIZATION

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1. Virus isolation

In total 240 samples, which included 4 ILI-NH, 49 ILI, 51 HOSPI and 136 SARI samples, positive for influenza viruses were used to attempt influenza virus isolation (Table 2). H3N2 virus positive samples were inoculated in MDCK-SIAT cells, and H1N1pdm09 and Victoria virus positive samples were inoculated in MDCK cells. After inoculation, cells were observed daily over a period of 72 hours post infection to check for the appearance of a characteristic cytopathic effect.

Table 2. Virus isolation from surveillance samples, season 2023-2024

Subtype	Isolated	Negative	Contaminated	Total
H3N2	92	19	20	**131**
H1N1pdm09	69	21	19	**109**
Total	**161**	**40**	**39**	**240**

A representative selection of these isolated influenza viruses were sent to the WHO Collaborating Centre at the Crick Institute in London (United-Kingdom), as part of the WHO-recognised National Influenza Centre's terms of reference, to be further characterised and compared with isolates from other countries in preparation of the Vaccine Composition Meetings to select the vaccine strains. There is currently no similar system of systematic exchange in place for SARS-CoV-2 viruses.

2. Antigenic characterization

The antigenic characteristics of an influenza virus are based on its interaction with post-infection ferret antiserum raised against a vaccine/reference influenza virus in the context of a Haemagglutination Inhibition assay (HI) that can utilise a range of Red Blood Cells (RBCs), commonly from either chicken (H1N1pdm09) or guinea pigs (H3N2).

In total 38 virus isolates were tested in HI. For 15 of them the HA titer was >4HAU/25µl and further antigenic characterization was performed (Table 3).

Table 3. Closest strain of the antigenically characterised influenza A viruses, season 2023-2024.

	Reference virus	SARI	ILI	HOSPI
H1N1pdm09	A/Sydney/5/2021			
	A/Victoria/2570/2019			
	A/Victoria/4897/2022			
	A/Wisconsin/67/2022	7		
H3N2	A/Catalonia/NSVH161512067/2022			3
	A/Darwin/9/2021	2		2
	A/Thailand/08/2022			
	A/Thuringen/10/2022			1
Total		**9**	**0**	**6**

Data were reported through TESSy in the strain-based record type INFLANTIVIR.

3. Sequencing

Whole genome sequencing using NGS Oxford Nanopore MinION technology is performed at the NRC influenza for influenza viruses and SARS-CoV-2.

3.1. INFLUENZA VIRUSES

Sequencing was attempted on only a subset of the ILI, SARI and HOSPI samples positive for influenza viruses. The selection was based on the qPCR typing and subtyping results and the corresponding Ct values of these assays. Sequence analysis allowed to classify the viruses in clades, as defined by WHO Euro / ECDC for reporting into TESSy (The European Surveillance System).

A total of 43 samples positive for H3N2 viruses were processed for sequencing and uploaded on GISAID (Table 4 and Figure 7). All viruses belonged to clade 3C.2a1b.2a.2a.3a.1.

Table 4. Clade distribution of the sequenced A/H3N2 viruses, season 2023-2024

Clade assignment	ILI	SARI	HOSPI	Total
3C.2a1b.2a.2a.3a.1	11	25	7	**43**

Fifty-nine samples positive for H1N1pdm09 viruses were processed for sequencing and uploaded on GISAID (Table 5 and Figure 8). Clade 6B.1A.5a.2a was predominant, with a subpopulation of isolates belonging to 6B.1A.5a.2a.1.

Table 5. Clade distribution of the sequenced H1N1pdm09 viruses, season 2023-2024

Clade assignment	ILI	SARI	HOSPI	Total
6B.1A.5a.2a	11	23	16	**50**
6B.1A.5a.2a.1	2	5	2	**9**

Three samples positive for influenza B type were processed for sequencing (Table 6). All samples belonged to the Victoria lineage, 2 belonged to clade V1A.3a.2, one sample was unassigned.

Table 6. Clade distribution of the sequenced B/Victoria viruses, season 2023-2024

Clade assignment	SARI
V1A.3a.2	2
unassigned	1

Twenty-nine viruses positive for influenza A were sequenced via the Crick Worldwide Influenza Centre, 15 H3N2 viruses and 14 H1N1pdm09 viruses.

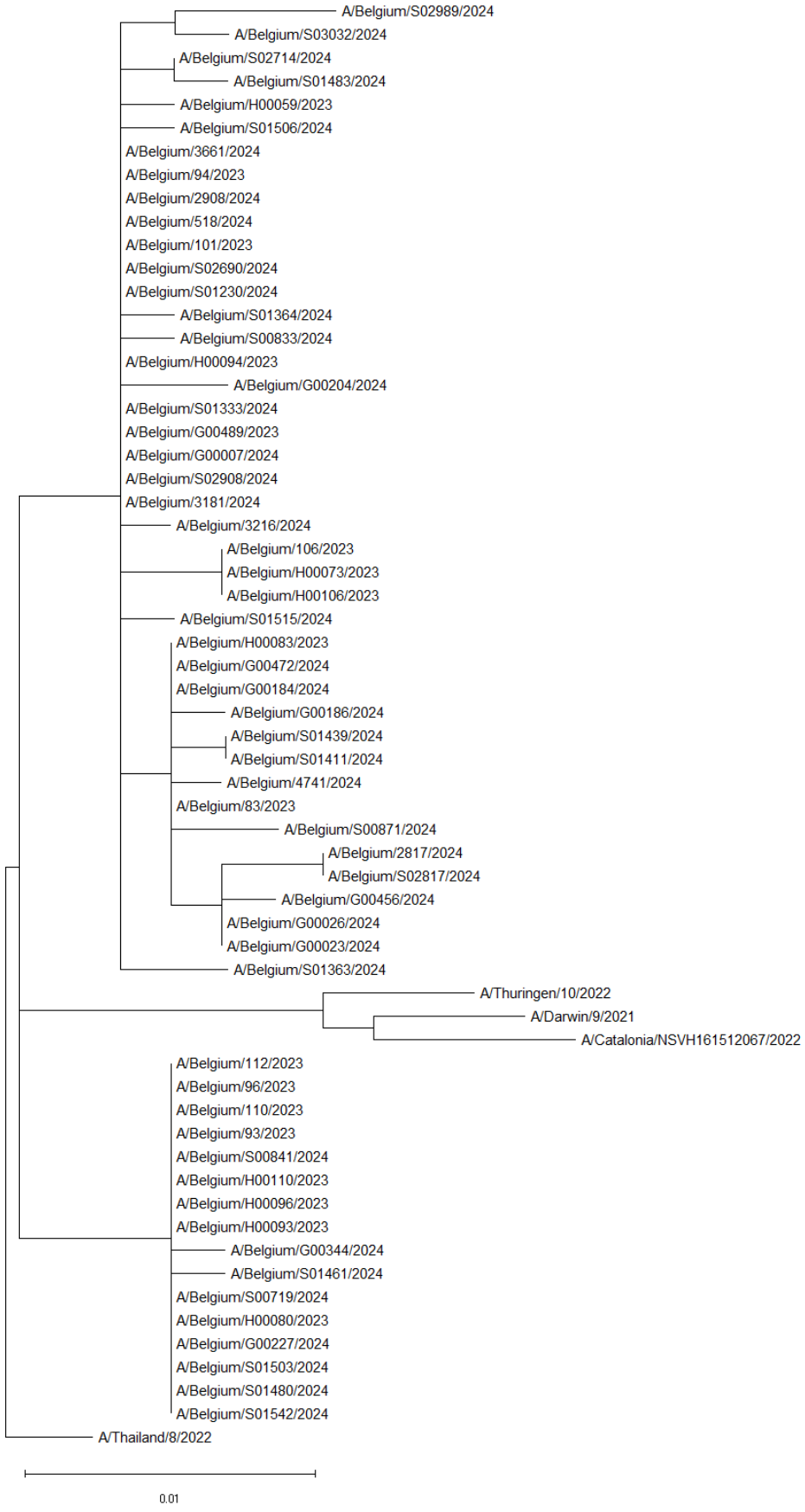

Figure 7. Phylogenetic tree based on amino acid sequences of the A/H3N2 viruses season 2023-2024. Phylogenetic relationships were estimated by using the maximum-likelihood method in MEGA12 software and the Jones-Taylor-Thornton substitution model with a gamma distribution of among-site rate. Branch length is proportional to genetic distance. Scale bar indicates amino acid substitutions per site.

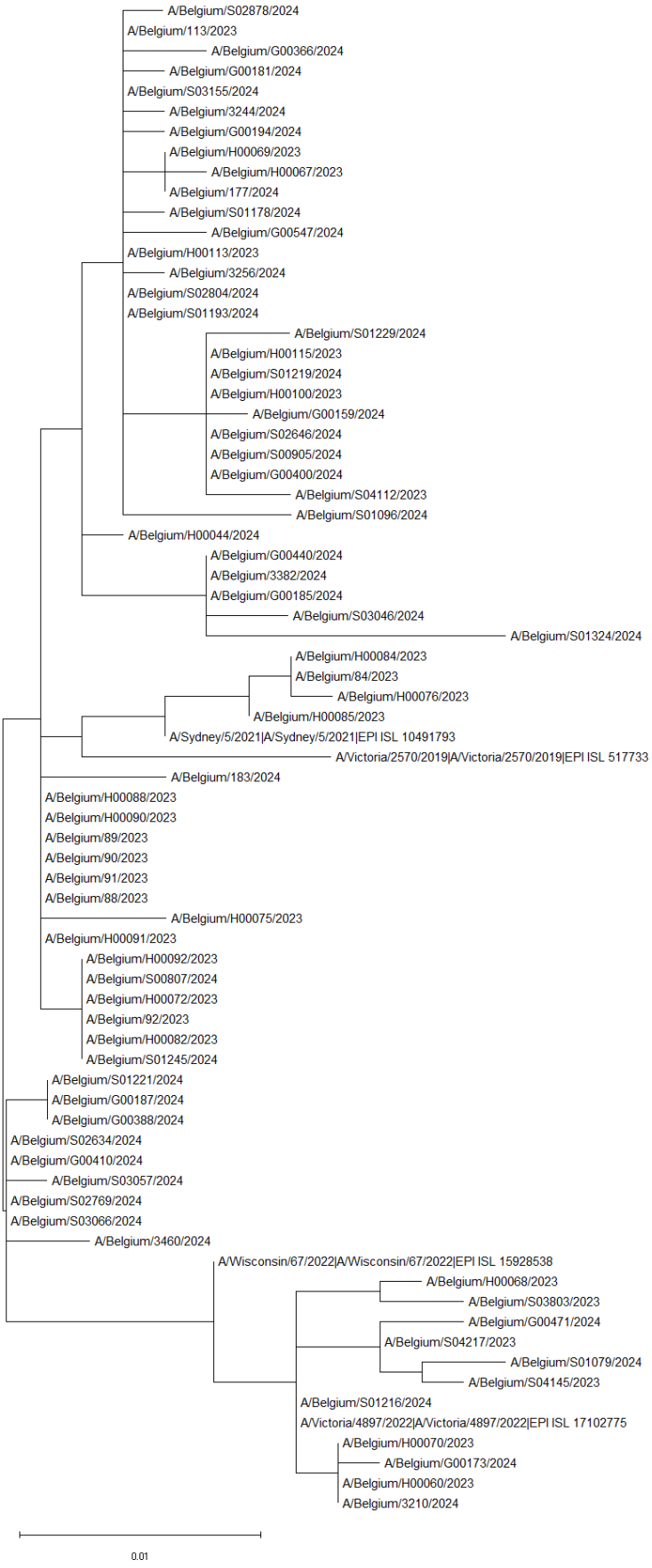

Figure 8. Phylogenetic tree based on amino acid sequences of the A/H1N1pdm09 viruses season 2023-2024. Phylogenetic relationships were estimated by using the maximum-likelihood method in MEGA12 software and the Jones-Taylor-Thornton substitution model with a gamma distribution of among-site rate. Branch length is proportional to genetic distance. Scale bar indicates amino acid substitutions per site.

3.2. SARS-COV-2 CORONAVIRUSES

Sequencing was performed on all SARI/ILI samples positive for SARS-CoV-2 with a Ct value ≤25. A total of 358 samples positive for SARS-CoV-2 coronavirus were selected for sequencing, the sequencing failed for 4 samples. Two systems are used for further subdivision to classify SARS-CoV-2 based on genomic analysis: Nextclade (Table 7) and Pangolin lineage (Table 8).
During the 2023-2024 season, Clades 23I was most prominent, followed by 24A and 23F.

Table 7. Clade distribution of the SARS-CoV-2 positive samples based on Nextclade system, season 2023-2024

Nextclade	ILI	SARI	Total
22F (Omicron)	1	3	4
23A (Omicron)	1	2	2
23B (Omicron)	1	2	3
23C (Omicron)	0	1	1
23D (Omicron)	2	6	8
23E (Omicron)	0	4	4
23F (Omicron)	8	9	17
23H (Omicron)	0	2	2
23I (Omicron)	50	201	251
24A (Omicron)	4	28	32
24B (Omicron)	1	11	12
JN.1.1 (Omicron)	0	1	1
JN.1.4 (Omicron)	0	1	1
Recombinant	1	13	14

Table 8. Clade distribution of the SARS-CoV-2 positive samples based on Pangolin system, season 2023-2024

Pangolin	ILI	SARI	Total
BA.2.86	0	2	2
BA.2.86.1	1	10	11
BA.2.86.3	1	0	1
DV.7.1	0	1	1
EG.5.1	2	2	4
EG.5.1.1	1	1	1
EG.5.1.1	3	2	5
FE.1.2	0	1	1
FL.1.5	0	1	1
FL.1.5.1	0	2	2
FL.15	1	2	3
FL.25	1	0	1
GE.1	0	1	1
GK.2	0	1	1
GS.4	0	1	1
GS.4.1	0	1	1
HK.3	1	2	3
HK.3.1	0	1	1
HN.5	0	1	1
HV.1	1	1	2
JD.1.1.1	1	0	1
JD.1.1.8	0	1	1
JG.3	1	2	3
JN.1	32	112	144
JN.1.1	6	44	50
JN.1.1.1	0	1	1
JN.1.1.2	0	1	1
JN.1.2	0	2	2

JN.1.4	5	16	21
JN.1.4.4	0	1	1
JN.1.4.7	0	1	1
JN.1.6	0	1	1
JN.1.7	0	3	3
JN.1.8	0	1	1
JN.1.8.1	1	1	2
JN.1.12	0	1	1
JN.1.16	1	1	2
JN.1.16.1	0	2	2
JN.1.18	0	3	3
JN.1.18.3	0	1	1
JN.1.48.1	1	1	2
JN.1.50	1	0	1
JN.2	0	2	2
JN.4	2	16	18
JN.6	0	1	1
JN.9	2	0	2
KP.1.1	0	1	1
KP.2	0	3	3
KP.2.3	0	2	2
KP.3	0	2	2
KP.3.1	1	2	3
KP.3.3	0	1	1
KS.1	0	6	6
LB.1.3	0	1	1
LB.1.4	1	0	1
LF.1.1.1	0	1	1
XBB.1.16.6	1	1	2
XBB.1.16.15	0	1	1
XBB.1.16.17	1	0	1
XBB.1.17.1	0	1	1
XBB.1.42	0	1	1
XBB.1.42.1	1	0	1
XBB.2.3.11	0	1	1
XDD	1	7	8
XDD.1.1	0	1	1
XDK	0	2	2
XDK.1	0	1	1
XDK.1.2	0	1	1
XDV.1	0	1	1

QUALITY MANAGEMENT

The NRC influenza is accredited by BELAC (Belgian Accreditation Body) according to the ISO 15189 norm.

As part of its requirements to maintain ISO 15189 accreditation and its recognition as National Influenza Centre by WHO, the NRC influenza takes part in several Proficiency Tests / External Quality Assessments (EQA).

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