

Surveillance of Influenza Summary of the Season 2016-2017

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Background

In Belgium, the influenza surveillance is performed by the National Influenza Centre and the Unit of Epidemiology of Infectious diseases. 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 were 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.

Six hospitals participated to the surveillance. The SARI case definition is: an acute respiratory illness with onset within the last seven days and fever of ≥ 38 C and cough or dyspnea, and requiring hospitalization (24h or more). The surveillance is carried out during the epidemic period of seasonal influenza. Clinical data and respiratory samples are collected from patients meeting to the case definition. Respiratory samples are analyzed by real time PCR for influenza (typing and subtyping) and other respiratory viruses. The hemagglutinin gene of a subset of influenza positive samples is also sequenced.

Methods

Patients

Pediatric and adult units collected clinical data and took nasopharyngeal swabs from patients who corresponded to the case definition. For each patient, information on gender, age, clinical symptoms, influenza vaccination status, antiviral treatment and risk factors was gathered.

Methods

- Real time RT-PCR for typing Influenza A/B
- Real time RT-PCR for subtyping Influenza A strains and determination of lineage of influenza B
- Multiplex (4 quadruplex for 15 different respiratory viruses : respiratory syncytial virus (RSVA and RSVB), parainfluenza viruses (PIV 1, 2, 3, 4), rhinoviruses/enterovirus (HRV/ENV), human metapneumovirus (hMPV), parainfluenza (HPeV), bocavirus (BoV), adenoviruses (ADV) and different coronaviruses (CoOC43, CONL63, Co229E)
- Sequencing the hemagglutinin gene of a subset of positive samples

MIX 1	MIX 2	MIX 3	MIX 4
RSV A HEX	PIV 1 ROX	Co 229F 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	

Results

From week 1-2017 to week 17-2017, 1422 respiratory samples from the sentinel network of hospitals were tested among which 563 (39.5%) were positive for influenza, with 556 (39%) influenza A and 7 (0.5%) influenza B. Among the analysed influenza viruses, 526 (93.4%) were A(H3N2), two (0.4%) was A(H1)pdm2009, 2 (0.4%) were influenza B/Victoria and 5 (0.9%) were influenza B/Yamagata (Fig.1). The percentage of positivity for influenza viruses was higher in the age group ≥ 65 years old and reached 60% in the elderly (Fig 2).

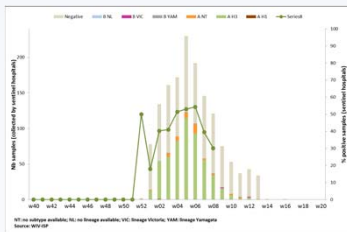


Figure 1. Weekly detection of influenza viruses season 2016-2017

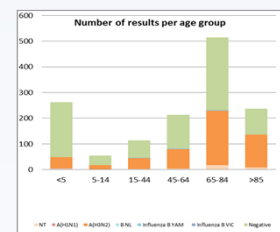


Figure 2. Age distribution of influenza SARI surveillance

Overall, 72% of the SARI patients were positive for at least one respiratory virus (including influenza virus and other viruses). Besides influenza virus, the most prevalent viruses were RSVB (8.8%), human rhinovirus/enterovirus (7.7%), hMPV (7.23%). The percentage of co-infection was overall 10,9 %, but reached 29% in children <5 years old.

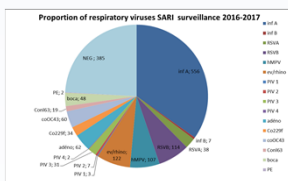


Figure 3. Proportion of the different respiratory viruses

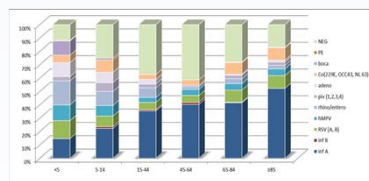


Figure 4. age distribution respiratory viruses season 2016-2017

Sequencing of a subset of the different viruses showed that the strains belonged to groups that were close to the corresponding vaccine strains.

A few A(H1N1)pdm2009 were sequenced and belonged to group 6B.1, represented by the reference strain A/Michigan/45/2015. These viruses are antigenically homologous and similar to the vaccine strain A/California/7/2009.

The majority of the A(H3N2) strains belonged to the newly emerging subclade 3C.2a1, represented by the reference strain A/Bolzano/7/2016 which is antigenically close to the vaccine strain A/Hong Kong/4801/2014 (Fig.5)

Independently of this surveillance, three influenza B Yamagata which were genetically characterized belonged to clade 3 represented by the vaccine strain B/Phuket/3073/2013 present in the quadrivalent vaccine.

Only one influenza B Victoria was detected during this season and belonged to clade 1A, the B/Brisbane/60/2008 clade which is present in the trivalent vaccine.

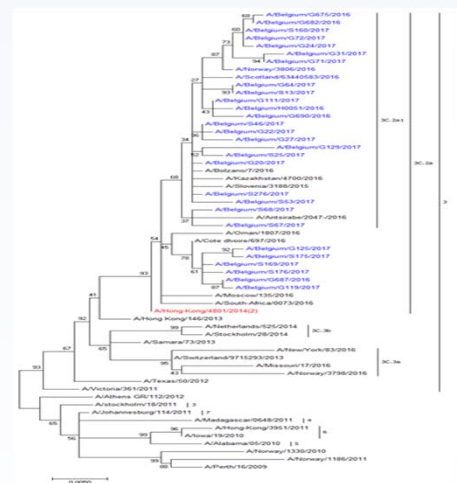


Figure 5. Phylogenetic analysis of the HA sequences of the A(H3N2) viruses analysed in Belgium during the 2016-2017

Conclusions

The 2016-2017 influenza epidemic was characterized by an early start, short duration and moderate intensity and severity. The predominant viruses were A(H3N2). As observed in other countries, a new subclade of A(H3N2) has emerged: the 3C.2a1 which remains however antigenically close to the vaccine strain A/Hong Kong/4801/2014. Sentinel surveillance of severe influenza cases has been successfully introduced in Belgium since six consecutive seasons.

Influenza virus was the main virus involved in SARI patients, but in 51% of the influenza virus-negative samples one or more other respiratory viruses were also detected.

Acknowledgements

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