Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
**Results:** Total 547 from 700 samples were detected as positive for viral infection 78.1% (547/700). Among them, PIC (RV/EV) (34.0%) was the most detected, followed by RSV (28.3%), HBoV (19.1%), HCoVs (10.7%), ADV (13.7%), Flu A/B (8.9%), PIV 1-3 (7.9%) and hMPV (5.0%). PIC (RV/EV) and RSV were the most dominant etiological agents among hospitalized children with ARIs in both city of China. The prevalence of RSV, HCoVs, hMPV and coinfection was significantly higher in Beijing than in Shanghai (P < 0.05). Different age and seasonal distribution of various viral infections between Beijing and Shanghai were also observed among hospitalized children with SARIs.

**Conclusions:** Different viral and epidemiological profiles existed between Beijing and Shanghai of China. The data provide a better understanding of the role of location and climate in the respiratory viral infection among hospitalized children with SARIs.

**http://dx.doi.org/10.1016/j.jcv.2016.08.223**

**Abstract no: 150**  
**Presentation at ESCV 2016: Poster 184**

**The “Snotbarometer”: Epidemiological data on respiratory infections**

A. Vankeerbergen1, K. Dierickx, A. Boel, K. Van Vaerenbergh, H. De Beenhouwer  
**Laboratory of Microbiology, OLVZ Aalst, Belgium**

Molecular detection of respiratory viruses was initiated in the Laboratory of Microbiology of OLVZ Aalst, Belgium, in 2003 with the detection of human metapneumovirus (hMPV) and respiratory syncytial virus (RSV). Since then, a constant elaboration of the portfolio was performed resulting in 8 multiplex in house real time PCR’s that detect 22 respiratory pathogens including viruses (RSV, hMPV, adenovirus, bocavirus, para-influenzavirus (PIV) 1, 2, 3 and 4, Influenza A and B, coronaviruses, enterovirus and rhinovirus) and atypical bacteria (M. pneumoniae, C. pneumoniae, B. pertussis, parapertussis and holmesii). Samples are mainly obtained from our hospital but also from other hospitals from the Flanders region. On each respiratory sample for which molecular diagnostics for at least one of these pathogens is requested, the complete PCR panel of 22 pathogens is performed. This increases the accuracy of a specific diagnosis, and it also results in “local” epidemiological data. These data are translated into a graphic representation, called the “snotbarometer”, which is made available for the hospital staff through the intranet, and on the website of the hospital. The “snotbarometer” consists of a weekly and a monthly report.

In the weekly report, the amount of positive samples for each pathogen separately is depicted in a graph and updated weekly. This presentation gives the physician an idea of the actually circulating pathogens, of the amount of samples analysed in the lab, and the percentage of samples positive for each pathogen.

In the monthly report a seasonal overview is given for the pathogens with epidemiological data available for multiple years, so one can start to extract the characteristic seasonal patterns. Examples are RSV, influenza A and B, PIV1, PIV2, PIV3 and PIV4. This year, Influenza B exceptionally preceded Influenza A which prolonged the influenza season. For other pathogens like adenovirus, bocavirus and M. pneumoniae the seasonality is less clear and one can observe a more fluctuating presence. Together, this information is very useful to predict the upcoming viruses.

**Conclusion:** Regional epidemiological data are powerful since they can give useful information to the physician, especially when a weekly follow-up is available.

**http://dx.doi.org/10.1016/j.jcv.2016.08.224**

**Abstract no: 181**  
**Presentation at ESCV 2016: Poster 185**

**Molecular characterization of human parainfluenza virus type 3 (HPIV-3) among hospitalized patients from central Israel**

I. Jornist1,∗, E. Mendelson1, D. Ram2, R. Azar2, M. Mandelboim1, M. Hindiyeh1

1 Chaim Sheba Medical Center & Tel-Aviv University, Israel  
2 Chaim Sheba Medical Center, Israel

Human parainfluenza virus 3 (HPIV-3) is an enveloped, non-segmented, negative sense RNA virus that belongs to the Paramyxoviridae family. HPIV-3 is a common cause of bronchiolitis and pneumonia in children less than 1 year of age and one of the leading causes of acute lower respiratory tract infections in children under five years of age. In Israel, the epidemiology of HPIV-3 infections is not well characterized.

In this study, epidemiology and molecular characterization of HPIV-3 was performed on patient samples collected between January 2012 and September 2015. Nasopharyngeal swabs (N = 15,946) were collected from hospitalized patients presenting with respiratory illness. Viral nucleic acid was extracted from patient sample using NucliSens easyMAG® (bioMérieux, France) and tested for the common human respiratory viruses (influenza viruses A and B, hMPV, adenovirus, RSV and HPIV-3) using validated real time PCR multiplex assays. Furthermore, molecular characterization of HPIV-3 complete HN gene (1722 bases) was performed after sequencing the complete HN gene. The Bayesian Markov chain Monte Carlo (MCMC) method was applied using a relaxed molecular clock, as implemented in the BEAST program (version 1.7.5). Trees were visualized and edited with the FigTree program (version 1.4.2) included in the BEAST software package.

Of the patient samples tested, 547 (3.43%) samples were positive for HPIV-3. Stratifying HPIV-3, by month revealed the virus major activity was during the winter and spring seasons. Not only that, but the majority of patients infected were children less than 1 year of age and elderly greater than 60 years of age. An increased HPIV-3 activity was seen in patients hospitalized in the oncology/transplants wards of the hospital. Of interest were patient’s co-infections with HPIV-3 and other respiratory viruses. Of the 547 patient infected with HPIV-3, 99 (18.1%) patients were co-infected with other human respiratory viruses. Of which, adenovirus (6.6%) and RSV (6.4%) were the most common.

Molecular characterization of the complete HPIV-3 HN gene from 50 different patients infected throughout the study period revealed that the majority of the HPIV-3 strains circulating in Israel belonged to the C1b and C3a clades. These HPIV-3 clades were mainly seen in the America’s and Saudi Arabia. In addition, one HPIV-3 isolate from the year 2012 did not match with any of the C1 clades, suggesting the possibility of being a new sub clade. HPIV-3 HN sequence analysis also revealed that the isolates characterized from Israel did not acquire the substitutions T193I and 1567V in the HN gene suggesting that in patients with severe infection and where Zanamivir treatment is warranted, this antiviral can be used to help in managing the HPIV-3 infection.

This is the first comprehensive study that characterized HPIV-3 infections in Israel. The high co-infection rate of HPIV-3 and other common human patients mandates careful evaluation of the clinical presentation of infected patients and their prognosis. In addition, in depth evaluation of the clinical presentation of patients infected with the different HPIV-3 clades should be entertained.

**http://dx.doi.org/10.1016/j.jcv.2016.08.225**