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more, for monitoring of intensity, RSV-specific denominators are needed.

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Herpes Simplex 1-2 in broncho alveolar fluid: A 5 years retrospective study

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Aim: Respiratory viruses are very often detected in pneumonia thanks to uniplex and multiplex real-time PCR techniques. Moreover viruses that are not primilarly the cause of respiratory infections may also be detected such as HSV 1-2, varicella zoster virus and cytomegalovirus.

The aim of our study was to analyze the prevalence of other respiratory infections among broncho-alveolar lavages (BAL) positive for HSV 1-2. The clinical outcome of patients according to the anti HSV 1-2 treatment was also analyzed.

Material and methods: Data from hospitalized patients suffering from serious respiratory symptoms and whose broncho-alveolar lavages were positive for HSV 1-2 by an in-house real-time PCR were analyzed.

Nucleic acids (NA) had been extracted with the MagNA Pure 96 DNA and Viral NA Small Volume kit® on the MagNA Pure 96™ instrument (Roche Molecular Diagnostics, Meylan, France).

Samples had been tested for 16 respiratory viruses (influenza A and B, parainfluenza 1–4, respiratory syncytial viruses A and B, human metapneumovirus, coronaviruses 229E, OC43 and NL63, rhinoviruses, enteroviruses, bocaviruses and adenoviruses) with a multiplex RT-PCR (Anyplex™ II RV16 Detection®, Seegene) on the CFX96™ Real-Time System (Biorad diagnostics).

NA had also been tested for cytomegalovirus, varicella zoster virus employing a monoplex in-house PCR on the Light Cycler or the Light Cycler 480™ (Roche Molecular Diagnostics, Meylan, France).

Data were analyzed on StataTM software (StataCorp, Texas) using the exact Fisher test.

Results: Between 2011 and 2015, 122 (73 males) patients attending an intensive care unit in the Toulouse University Hospital were selected with a HSV 1-2 positive result (mean age 62; 24–86). 119 samples were HSV-1 and three were HSV-2.

117 had been tested with the Anyplex™ II RV16 Detection Seegene®. All the viruses of the panel had been detected except parainfluenza 1, 2 and 4, human metapneumovirus and bocavirus; Influenza viruses were the most detected ($n = 13$), followed by rhinovirus ($n = 6$), respiratory syncytial virus ($n = 5$) and adenovirus ($n = 4$). 117 samples had been tested for cytomegalovirus (26 positive), and 90 for varicella zoster virus (negative).

28 among the 78 samples that tested positive for HSV 1-2 during the winter season (November to April) were also positive for another respiratory virus. During the summer season (May to October) 44 samples tested positive for HSV 1-2 with only 4 in coinfection ($p < 0.005$).

The mortality rate did not differ between the HSV 1-2 positive patients treated with acyclovir or valacyclovir ($n = 57$) and those who were not ($p =$ ns).

Conclusions: Our results indicate that HSV 1-2 infection is frequent among patients hospitalized in intensive care unit. During the winter season this infection is linked to other respiratory viruses.

The apparent clinical inefficiency of anti HSV 1-2 treatment indicates that the presence of the virus is more a witness of a clinically poor condition rather than a cause of it.

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Three years (2013–2016) of human respiratory syncytial virus surveillance at a tertiary hospital in Catalonia, Spain

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Background: Human respiratory syncytial virus (HRSV) is the most common respiratory pathogen and the main cause of lower respiratory tract infections among infants and young children. Its genome is a lineal single-stranded negative-sense RNA of approximately 15 kb that contains 10 genes encoding 11 proteins. The G glycoprotein in the viral envelope plays an essential role in the virus attachment. Antigenic and genetic differences in this protein lead classify HRSV into two different groups, HRSV-A and HRSV-B. Furthermore, based on the hypervariable region 2 (HVR-2) located in the C-terminal domain of the G protein several genotypes have been described. Selection pressure drives G protein to continuously evolve, resulting in the likely replacement of predominant genotype season by season. In the present study the epidemiology of HRSV viruses detected in respiratory specimens from patients attended at the Hospital Universitari Vall d'Hebron in Barcelona (Spain) during three consecutive years (from 2013 to 2016) has been described.

Material and methods: From October 2013 (week 40) to March 2016 (week 20) respiratory specimens from patients were collected for laboratory confirmation of respiratory virus infection using immunochromatography (Binax Now RSV Card, Allere Scarborough Inc, USA), immunofluorescence (D³ *Ultra 8*™ DFA Respiratory Virus Screening & Identification Kit, Diagnostic HYBRIDS, USA) or real-time multiplex RT-PCR (Anyplex II RV16 Detection Kit, Seegene, Korea) assays. A nucleoprotein-specific real time RT-PCR was performed to determine HRSV group. In addition, phylogenetic analyses and molecular characterizations were carried out using MEGAv5.2 software based on the HVR-2 sequence from a representing sampling of HRSV per week.

Results: A total of 16552 specimens were collected, of which 1324 (8.3%) were positive for HRSV. The virus showed a seasonal pattern of circulation, previous to influenza annual epidemics, with a maximum detection rates in the weeks 52 or 53 in all three seasons. Viruses belonging to both HRSV groups were detected: HRSV-A (662; 50%), HRSV-B (579, 44%), HRSV-A/B co-infection (8; <1%), and 75 (6%) remained unsubtyped. There was an alternation in the predominance of HRSV group by season; while HRSV-B was predominant during the first two seasons, HRSV-A became it during the third. Based on HVR-2 phylogenetic analyses, HRSV-A viruses belonged to ON1 genotype (153; 99%), but 2 (1%) to NA1.