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.

Abstract No: 1570

Presentation at ESCV 2015: Poster 1

The Respiratory Virus Network – An initiative to collect and provide data on respiratory virus diseases via internet

R. Kaiser[1,*], E. Knops[1], M. Neumann-Fraune[1], M. Timmen-Wego[1], B. Gärtner[2], O. Adams[3]

[1] *Institute of Virology, University of Cologne, Germany*
[2] *Institute for Microbiology, University Hospital of Saarlandes, Germany*
[3] *Institute of Virology, University Hospital of Düsseldorf, Germany*

Background: The Respiratory Network was founded in 2009 on the initiative of the section "Clinical Virology" of the "Gesellschaft für Virologie" (GfV) and is meanwhile supported by the "Deutsche Vereinigung zur Bekämfung von Viruserkrankungen" (DVV) and the "Paul Ehrlich Gesellschaft" PEG. Meanwhile more than 30 laboratories from Germany, Austria, Switzerland and Netherlands are members of the network. Using an online platform, the following data are collected: positive and negative results of respiratory virus tests, detection method, and – optionally – basic patient characteristics. Molecular techniques, e.g. multiplex PCRs such as realtime or Luminex-approaches are meanwhile state of the art.

Methods: Most of the samples are nasal swabs taken with commercially available flocked swabs in transport medium (e.g. eNAT from COPAN, Brescia, Italy). Subtyping of viruses is performed in specialized centers. Most of the samples tested derived from hospitalized patients. The members have direct and real-time access to the cumulated data. The network has an internal site for the members and a freely accessible one, which can be reached via http://rvdev.medical-dpc.com/without registration.

Results: So far, data from more than 35,000 patients are in in the database. Seasonal variations of the beginning, intensity and end of virus activities could be found not only for influenza viruses but also for viruses which are not routinely documented in other surveillance programs, like RSV, HMPV, Rhino-, Entero-, Adeno-, Parainfluenza- and Human Coronaviruses. Data from the RSV-epidemiology are of special interest for the RSV-prophylaxis with Palivizumab in preterm infants.

Conclusions: The Respiratory Network has proven to be a powerful tool in synergy to previously established surveillance systems of public health authorities in Germany. While the latter are focused on Germany and mainly collecting data on Influenza viruses from outpatients in Germany, the spectrum of the patients and the spectrum of viruses is broader in the Respiratory Network, most samples derive from inpatients and the data are collected also from Austria, Switzerland and The Netherlands. Electronic export functions of the database are established for the exchange with other databases. The current activity has extended the data collection under coordination of bacterial specialists to the collection of respiratory bacteria, beginning with Mycoplasma pneumoniae, Chlamydia pneumonia, Bordetella pertussis and expanding to others.

http://dx.doi.org/10.1016/j.jcv.2015.07.106

Abstract No: 1571

Presentation at ESCV 2015: Poster 1

Molecular characterisation of influenza viruses during the 2014–2015 season at a tertiary university hospital in Catalonia, Spain

C.A. Vergés*, L. Gimferrer, M. del Carmen Martín, F. Fuentes, A. Antón

Virology Unit, Microbiology Department, Hospital Universitari Vall d'Hebron, Universitat Autònoma de Barcelona, Spain

Background: Seasonal influenza epidemics represent a substantial public health burden because of significant morbidity and mortality. The aim of this study was to describe the genetic diversity of circulating influenza viruses detected at our hospital during the 2014–2015 season.

Methods: From week 40/2014 to week 20/2015 respiratory tract specimens were collected for laboratory-confirmation of influenza virus infection from patients attended at the emergency care unit or admitted to our hospital. The detection of influenza viruses was carried out by either immunofluorescence or PCR-based assays. A specific real- time one-step multiplex RT-PCR was performed for influenza subtyping (Anton A et al., 2010). The complete HA1-domain coding regions of influenza viruses detected in respiratory samples were sequenced for molecular characterisations and phylogenetic analyses.

Results: A total of 5188 specimens (3686 cases) were received at the Virology Unit for viral respiratory infection diagnosis. 937 (18%) specimens that were laboratory-confirmed for influenza viruses were collected from 900 (24%) patients (675 for influenza A, FLUAV, and 225 for influenza B, FLUBV), of which about 80% were hospitalised. The majority (666) of FLUAV strains were H3 (391, 59%) and H1pdm09 (172, 26%), while the remaining 103 (15%) were unsubtyped. The phylogenetic analyses showed that the 78% (189/244) A(H3) strains belonged to the A/HongKong/5738/2014 (3C.2a) phylogenetic group, which had significant antigenic differences compared with the vaccine strain (A/Texas/50/2012), included in the 2014–2015 Northern Hemisphere vaccine, according to WHO data (http://www.who.int). All (114) A(H1)pdm09 strains fell within the A/SouthAfrica/3626/2013 phylogenetic group, which remained antigenically similar to the vaccine strain (A/California/07/2009). All (103) FLUBV sequences fell within the B/Phuket/2073/2013 genetic clade (B/Yamagata lineage), but one belonging to B/Victoria lineage. A(H1)pdm09 strains detected in almost all hospitalised patients did not carry the D222G/N mutation in the HA receptor-binding-site unlike reported in previous seasons.

Conclusions: The large circulation of drifted A(H3) strains during the 2014–2015 season remarks the need to improve the prediction of the predominant influenza viruses in the upcoming seasons in the current vaccine production strategy to enhance protection. A(H1)pdm09 remained antigenically similar to vaccine virus since its emergence in 2009, and it is the cause of severe respiratory infection of a high percentage of influenza cases, too. However, the only genetic marker (D222G/N) related to severity was not detected in strains from hospitalised patients unlike in previous seasons.

http://dx.doi.org/10.1016/j.jcv.2015.07.107