27th ECCMID Vienna, Austria 22 – 25 April 2017

The congress of ESCMID

Session: P040 Epidemiology of viral infections

Category: 1f. Viral molecular epidemiology (other than hepatitis & HIV)

23 April 2017, 13:30 - 14:30
P0886

Molecular epidemiology of influenza B virus among hospitalized paediatric patients in northern Italy during the 2015-16 season

Antonio Piralla*[1], Giovanna Lunghi[2], Luca Ruggiero[3], Alessia Girello[4], Sonia Bianchini[3], Francesca Rovida[5], Silvia Caimmi[6], Gian Luigi Marseglia[6], Nicola Principi[3], Fausto Baldanti[7], Susanna Esposito[8]

[1]*Fondazione Irccs Policlinico San Matteo; Molecular Virology Unit, Microbiology and Virology Department*

[2]*Irccs Fondazione Ca' Granda Ospedale Maggiore Policlinico DI Milano; U.O.S Virology*

[3]*Fondazione Irccs Ca' Granda Ospedale Maggiore Policlinico, University of Milan; Pediatric Highly Intensive Care Unit*

[4]*Fondazione Irccs Policlinico San Matteo; Microbiology and Virology Department, Molecular Virology Unit*

[5]*Fondazione Irccs Policlinico San Matteo; Molecular Virology Unit, Microbiology and Virology Department; Molecular Virology Unit, Virology and Microbiology Departmentnt*

[6]*University of Pavia, Fondazione Irccs Policlinico San Matteo; Pediatric Clinic*

[7]*University of Pavia; Clinical, Surgical, Diagnostic and Pediatric Sciences*

[8]*Fondazione Irccs Ca' Granda Ospedale Maggiore Policlinico, University of Milan*

Background: Currently, the influenza B viruses belong to two lineages distinct by their genetic and antigenic characteristics, which are referred to as the Yamagata and Victoria lineages, designated after their original isolates, B/Yamagata/16/88 and B/Victoria/2/87. The assessment of the lineage and the group prevalent in circulation is of importance, in order to select the virus to be included in influenza vaccines and to evaluate the efficacy of vaccination. Main aim of this study was to evaluate molecular characteristics of influenza B viruses circulating in a Region of Northern Italy, Lombardia during the influenza season 2015-2016.

Material/methods:
Influenza B virus was detected using a respiratory virus panel of assays and with an influenza B-specific real-time polymerase chain reaction. Complete influenza B HA gene was amplified and sequenced directly from clinical specimens. Phylogenetic analysis were performed using nucleotide sequences. Tests for positive selection were conducted using different methods.

Results:
A total of 71 hospitalized pediatric patients were influenza B positive. Phylogenetic analysis showed that the great majority of influenza B strains (66/71, 93.0%) fall in a clade defined by amino acid substitutions I117V, N129D and V146I (based on B/Brisbane/60/2008 numbering). These strains belonged to the Victoria-lineage and were antigenically similar to the vaccine strain (B/Brisbane/60/2008) included only in the quadrivalent vaccine. In our influenza B strains, a series of amino acid changes were observed in the antigenic regions: I117V, V124A, N129D, V146I, D197N, T199A, and A202T. However, only 2 amino acid changes were observed in HA regions involved in the receptor binding or in the antibody recognition. In detail, three influenza B strains harbored the N197D substitution, while one strain the amino acid change T199A. Interestingly, these changes lead to the loss of a glycosylation site near the receptor-binding region (helix-190). In addition, 3 out of 4 (75.0%) patients with these influenza B variants had signs and symptoms of bronchopneumonia or pneumonia. These three patients were hospitalized for a period ranging from 9 to 22 days. A global analysis of selective pressure made using the SLAC model indicated an estimated overall *dN/dS* ratio of 0.175. Overall, no sites were identified as being under positive selection by site-specific analyses in the influenza B alignment by at least three of the methods used (SLAC, FEL, REL, FUBAR and MEME).

Conclusions:
All the influenza B strains identified in this study belonged to the influenza B Victoria-lineage not included in the vaccine administered among pediatric population during the 2015-16 in Italy. The great majority of influenza B strains were similar to those circulating in Europe in the same period. However, three strains were closely related with “old” influenza B strains circulated in previous seasons.