

4th World Congress on **Virology**

October 06-08, 2014 Hilton San Antonio Airport, TX, USA

Molecular sign of influenza A and B viruses in Cuba during two consecutive years

Alexander Piñón
USA

The data contribute to a better understanding of the circulation of influenza viruses in Cuba, sub-tropical country located at the Caribbean area. The objective of this work was to determine circulation and molecular characterization of influenza viruses in Cuba. From January/2012-December/2013, Cuban National Influenza Centre received 7783 clinical samples of individuals presenting influenza-like illness symptoms, severe acute respiratory infection or fatal cases. Samples were tested for seasonal A(H3N2), A(H1N1)pdm09 and B influenza viruses by real-time reverse transcription-polymerase chain reaction. Nucleotide sequences from hemagglutinin HA1 region segment were obtained directly from clinical samples obtained from positive cases. Genetic distances were calculated using MEGA v.5.05. Phylogenetic tree was constructed using Mr.Bayes v.3.1.2 software. Potential N-Glycosylation sites were predicted using NetNGlyc server 1.0. Of the 1335 samples positives to influenza virus, 48% were positive to influenza A(H1N1)pdm09, 31% to influenza B and 21% to influenza A(H3N2). Year 2012 was marked by low circulation of H3N2 subtype, with only 23 detections. Sequences obtained directly from clinical samples, belong to the clade 6. In year 2013 circulation of H3N2 subtype was highest, all of them grouped into the clade 3C (3C.2 and 3C.3), related to the vaccine strain signed by lineage A/Texas/50/2012. Circulation of influenza A(H1N1)pdm09 was highest in 2013 (26,2%) respect 2012 year (8,3%). Studied sequences distributes into three distinct clades: sequences from 2012 year belong into the clade 7, sequences from January 2013 belong into the clade 7 mainly and one of them into the clade 6C together with sequences from May 2013, last sequences from November 2013 belong into the clade 6B. Influenza B viruses were detected during the two studied years, characterized by the circulation of lineage B/Victoria in 2012 (20.5% of influenza detections) and lineage B/Yamagata in 2013 (7.4% of influenza detections). Strains of B/Victoria lineage grouped with the vaccine strain B/Brisbane/60/2008, while strains of the B/Yamagata lineage belong into the clade 2 represented by the vaccine strain B/Massachusetts/02/2012. It remains to be defined if these viral variants represent an important antigenic drift that would enable viral immune evasion and/or affect influenza vaccine effectiveness.

alexpr@infomed.sld.cu, alexpr230975@gmail.com