

# 2014/15 INFLUENZA SEASON IN AN INLAND PORTUGUESE REGION

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## Introduction

Each year, influenza affects hundreds of millions of people around the World<sup>1</sup>. While both influenza A subtypes and both type B lineages co-circulate every year, the extent to which each subtype circulates varies between and within seasons<sup>2</sup>.

Influenza surveillance is an important tool to identify emerging/reemerging strains and to define seasonality of the circulating strains.

Based on Influenza surveillance networks in the Northern Hemisphere, in February the World Health Organization (WHO) recommends which influenza viruses must be included in influenza vaccines for the forthcoming winter. In December 2014 the CDC health alert network notified an antigenically drifted influenza A(H3N2) virus, antigenically distinct from the A(H3N2) vaccine virus, A/Texas/50/2012<sup>3</sup>.

The aim of this work is to compare the circulating strains detected by Centro Hospitalar Cova da Beira - EPE, from an inland north region of Portugal, with the strains circulating among Europe during 2014/2015 Influenza season.

## Material and Methods

In the present review, 249 nasopharyngeal swabs were analyzed by real time PCR techniques, designed to amplify Influenza A and Influenza B virus. All the positive samples were sent to the Portuguese Influenza Reference Laboratory in order to subtype influenza A virus and to perform genetic characterization (genomic sequencing of HA1 subunit of hemagglutinin gene) and antigenic characterization (by hemagglutination inhibition assay with reference antisera) of detected viruses.

## Results

During 2014/2015 season 109 (44%) out of 249 samples tested positive for Influenza viruses: 62 (58%) Influenza A and 47 (42%) Influenza B (Figura 1).

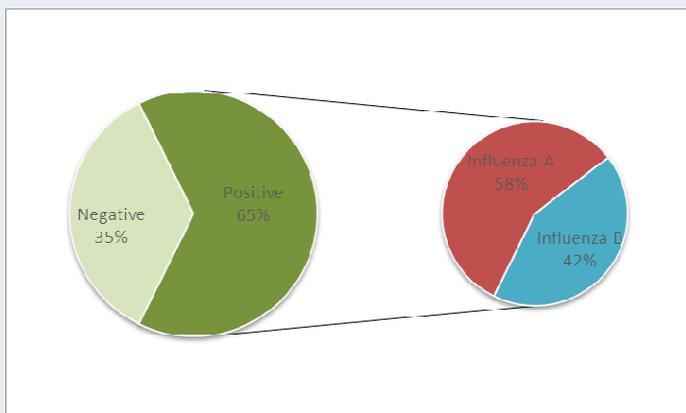


Figure 1: Percentage of Influenza positive samples during 2014/2015 season

In the present season, all seasonal types/subtypes of influenza virus circulated. A(H3) and B strains co-circulated between weeks 1/2015 and 11/2015 with peak activity in weeks 6 and 7/2015. Influenza A was responsible for 58% (63/109) of positive cases, mainly in the last weeks, between week 4 and 10. Influenza B strains were responsible for 42% (46/109) of positive influenza cases, mainly in the first seven weeks of the year (weeks 2 to 8).

The influenza A(H1)pdm strain circulated at a low level, ~5% (5/109) of the positive samples, between 6/2015-9/2015 weeks. However, as only 2/3 of the influenza A samples were subtyped, the percentage of influenza A(H1)pdm strain can be higher than the presented one (Figura 2).

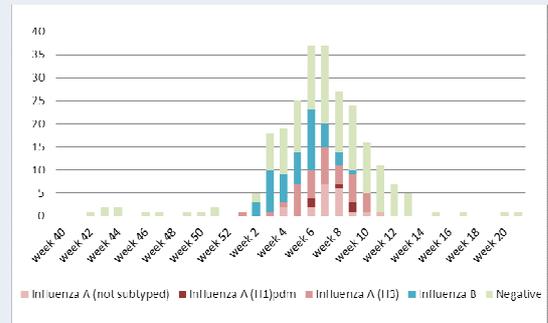


Figure 2: Number of negative / positive specimens tested for influenza virus, by (sub)type and week of specimen collection, weeks 40/2014-20/2015

Antigenic characterization was performed in 11 isolated strains (7 influenza B, 3 AH3 and 1 AH1pdm).

All influenza B strains characterized were from B/Yamagata lineage. Majority of influenza B were well recognized by B/Phuket/3073/2013 antiserum. 19% of influenza B detected strains were selected for genetic characterization. All belonged to genetic clade 3, represented by B/Phuket/3073/2013.

The 9 Influenza A strains genetically characterized, showed the circulation of the new drifted A/H3 variant. 56% (5/9) belonged to genetic subgroup 3C.2a, represented by A/Hong Kong/5738/2014, dissimilar to the 2014/2015 A(H3N2) vaccine strain. 44% (4/9) belonged to A/Samara/73/2013 (genetic group 3C.3), antigenically similar to the current A (H3N2) vaccine (Figura 3).

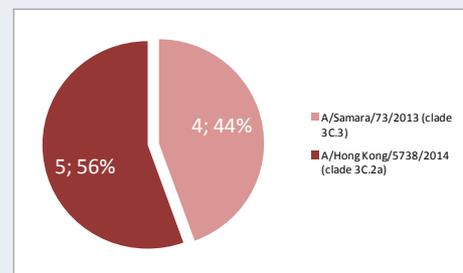


Figure 3: Genetic characterization of influenza A(H3) viruses detected during 2014/2015 season.

## Discussion

The co-circulation of influenza types/subtypes was similar to the one described in Europe but in this Portuguese region the influenza B circulated in first part of the epidemic period, followed by influenza A(H3) virus at the end of epidemic period. This situation was opposite to what happened in Europe, where influenza A viruses had dominated from the start of the season, while influenza B viruses have done so since week 11/2015<sup>4</sup>.

The influenza genetic characterization observed in Portugal was similar to the one from ECDC data either for influenza A and influenza B viruses.

Relatively to influenza A the majority of detected viruses were from the drift detected in December 2014, which is dissimilar to the 2014/2015 A(H3) vaccine virus. The drifted virus' proportion found in this study is similar to the one observed in Europe in spite of the low number of strains genetically characterized<sup>4</sup>.

## References

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- 2- European Centre for Disease Prevention and Control. Circulation of drifted influenza A(H3N2) viruses in the EU/EEA – 22 December 2014. Stockholm: ECDC; 2014.
- 3- Centers for Disease Prevention and Control. CDC Health Advisory Regarding the Potential for Circulation of Drifted Influenza A (H3N2) Viruses. 3 Dec 2014
- 4- European Centre for Disease Prevention and Control/WHO Regional Office for Europe. Flu News Europe, Joint ECDC-WHO weekly influenza update, week 20/2015.