Influenza in Portugal, 2014/2015 season

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Background

Influenza activity in Portugal has been monitored since 1953 at the National Institute of Health. Clinical and virological data is analysed and Influenza-like Illness (ILI) incidence rates are estimated weekly. Information is forwarded to National Health Authorities, contributing for the management of the disease. The National Influenza Surveillance Programme collects and integrates information generated through 2 sentinel surveillance structures, the General Practitioner's Sentinel Network (since 1990) and the Network of Emergency Units (since 1999). The Programme also integrates the information from the Portuguese component of the IMOVE project. Here we provide a snapshot of the influenza activity in Portugal during the 2014/2015 winter, based on the information generated through the Portuguese Influenza Surveillance System.

Materials and Methods

ILI cases were reported to the National Influenza Reference Laboratory and to the Epidemiology Department of the National Institute of Health, in the context of the National Influenza Surveillance Programme, from week 38/2014 through week 20/2015. The intensity and duration of the epidemic periods were described based on the weekly incidence rates for ILI. Nasopharyngeal swabs were collected for virological characterisation of influenza viruses circulating during this period. The detection of influenza viruses was performed by real time RT-PCR. Influenza virus culture was performed in MDCK cells and a sample of isolates was taken for sequence analysis of the HA1 gene segment.

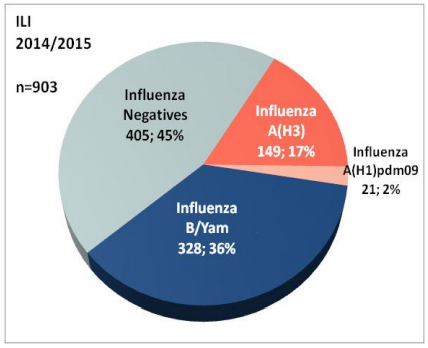

Figure 1 – Influenza laboratory diagnosis in ILI cases from the 2014/2015 season.

Results

During the 2014/2015 winter, between September 2014 and May 2015, 903 nasopharyngeal swabs from ILI cases were sent to the Portuguese NIC (Figure 1 and 2). Influenza activity was high with an epidemic period of 8 weeks (from week 1 to 8/2015) with a max. 148 ILI cases / 10^5 inhabitants in week 4/2015 (Figure 2). Influenza viruses were detected in 498 (55%) ILI cases: 328 (36%) influenza B/Yamagata viruses, 149 (17%) influenza A(H3) viruses and 21 (2%) pandemic influenza A(H1) viruses (Figure 1).

A(H3) positive cases were recorded in higher percentage in children (0 to 4 years: 40.0% and 5 to 14 years: 41.5%) and in adults over 65 years (36.2%), as seen in Figure 3.

The antigenic and genetic analysis of circulating influenza A(H3) and B virus showed differences regarding 2014/2015 influenza vaccine strains (Figure 4 and Table I). Most A(H3) viruses belonged to subgroup 3C.2a, antigenically different from vaccine strain A/Texas/50/2012. Although genetically all Influenza B belong to B/Phuket/3073/2013 group, antigenically 21% of them were low reactors to this antiserum (Figure 4). A(H1)pdm09 viruses were similar to the vaccine A/California/7/2009 strain. In general, the detected influenza viruses were similar to those recommended strains for next winter`s vaccine 2015/2016.

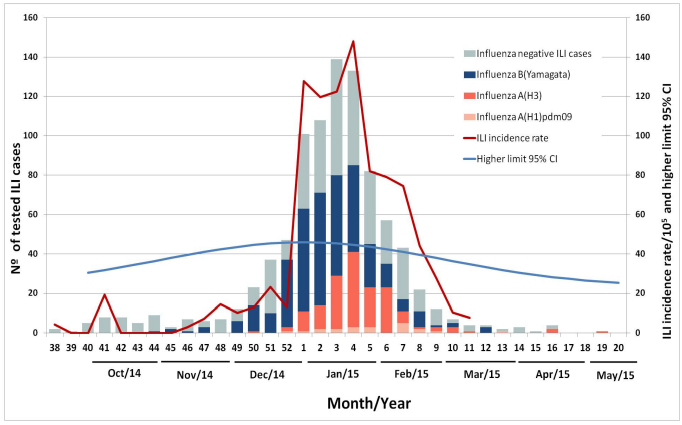

Figure 2 – Weekly distribution of ILI incidence rates and influenza positive and negative cases, season 2014/2015.

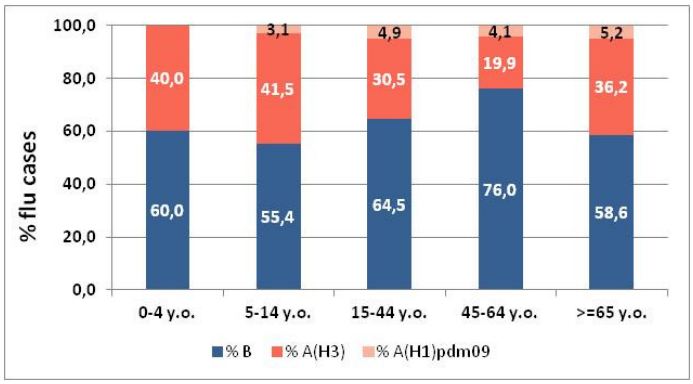

Figure 3 – Distribution of influenza positive cases by age group, season 2014/2015..

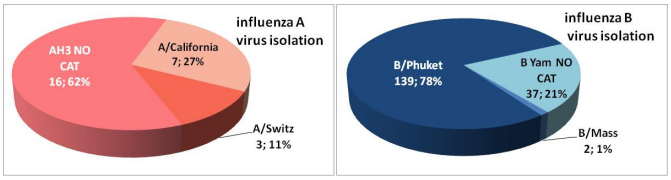

Figure 4 – Antigenic characterisation of influenza A and B viral strains, isolated during the 2014/2015 season.
A/California = A/California/7/2009-like; A/Switz = A/Switzerland/9715293/2013-like;
B/Phuket = B/Phuket/3073/2013; B/Mass = B/Massachusetts/2/2012.

Table I – Genetic characterisation of influenza A and B viral strains, isolated during the 2014/2015 season.

Subtype/Lineage	Phylogenetic group	N. of viruses
A(H1)pdm09	A/Hong Kong/5659/2012 (group 6A)	0
	A/South Africa/3626/2013 (group 6B)	10
	A/Dakar/04/2014 (group 6C)	0
A(H3)	A/Texas/50/2012 (subgroup 3C.1)	0
	A/Samara/73/2013 (subgroup 3C.3)	18
	A/Hong Kong/5738/2014 (subgroup 3C.2a)	37
B/Yamagata	B/Massachusetts/2/2012 (group 2)	0
	B/Phuket/3073/2013 (group 3)	56
Total of sequenced viruses		121

Conclusions

- Influenza activity was high. B/Yamagata viruses were dominant during most weeks of the 2014/2015 flu season, but co-circulated with influenza A(H3). Sporadic cases of A(H1)pdm09 were detected.
- Most influenza A and B viruses were antigenically distinct from the 2014/2015 vaccine strains.
- Influenza A(H3) detections reached the highest percentages in the age groups of the children and elderly.

Acknowledgments

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