Influenza surveillance during 2015/2016 season in Portugal

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Background

The National Influenza Surveillance Program ensures influenza epidemiological surveillance, integrating clinical and laboratory data. The clinical component describes the transmissibility over time, the virological component detects and characterizes influenza virus in circulation. Data is generated through 2 sentinel surveillance structures, the General Practitioner's Sentinel Network (since 1990) and the Network of Emergency Units (since 1999). Here we provide the evaluation of 2015/2016 influenza season in Portugal.

Methods

Influenza-Like illness (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 Program, from week 39/2015 through week 22/2016. The intensity and duration of the epidemic period were described based on the weekly ILI incidence rates. Nasopharyngeal swabs were collected for influenza and other respiratory viruses (RV: respiratory syncytial virus, adenovirus, rhinovirus, metapneumovirus, coronavirus, parainfluenza virus) diagnosis and characterization. The detection of influenza and RV was performed by multiplex real-time RT-PCR. Influenza virus isolation, antigenic analysis (hemagglutination inhibition assay) and genetic characterization (HA1 gene segment) were performed.

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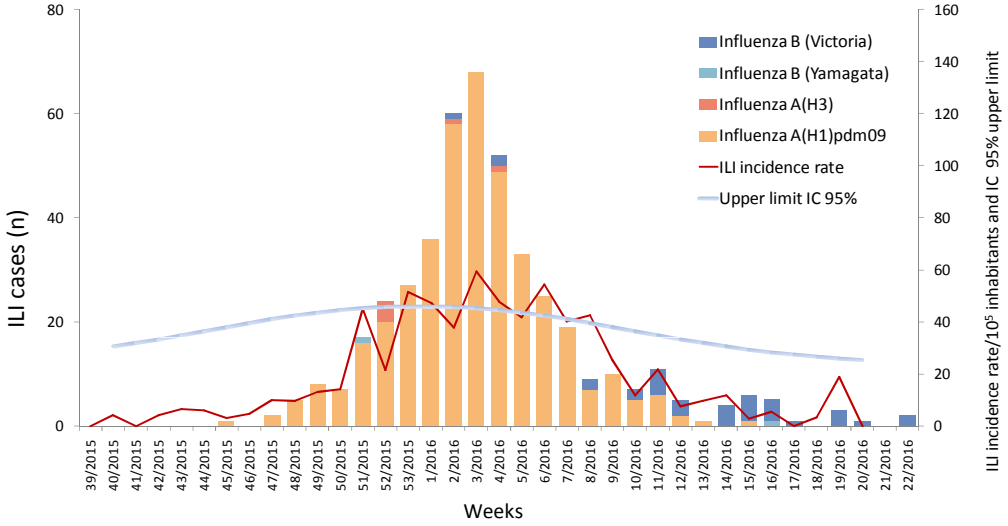

Figure 1 – Weekly distribution of ILI incidence rates and influenza positive cases, season 2015/2016.

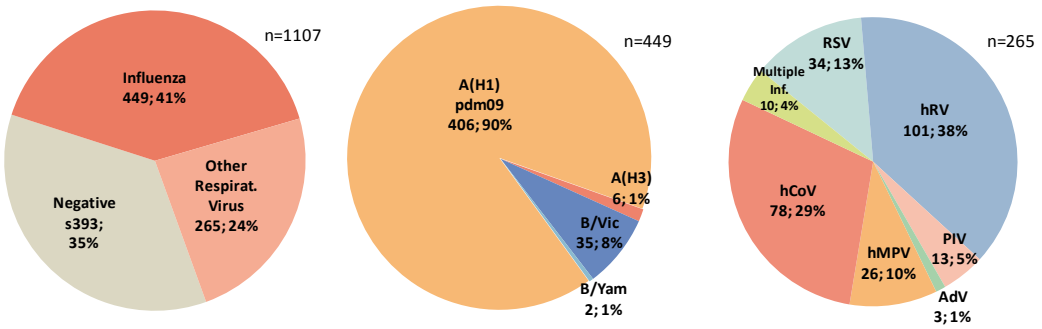

Figure 2 – Influenza ans other respiratory virus laboratory diagnosis in ILI cases from the 2015/2016 season.

Results

- Influenza activity was low and the epidemic period occurred between week 53/2015 and 8/2016 with a maximum of 59.4 ILI cases per 10^5 inhabitants in week 3/2016.
- The influenza A(H1)pdm09 was predominant (91% of flu confirmed cases). Influenza B/ Victoria was identified sporadically (7% of flu cases) in late season.
- Other respiratory viruses were detected in influenza negative cases, being rhinovirus (101; 38%) and coronavirus (78; 29%) found in higher frequencies.
- Influenza A(H1)pdm09 showed similarity with vaccine strain. The majority of influenza B virus belonged to Victoria lineage and clade 1A, dissimilar from 2015/16 vaccine strain. Although few A(H3) viruses in circulation, almost all were similar to strain recommended for next season, 2016/2017, influenza vaccine.
- None of the 420 A(H1)pdm09 viruses analysed showed the H275Y substitution (correlated to high reduced susceptibility to oseltamivir).

Conclusions

Influenza activity during 2015/2016 flu season was low, that can be linked with a higher influenza activity in last season and exceptional climatic conditions during the winter (higher temperature than usual). A(H1pdm)09 viruses were dominant, although in co-circulation with influenza B/Victoria. Situation that contrasts with European influenza picture, that showed a late peak of influenza B/ Victoria. Most influenza detected viruses were similar to the 2015/2016 vaccine strains, although circulating influenza B/Victoria were from a different lineage comparing with vaccine strain. Observed mortality from all causes was within expected values during the study period.

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