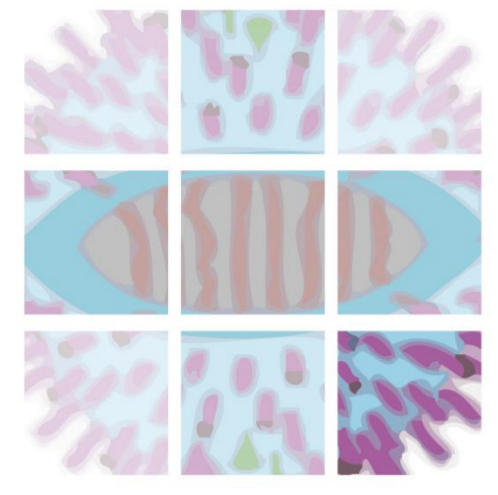


Severe acute respiratory infections in the 2012/2013 season studied by the Portuguese Laboratory Network for Influenza



REDE PORTUGUESA DE LABORATÓRIOS PARA O DIAGNÓSTICO DA GRIPE



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Background:

During the 2009/10 influenza pandemic, a network of 14 laboratories located in the main reference hospitals from Portugal mainland, Madeira and Azores was established for the diagnosis of the new influenza A(H1N1)2009 pandemic strain. Since then, the network performs laboratory diagnosis of influenza as well as other respiratory pathogens, thus contributing to the laboratory diagnosis of respiratory disease in Portugal. This network is a valuable complement of the National Influenza Surveillance Programme (mainly based on primary healthcare units), enabling a more accurate knowledge of the aetiology of the severe respiratory infections, especially in hospitalized cases. The present study describes the severe acute respiratory infections, in the 2012/2013 season, diagnosed by the laboratory network.

Material and Methods:

From the 14 laboratories, 11 reported cases of respiratory disease during 2012/2013 season. The laboratory network performs diagnosis of influenza A and B viruses and other respiratory agents by PCR based methods, enabling the detection of mixed infections. All 14 laboratories perform the detection of influenza A(H1)pdm09, 4 perform the influenza A(H1) seasonal and A(H3) subtyping, and 10 participants also detect influenza B. Eight laboratories implemented methodologies for the detection of other infectious agents associated with respiratory disease. The antigenic characterization of 16 isolated viruses [9 B/Yamagata, 6 A(H1)pdm09 and 1 A(H3)] was performed at the National Influenza Reference Laboratory. The genetic analysis of the HA1 subunit of the hemagglutinin gene was performed in 22 viruses [9 A(H1)pdm09, 2 A(H3) and 11 B/Yamagata]. Twenty nine A(H1)pdm09 and 5 B/Yamagata were tested for antiviral susceptibility [PCR(NA)-H275Y and/or MUNANA phenotypic assays for oseltamivir and zanamivir].

Results:

The 11 laboratories reported a total of 1511 respiratory disease cases, from week 39/2012 to 24/2013 [peak of 208 (13.8%) cases during week 10/2013]. Influenza was identified in 512 cases. Influenza A was detected in 352 (68.8%) cases: 297 (58.0%) cases were A(H1)pdm09, 48 (9.4%) cases were not subtyped, and 7 (1.3%) cases were A(H3). Influenza B was identified in 157 (30.7%) of the influenza cases (Figure 1). Were also identified 2 cases (0.4%) of flu A + flu B mixed infections as well as one case of infection by influenza C (0.2%).

From the 1511 reported cases, were notified 312 ICU cases. The causal agent was identified in 148 (47.4%) ICU cases. Influenza was identified in 121 (38.8%) patients. Among ICU influenza cases, the most detected virus was A(H1)pdm09 (76; 62.8%). However, cases of A(H3) (2; 1.7%), A untyped (5; 4.1%) and B (26; 21.5%) were also detected (Figure 2). As expected, the highest number of ICU influenza positive cases was detected in week 8 and 10/2013 (18; 14.9% each), almost coincident with the highest number of influenza cases during all season (Figure 1).

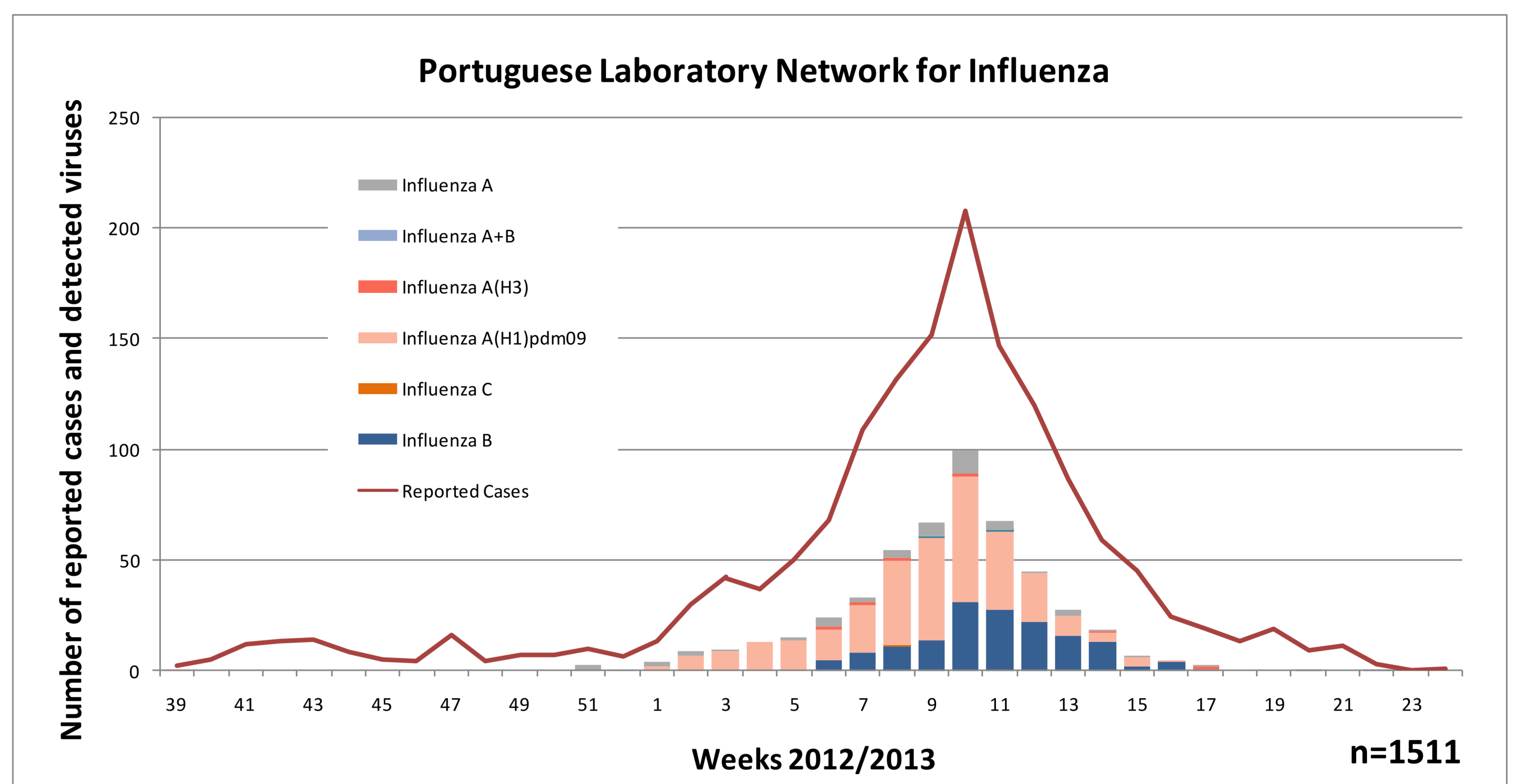


Figure 1 – Number of ILI cases and detected influenza viruses reported by the Portuguese Laboratory Network for Influenza in 2012/2013, by week.

ICU flu cases were detected predominantly in individuals between 45-64 years (55; 45.4%) mainly associated with AH1pdm09 virus. Influenza B virus were responsible for almost all ICU flu cases in the age group of 5-14 years (Figure 3). From the ICU reported cases, 6 (1.9%) died. The influenza A(H1)pdm09 virus was detected in 2 men between 50-59 years old from these 6 fatal outcomes.

Differential diagnosis of other respiratory agents enabled the detection of multiple infections between influenza and other respiratory agents in 12 cases. Bacteria were identified in 9 (8.0%) of these cases (Figure 2).

The isolated influenza A viruses were antigenic and genetic similar to the 2012/2013 vaccine strains. The influenza B/Yamagata viruses showed a greater antigenic and genetic variability. Most of the B/Yamagata viruses were B/Massachusetts/2/2012-like (future 2013/2014 vaccine strain). All the 34 viruses analysed geno- and/or phenotypically showed no reduction in susceptibility to neuraminidase inhibitors, oseltamivir and zanamivir (data not shown).

Conclusions:

The Portuguese Laboratory Network for Influenza Diagnosis plays a major role in the diagnosis of acute respiratory infections in Portugal, providing a more accurate knowledge of the respiratory agents involved. During the 2012/2013 season, the influenza A(H1)pdm09 virus co-circulated with influenza B virus. The A(H1)pdm09 virus was the responsible for the majority of the flu cases admitted in the ICU and may have been the cause of death in two cases. Bacterial and other viral agents have been identified in some of the severe cases reported.

The majority of the characterized influenza viruses were similar to the vaccine strains and reduction in susceptibility to neuraminidase inhibitors was not detected.

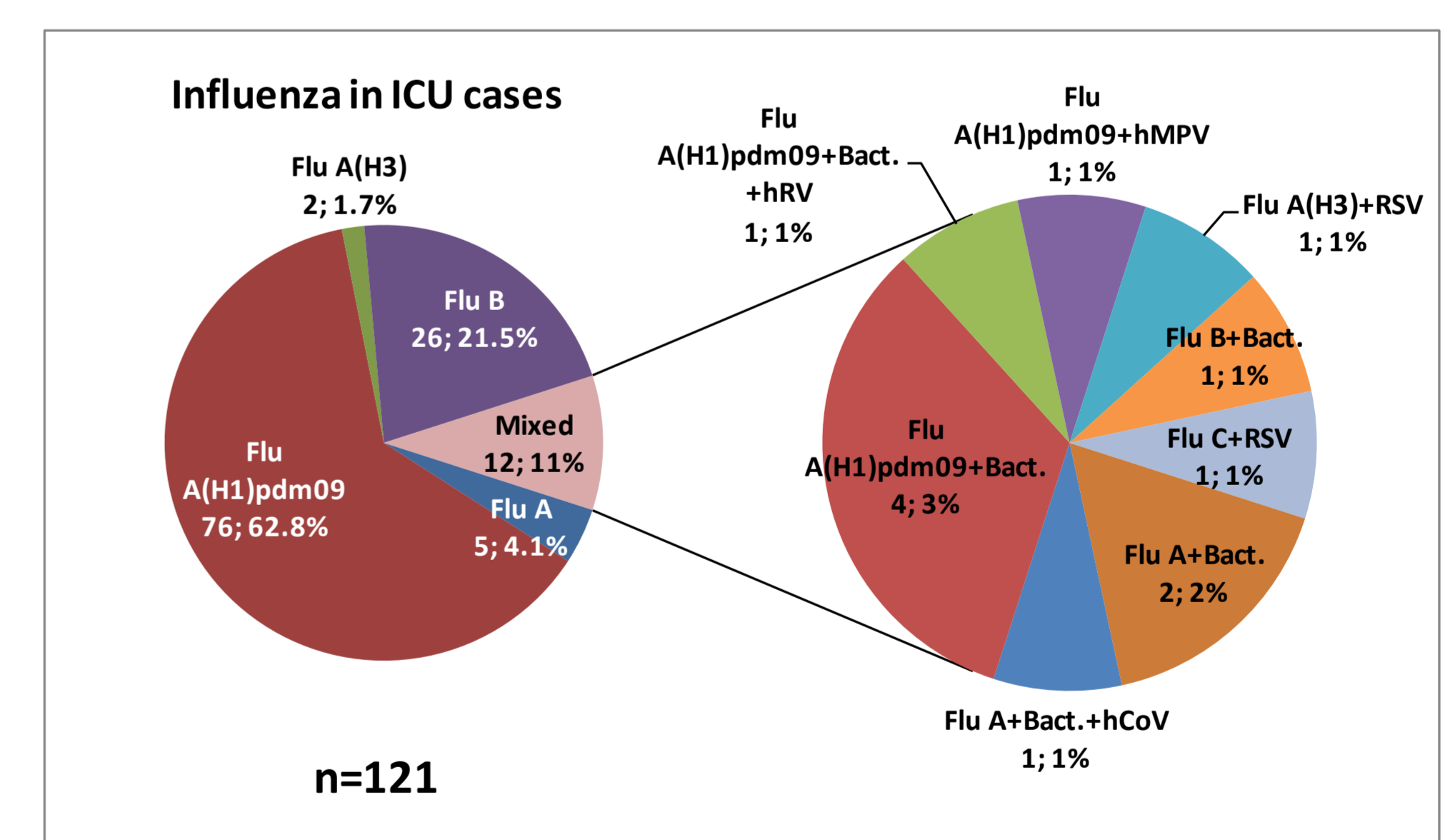


Figure 2 – Influenza viruses detected in ICU cases, reported by the Portuguese Laboratory Network for Influenza in 2012/2013.

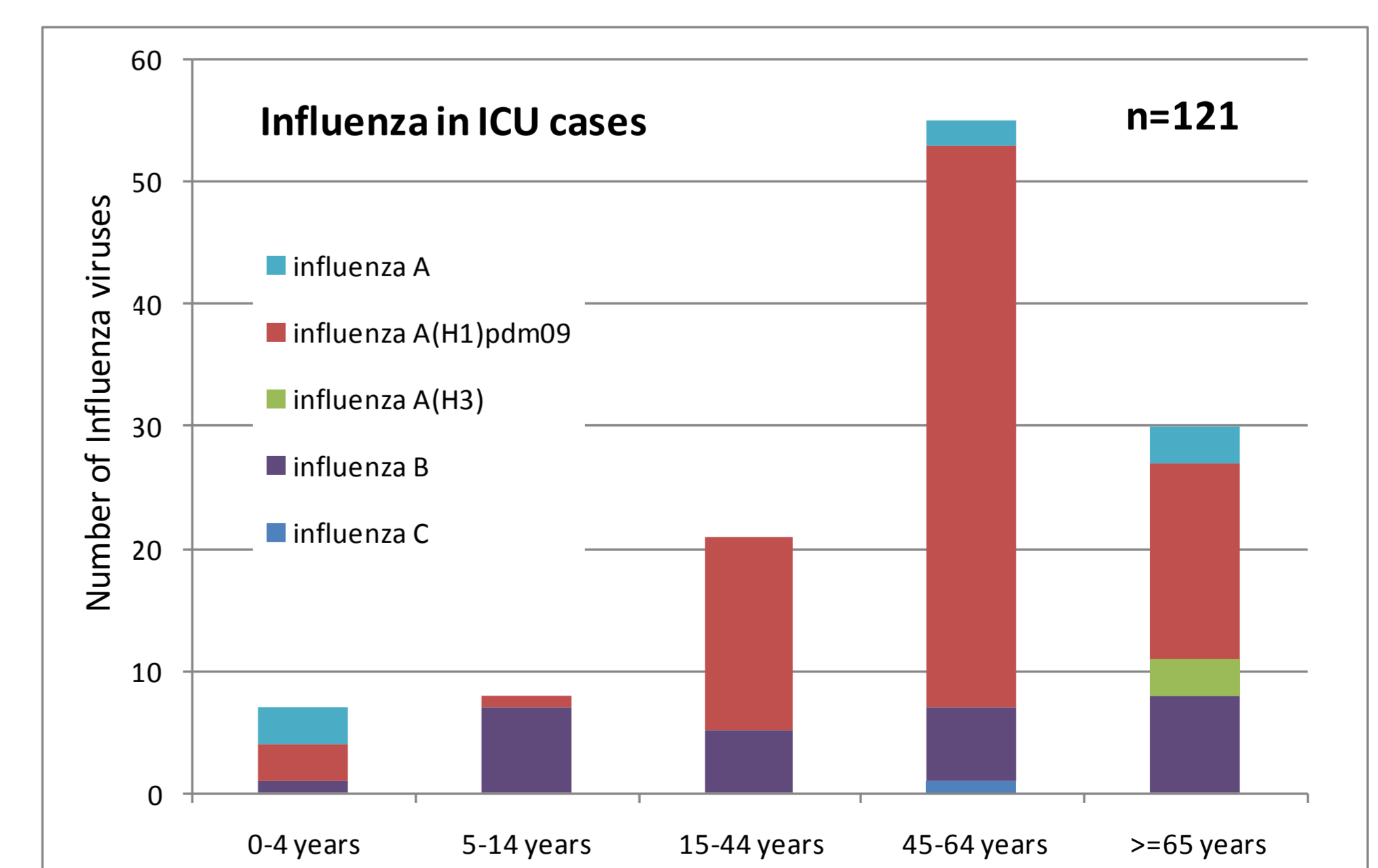


Figure 3 – Influenza ICU cases, reported by the Portuguese Laboratory Network for Influenza in 2012/2013 by age group.