Molecular epidemiology of Respiratory Syncytial Virus between 2010-2015, in Portugal

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Background

Respiratory syncytial virus (RSV) is one of the major causes of respiratory infection and complications in younger children and elderly. Genetic diversity of RSV A and RSV B was for the first time investigated in influenza like illness (ILI) cases, reported in the scope of the Portuguese Influenza Surveillance Programme, between 2010-2015.

Materials and Methods

During 2010-2015, nasopharyngeal swabs sent to the National Influenza Reference Laboratory from sentinel and non-sentinel network were tested for RSV A and RSV B by real time multiplex RT-PCR. Nucleotide sequence of a fragment of the hypervariable C-terminal region of the G protein gene and the phylogenetic analysis was performed for an half of detected RSV.

Results

Over the study period were detected 114 (5.2%) RSV in 2187 tested NPS. Of these 67 (59%) were from subtype A and 47 (41%) from subtype B. Circulation of RSV preceded or was coincident with the influenza epidemic period. RSV A was predominant in each winter with exception for 2014/2015 winter when RSV B was predominantly detected. Of the RSV positive samples, 53 (46,5%) were successfully sequenced and genetically characterized: 24 (45%) RSV A and 29 (55%) RSV B. RSV A clustered in two genotypes (Figure 1): most viruses (n=20; 83%) belonged to ON1 genotype while 4 (17%) viruses belonged to NA1 genotype. Since 2012/2013 season, only ON1 genotype was detected. All RSV B present a BA-like genotype (Figure 2). Most of them (19/29; 66%) clustered within BA9 genotype, the other strains clustered within BA10 genotype. BA9 and BA10 genotypes were detected over all the study period.

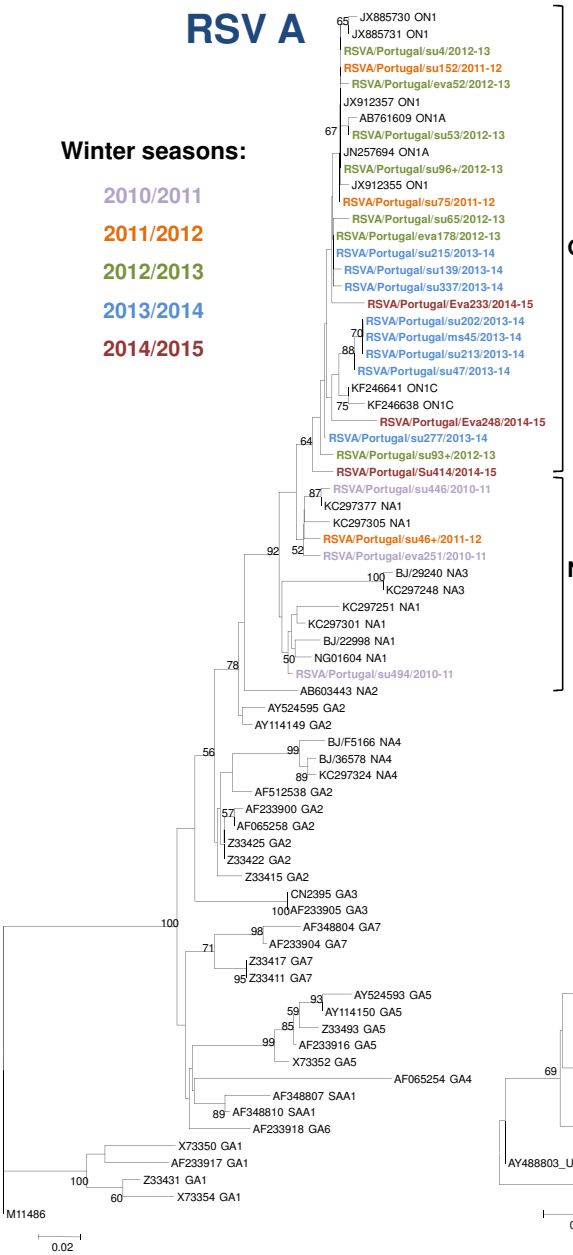

Figure 1 – Neighbour Joining phylogenetic tree based on the C-terminal region of G protein coding sequence of detected RSV A. Was used the Kimura-2 parameter substitution model, bootstrap values above 50 are shown (500 replicates).

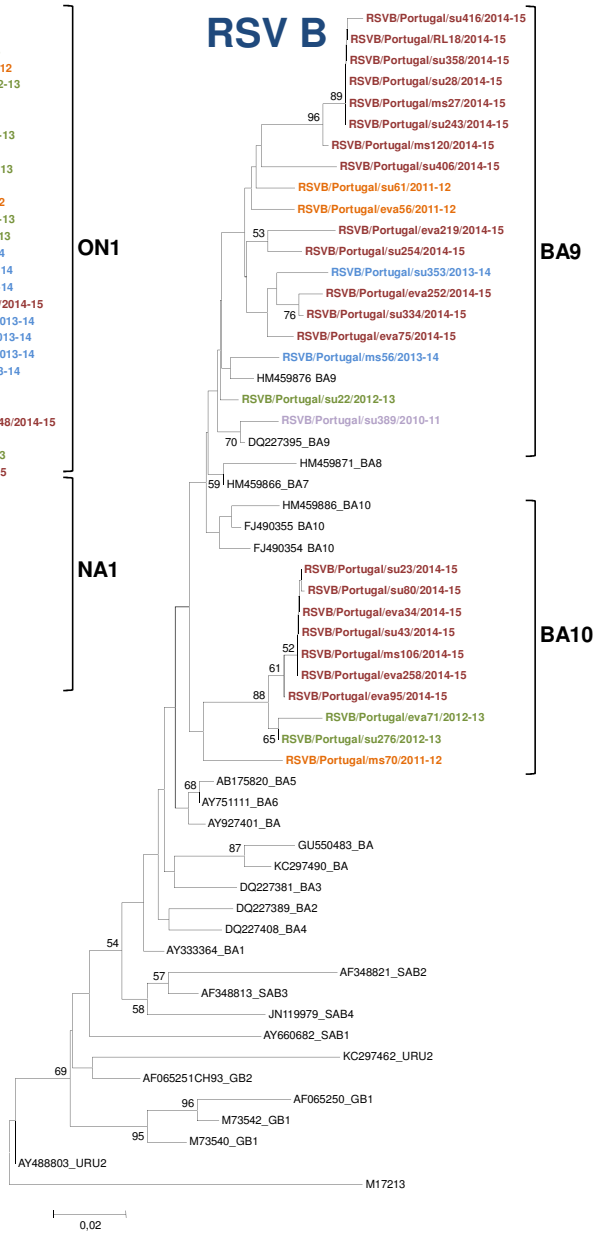

Figure 2 – Neighbour Joining phylogenetic tree based on the C-terminal region of G protein coding sequence of detected RSV B. Was used the Kimura-2 parameter substitution model, bootstrap values above 50 are shown (500 replicates).

Conclusions

Our study highlights the importance of RSV in ILI cases, showing a seasonal circulation each winter season during influenza epidemic. RSV accounted for 5.2% of the cases reported in the scope of influenza surveillance, assuming a huge importance in young children and elderly. Molecular data for RSV A revealed co circulation of NA1 and ON1 between 2010-2012. After this period, ON1 was exclusively detected suggesting a strain replacement by this antigenically advantageous genotype. Globally ON1 is also predominantly detected. For RSVB subtype was observed the circulation of only BA genotypes (BA9 and BA10), which were first identified in 1999 in Buenos Aires and since then are predominant in many countries.

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