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**Recent advances in molecular diagnosis and epidemiology of viral respiratory infections**

# Predominance of ON1 and BA9 genotypes among circulating human respiratory syncytial viruses at a tertiary care university hospital in Catalonia (Spain) during the 2013-2014 season

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**OBJECTIVE:** Human respiratory syncytial virus (HRSV) is the most common respiratory pathogen and the main cause of lower respiratory tract infections among infants and young children. HRSV is also recognised as a significant respiratory pathogen among immunosuppressed and elderly patients. Antigenic and genetic differences led to classify HRSV in two different groups, HRSV-A and HRSV-B. In addition, several genotypes of each HRSV group have been described. Palivizumab, an HRSV-specific humanized monoclonal antibody that binds a highly conserved region of the HRSV fusion (F) protein, is currently used as prophylaxis for paediatric patients at high risk of severe infection. Mutations within this region might be associated with resistance. In the present study we describe the genetic diversity of circulating HRSV strains from patients attended at the Hospital Universitari Vall d'Hebron in Barcelona (Spain) during the 2013-2014 season.

**METHODS:** From October 2013 to May 2014, respiratory specimens were collected from infants, children and adults for laboratory confirmation of HRSV infection using immunochromatography, immunofluorescence or real-time multiplex RT-PCR methods. A nucleoprotein-specific real time RT-PCR was performed to differentiate between HRSV-A and –B groups. Phylogenetic analysis and molecular characterisation from a representative sampling of laboratory-confirmed cases were carried out based on the complete sequences of the second hypervariable region (HVR-2) of the attachment G protein. Molecular characterisation of the antigenic site A of the F protein was also done from a random selection of strains belonging to the different genotypes.

**RESULTS:** A total of 3571 specimens (2271 patients) were collected, of which 334 (9%) specimens from 320 (14%) patients were positive: HRSV-A (74; 23%), HRSV-B (224, 70%), HRSV-A/B coinfection (6; 2%) and HRSV untyped (16; 5%). The maximum detection rate was in the 52/2013 week. Almost 70% of confirmed cases were infants aged under two years. The phylogenetic analysis (50 HRSV-A and 80 HRSV-B strains) revealed that the HRSV-A strains belonged to the genotypes ON1 (49, 98%) and NA1 (1, 2%); and HRSV-B strains belonged to the genotypes BA9 (77, 96%), BA10 (2, 3%) and an undefined BA (1, 1%). Some phylogenetic subgroups could be differentiated in the most representative genetic clusters. Molecular characterisation of the F protein (52 strains) revealed two amino acid substitutions, of which the K272M mutation was previously related to Palivizumab resistance.

**CONCLUSION:** The present study reports recent valuable data that describes the genetic diversity of the HRSV strains during the 2013-2014 season in Spain. Co-circulation of both HRSV-A and HRSV-B was reported, with the high predominance of the HRSV-B. Although several genotypes have been described in this study, the great predominance of ON1 (HRSV-A) and BA9 (HRSV-B) genotypes on circulation should be noted. This report also highlights the importance of an active surveillance for the likely emergence of Palivizumab resistant strains.