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Molecular characterization of rhinoviruses detected at a tertiary university hospital during the 2014-2016 seasons in Catalonia (Spain)

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Background: Rhinoviruses (RVs) are usually related to the common cold, and indeed, to the majority of non-influenza-related viral mild upper respiratory tract infections. But RV infection has been increasingly associated with severe respiratory diseases such as bronchiolitis, pneumonia and asthma exacerbations. On the basis of genetic and antigenic features, more than 100 RV types can be distinguished within the main three species (A, B and C). The aim of this study was to describe the genetic diversity of RV from patients who were attended at Vall d'Hebron University Hospital from 2014 to 2016 in Catalonia, Spain.

Material/methods: From October 2014 (week 40/2014) to November 2016 (week 47/2016), including the 2015 and 2016 inter-seasonal periods, respiratory tract specimens from patients with suspicion of respiratory tract infection (RTI), who were attended at the emergency care unit or admitted to our hospital, were collected for respiratory viruses laboratory-confirmation. The RV detection was carried out by PCR-based assays (Anyplex II RV16 Detection Kit, Seegene, Korea). A specific quantitative real-time one-step qRT-PCR (Granados A et al. 2012) was additionally carried out to establish a cycle-threshold cut-off to determine the suitability of molecular characterisation based on VP4/2 sequencing. Those samples with a Ct value under 35 were genetically characterised by phylogenetic analysis of VP4/2 sequences.

Results: A total of 14,313 specimens (9,105 cases) were received at the Virology Unit, of which 1822 (12.7%) samples (1176 patients, 13%) were RV laboratory-confirmed. A clear pattern of circulation could not be defined based on weekly-detection distribution. A 73.4% (1337) of samples showed Ct values under 35, which were selected for molecular characterisation. Phylogenetic analysis of 995 (74%) VP4/2 sequences revealed that 632 (63.5%) belonged to specie RV-A, 56 (6%) to specie RV-B, and 264 (26.5%) to specie RV-C. A high genetic diversity were found within the three RV species, but the predominant RV types by specie were A19 (21, 3.3%), A29/44 (19, 3%), A31/47 (20, 3.1%), A49 (32, 5%), A50 (20, 3.1%), A78 (24, 3.8%) in specie RV-A; B70 (6, 11%) and B72 (6, 11%) in specie RV-B; and C12 (31, 12%), C15 (20, 7.5%), C2 (34, 13%), C25 (20, 7.5%) in specie RV-C. No statistically significant differences were found between the different species and group ages ($p=0.56$).

Conclusions: Based on phylogenetic analysis of VP4/2 sequences, multiple RV types were detected in patients with RTI attended in our hospital. Co-circulation of RVs belonging to the three species was reported in the present study, although those belonging to RV-A showed the highest predominance. But, further studies should be done to associate these virological findings with clinical features to describe a likely relationship of a particular RV specie or type with the clinical outcome.