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P0102 High genetic similarity between rhinoviruses and enteroviruses remains as a pitfall for molecular diagnostic tools: a three-year overview

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Background

Enteroviruses (EVs) and rhinoviruses (RVs) belong to the *Enterovirus* genus within the *Picornaviridae* family, and show a high genetic similarity. Both viruses are mostly related to mild diseases, especially RVs, but EVs infections can sometimes lead to more severe complications, such as myocarditis, meningitis or acute flaccid paralysis. Hence, current diagnostic molecular techniques should discriminate between both viruses for an exact diagnostic result. The aim of the present study was to revise the EV and RV PCR-confirmed specimens by using a sequencing method for their genetic characterisation.

Materials/methods

From October 2014 (week 40/2014) until May 2017 (week 20/2017), respiratory tract specimens were collected from patients attended at Vall d'Hebron University Hospital with suspicion of respiratory infections. Respiratory viruses' laboratory-confirmation was carried out by commercial multiplex real-time RT-PCR assays (Anyplex II RV16 detection kit or Allplex Respiratory Panel Assays, Seegene, Korea). Genetic characterisation of all EV and RV with Ct values under 35 was performed based on the phylogenetic analyses of partial VP1 and VP4/2 sequences, respectively.

Results

From 19,957 tested specimens, 309 (1.5%) were EV-positive, 2,546 (12%) were RV-positive, and 233 (1%) were EV/RV co-detections. The phylogenetic analysis of the partial VP1 and VP4/2 sequences revealed that: among single EV detections, 177/309 (57%) were characterised as EV, 2/309 (1%) as RV, and 130/309 (42%) could not be typed; among single 1,771 RV detections (Ct<35), 1,651/1,771 (93%) were characterised as RV, 3/1,771 (0.3%) as EV (2 EV-D68 and 1 CV-B5) and 117/1,771 (6.7%) could not be typed. Among EV/RV co-detections, 62/233 (27%) were characterised as EV, 130/233 (56%) as RV and 41/233 (17%) could not be typed.

Conclusions

The number of EV/RV co-detections by a multiplex PCR assay was small. However, the genetic characterisation confirmed that an important percentage of these co-detections (56%) were real RVs, and in a minor proportion (27%), EV. Diagnostic PCR-based assays are still not able to discriminate correctly between both viruses. The potential relatedness of EV to neurological complications makes their monitoring mandatory, so the differentiation of both viruses in commercial PCR assays should be more accurate for an early detection.