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A novel human metapneumovirus carrying a 180-nucleotide duplication within the coding G protein region detected at a tertiary university hospital in Catalonia since the 2104-2015 season

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Background: HMPV is an aetiologic agent of respiratory tract infection (RTI) in both children and adults. It shows a seasonality pattern with detection peaks in late winter and spring. It is an enveloped, negative-sense, single-stranded RNA virus belonging to *Pneumoviridae* family together with human respiratory syncytial virus (HRSV). Fusion (F) and glycosylate (G) proteins are the major envelope glycoproteins, and the most widely used for epidemiological studies. HMPV is classified into two genotypes (A and B), subdivided into 4 subgenotypes (A1, A2, B1 and B2) and even into lineages (A2a and A2b).

Material/methods: Respiratory specimens from patients with RTI suspicion attended at Hospital Universitari Vall d'Hebron (Barcelona, Spain) were collected from October 2014 to October 2016 for virological diagnosis. All samples were HMPV laboratory-confirmed by immunofluorescence or real-time multiplex RT-PCR assays. Both partial viral coding G and F protein regions were sequenced to perform phylogenetic analyses and molecular characterisations with MEGA v5.2.

Results: A total of 13,742 specimens were studied from 10,010 patients, of which 270 (2%) samples of 255 (3%) patients were HMPV laboratory-confirmed. Its prevalence increased from 2.44% (2014-2015) to 3.15% (2015-2016). Detection peaks were shown from February to April in both seasons. While during the 2014-2015 season HMPV mainly affected children under 5 years of age (48/90, 53%), in the 2015-2016 season HMPV affected the elderly population (60/151, 40%). Both HMPV genotypes simultaneously co-circulated, but HMPV-B was predominant in the 2014-2015 season whereas HMPV-A was predominant in the 2015-2016 season.

Phylogenetic analyses revealed that 10 (4%) viruses belonged to A2a, 121 (47%) to A2b, 64 (25%) to B1 and 48 (19%) to B2. Within A2b, sequences were distinguished as A2b1 (34, 28%) and A2b2 (87, 72%) sublineages. Twelve (5%) sequences could not be amplified and one (>1%) was detected as a coinfection A/B. Molecular characterisation of partial coding G protein region revealed that 18/87 (21%) A2b2 viruses were carrying a 180-nucleotide duplication within the G protein, in addition to 2 (2%) carrying a 111-nucleotide duplication in a close region. Moreover, viruses carrying the 180-nucleotide duplication seem to increase their prevalence in the second season (2014-2015, 2/13, 15%; 2015-2016, 15/66, 23%; interseason 2016, 1/8, 13%), but without statistical differences (P=0.55).

Conclusions: Recent and valuable data about prevalence, seasonality and genetic diversity of HMPV in Catalonia is reported. The present study is the first description of HMPV carrying a genetic duplication event within the coding G protein region. Due to the higher relative percentage of 180-nt duplication viruses during the last season, these might become predominant in the future, as already described for ON-1 and BA HRSV. However, continuous virological surveillance is required both to monitor their spreading and to associate them with changes in clinical features.