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**Genotype variability of human metapneumovirus isolated from Korean children, 2007-2013**

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**Background:** Human metapneumovirus (hMPV) is a pathogen of the respiratory tract with a worldwide distribution. hMPV is subdivided into several genotypes with a predominant circulating genotype that varies from year to year. The purpose of this study was to evaluate the contribution of hMPV to viral respiratory tract infections and to determine the genotype variability of hMPV in Korean children.

**Material/methods:** We investigated 14,853 nasopharyngeal aspirates of pediatric patients who were referred for a respiratory virus test by reverse transcription polymerase chain reaction (RT-PCR). hMPV genotype analysis was performed using a nested PCR-restriction fragment length polymorphism (RFLP) assay for the fusion (F) gene. Fifteen unidentified samples, which revealed previously unknown bands in genotyping, were sequenced and subjected to phylogenetic analysis.

**Results:** Seven hundred and ninety-three of 14,853 (5.3%) aspirates were positive for hMPV. Nested PCR-RFLP analysis clearly identified four hMPV genotypes (A2a, A2b, B1, and B2) in 98.0% of patients. The predominant genotype of hMPV changed over the 7-year period in the following order: A2a - B2 - B2 - A2a - B1 - B1 - B2. Throughout the entire period, the most common genotype was A2a (43.3%). Results of sequencing and phylogenetic analysis showed that the sequences of unidentified strains were very similar to genotype B1 or B2, though several had not been reported previously.

**Conclusions:** This large-scale, 7-year study determined the contribution of hMPV to viral respiratory tract infections and identified the genetic diversity of hMPV in Korea. We expect that this study may help reveal the characteristics of hMPV propagation.