

**P1133 Ten year molecular epidemiology of human metapneumovirus in South Korea**Mi-Kyung Lee<sup>\*1</sup>, Yong Kwan Lim<sup>1</sup>, Oh Joo Kweon<sup>1</sup>, Hye-Ryoun Kim<sup>1</sup>, Tae-Hyoung Kim<sup>2</sup><sup>1</sup> Department of Laboratory Medicine, Chung-Ang University College of Medicine, <sup>2</sup> Department of Urology, Chung-Ang University College of Medicine

**Background:** Human metapneumovirus (hMPV) is one of the most common cause of upper and lower respiratory tract infections. hMPV could be classified into several genotypes, however data on long-term circulation of genotypes are limited. We analyzed a long-term surveillance series on hMPV in Korea from 2007 to 2016, and characterized seasonal dynamics in virus prevalence and genotype variability.

**Materials/methods:** Total 23,550 upper respiratory specimens were enrolled in this study. For hMPV positive samples, hMPV genotyping analysis was performed using a nested PCR-restriction fragment length polymorphism assay or direct sequencing analysis targeted to the fusion (F) gene.

**Results:** 1,272 of 23,550 specimens (5.4%) were positive for hMPV. hMPV genotyping could identify four hMPV genotypes (A1, A2a, A2b, B1, and B2) in 91.4% of patients. Prevalence was low in summer and fall, but increased in winter with a peak in April. The most common hMPV genotypes were following order; A2a, B1, B2, A2b, and A1.

**Conclusions:** This large-scale, 10-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.

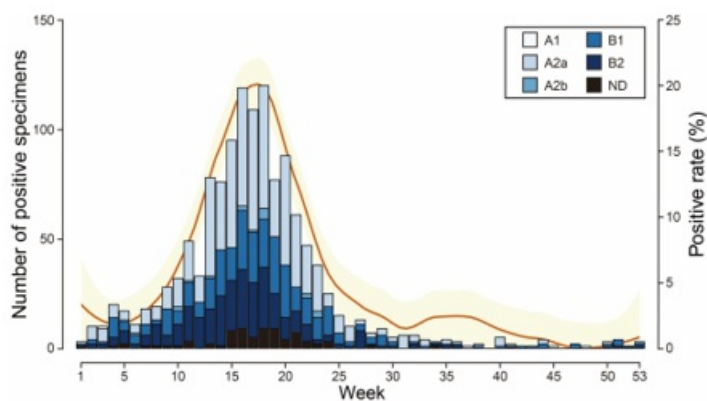


Figure 1. Number of human metapneumovirus (hMPV) positive specimens (blue boxes) and hMPV positive rate (orange line) with 95% confidence interval.