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Abstract (poster session)

**Genotype variability and clinical features of human metapneumovirus Isolated from Korean children, 2007-2010**

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**Objectives:** Human metapneumovirus (hMPV) has been divided into five subgroups based on variations of the hMPV F gene. This study was undertaken to determine the genotype variability of hMPV, its circulation pattern in over a 3.5 year period, and to evaluate its clinical characteristics in Korean children. **Methods:** We investigated 325 of 4599 pediatric patients with a positive nasopharyngeal aspirate that were referred for a routine respiratory virus test for hMPV by RT-PCR. HMPV genotype analyses were performed using a nested PCR-restriction fragment length polymorphism (PCR-RFLP) assay. Clinical and laboratory data obtained from medical records were reviewed retrospectively. **Results:** 325 (7.1%) of the 4599 samples tested were positive for hMPV, and the co-infection rate among these 325 was 16%. Nested PCR-RFLP analysis clearly identified four of the five previously described hMPV genotypes (A2a, A2b, B1 and B2) in 97.8%. The predominant genotype of hMPV changed over the 3.5-year study period from genotype A2a to B2 and then back to A2a. The most common genotype was A2a (214/325, 65.8%). Evidence of recurrent infection was obtained in one child only. Lymphocytosis was more frequent in children with a co-infection, but sputum was less frequent than in children with a single infection ( $P < 0.05$ ). In genotype A2a hMPV infected-children, sneezing and neutrophilia were more frequent than in genotype B1 or B2 hMPV-infected children **Conclusion:** This 3.5-year study broadens knowledge regarding the prevalence, the seasonal incidence, the occurrences of co-infection and re-infection, and the genotype diversity of hMPV in Korea.