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Abstract (poster session)

Co-circulation of genetically distinct human metapneumovirus and human bocavirus strains in children with respiratory tract infections in southern Greece

V. Pogka*, A. Moutousi, A. Kossyvakis, M. Giannaki, D. Sgouras, A.F. Mentis (Athens, GR)

Objectives: Our aim was to evaluate the genetic diversity of the newly recognized and poorly studied, within the Greek population, human metapneumovirus (hMPV) and human bocavirus (hBoV) positive strains, during the winter period of three consecutive years (2005-2008), comparing them with the main, already characterized, genetic lineages for each virus. Methods: Rhinopharyngeal or throat swabs from 3307 patients aged 0-18 yo, diagnosed with respiratory tract infections (RTI), were collected over the winter period of the years 2005-2008. Molecular assays, including a conventional PCR specific for the F gene of hMPV and a real-time PCR specific for the NP gene of hBoV, were employed for detection of the viruses. Viral strains selected throughout the study period where further amplified using non-conserved regions, including full-length G gene of hMPV (Hoogen et al, Emerg Infect Dis 2004) and VP1/VP2 gene of hBoV (Chieochansin et al, Virus Res 2007), for genotypic characterization. Results: HMPV presence was confirmed in 188 (5.7%) samples and hBoV presence in 193 (5.8%) samples. Twenty four hMPV-positive samples were characterized at the molecular level and presented with a nucleotide (nt) identity of 92-100% and an amino acid (aa) identity of 85.9-100.0% to each other. Phylogenetic analysis revealed circulation of 4 different subclusters, based on the number of aa differences, belonging to genetic lineage B2 within the Greek population. Sequencing analysis of 26 hBoV positive strains showed a nt identity of 98.2-100.0% and a deduced aa identity of 95.6-100.0% to each other. The above analysis also indicated that 2 (7.7%) of them clustered into genotype St1 and 22 (84.6%) into genotype St2. Co-circulation of hBoV genotypes St1 and St2 was observed during the second and the third study period. The remaining 2 (7.7%) studied strains formed a third cluster that may have resulted from a recombination event between different viral isolates circulating during the same period. Conclusion: Phylogenetic analysis revealed circulation of different subclusters of hMPV, based on the number of aa differences they shared and a mixture of hBoV genotypes, circulating within the Greek population during the winter season of three consecutive years. All hMPV strains belonged to lineage B2 while hBoV genotype St2 predominated. Similar results were also observed in other European studies, such as Spain, Italy and Germany.