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Prevalence and genetic characterization of enterovirus D68 among children with severe acute respiratory infection in China

W. Tan 1, 2, *, Y. Wang 1, 2, Y. Zhao 1, 2, R. Lu 1, 2
1 National Institute for Disease Control and Prevention, China
2 CDC, Beijing 102206, China

To understand the prevalence and molecular typing of enterovirus D68 among children with severe acute respiratory infection (SARI) in Beijing and Shanghai, 385 respiratory samples were collected from in Beijing during 2008–2010, and 441 respiratory samples were collected in Shanghai city between 2013 and 2014. All the samples were used for the screening of EV-D68 by nest RT-PCR and sequencing, then EV-D68-positive samples were used for the complete genome sequencing through overlapping PCR. All available EV-D68 full-length genomes collected from GenBank were used for phylogenetic analysis and comparison of EV-D68 types prevalent in China and America. One (0.4%) from 385 respiratory samples in Beijing was positive for EV-D68, and 4 (0.9%) among the 441 samples from Shanghai were positive for EV-D68. Phylogenetic analysis of full length genome indicated that the EV-D68 prevalent in Beijing (BJ24) belong to Clade A2 and Clade B2, different from the American popular strains (Clade A1, Clade B1, Clade B4 and Clade B5). Partial sequence analysis declared phylogenetic conflict among different gene sequences. We concluded that the prevalence rate of EV-D68 among SARI Children in Beijing and Shanghai currently was lower (5/700; <1%), and the EV-D68 genotype prevalent in China and America belong to different clusters. Partial sequence analysis indicated that intratypic recombinant events may occur in EV-D68 prevalent in China.

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Replication and immune response in HAE of HCoV-HKU1 isolate from a pediatric patient with severe acute respiratory infection

N. Zhu *, R.J. Lu, W.J. Tan
National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China

Human coronavirus HKU1 (HCoV-HKU1), a fastidious cultured β-coronavirus, was associated with acute respiratory infection in the aged and children. Human airway epithelium cells (HAE) provide the first line of defense in the respiratory tract and are the main target of HCoV-HKU1. However, little attention has been devoted to immune response of HAE induced by HCoV-HKU1, maybe due to its fastidious culturing. Here, we isolated a novel strain of HCoV-HKU1 (BJ-01) from a pediatric patient with severe acute respiratory infection (SARI) and propagated on HAE. This strain of virus owned the typical morphology of coronavirus with the diameter of 120–130 nm. The genome HCoV-HKU1 BJ-01 is divided into different groups: Chemokines (CCL4, CCL13, CCL15, CCL16, CCL24, CCL26, CCLX13, XCL1), Hematopoietins (IL23R, TSLP, PRL, GHR), PDGF family (PDGFC, KITLG), IL-10 family (IL20RA), IL-1 family (IL1R1), TNF family (SF11B, LTA, SF1B), TGF-β family (BMP7, BMPR1B), which mainly affect Chemokine/NF-KAPPA B/PI3K-AKT/JAK-STAT signaling pathway on HAE cells. This work was the first report on immune response in HAE of a novel HCoV-HKU1 strain (HCoV-HKU1 BJ01) from a pediatric patient with SARI.

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Development of an external quality assessment panel for the molecular detection of respiratory viruses

E. Elenoglou *, F. Kartal, B. Kele, H. Seyedzadeh, P. Jovanovic, S. Rughooputh, C. Walton
Public Health England, United Kingdom

Background: Respiratory virus infections occur commonly and are responsible for a significant amount of morbidity worldwide. In the developed world respiratory viruses are responsible for a considerable amount of morbidity which has a significant economic impact. Mortality rates however are low. In contrast, in developing countries, viruses are responsible for approximately 20–30% of respiratory deaths in children. The spectrum of disease ranges from upper respiratory tract infections such as common colds to infections of the lower respiratory tract manifesting as bronchiolitis or pneumonia.

Respiratory Syncytial Virus (RSV) is the most common cause of lower respiratory tract infection in infants and children worldwide. Most frequent types of influenza viruses that affect individuals are Influenza A and B, however rhinoviruses are the common cause of coughs and colds during winter with a peak season in the UK to be between January and March.

The elderly and infant population tend to be the most susceptible to these viral illnesses. The availability of an External Quality Assessment (EQA) panel for the Molecular Detection of Respiratory viruses is crucial for providing objective evidence in the quality of testing with a request.

Materials and methods: A pilot distribution, containing 9 specimens was sent out to 23 participants. Three simulated throat swabs and six simulated freeze-dried nasopharyngeal aspirate material (Specimen numbers were 3642–3650) were dispatched for testing for respiratory pathogens using molecular methods. The swab specimens were distributed in a Phosphate Buffer Solution (PBS) based solution with a different cell line added in each of them. The freeze dried specimens were distributed in a sucrose based matrix. Simulated specimens were positive for Parainfluenza virus type one (PIV-1), Adenovirus type 2 (AdV-2) and Influenza B (FluB).

Results: Out of 23 participants, 21 returned their results. Only one laboratory detected PIV-1 in specimen 3642. PIV-1 was correctly reported for specimen 3643 mainly by those laboratories who have used in-house real-time multiplex/single target PCR assays. RespiFinder was the only commercially available multiplex real-time assay that was able to detect PIV-1 in specimen 3643.

Adenovirus type 2 was successfully detected for specimens 3644, 3645 and 3649 by all those laboratories tested 100% for PIV-1. PIV-1 was co-distributed for specimen 3643 mainly by those laboratories who have used in-house real-time multiplex/single target PCR assays. RespiFinder was the only commercially available multiplex real-time assay that was able to detect PIV-1 in specimen 3643.