

Abstract

Background: Human coronavirus NL63 (HCoV-NL63) is an important global respiratory pathogen among infants and young children. We evaluate the epidemics and diseases spectrum about the HCoV-NL63 infection in children in Taiwan.

Material and methods: Children with respiratory diseases who admitted to NTUH were enrolled in this study from May 2004 to Apr 2005. Real-time RT-PCR designed for nucleocapsid gene of HCoV-NL63 was used to screen the nasopharyngeal aspirate (NPA) samples and 1b gene primers were used for reconfirmation. Other respiratory virus pathogens were detected by virus culture, antigen test, serology and RT-PCR. The NC gene of positive samples were sequenced and compared to those reported in the literature.

Results: 539 NPA samples from children with respiratory diseases was enrolled in one year and at least one viral pathogen was detected in 187 samples. Seven cases (1.3%) of positive HCoV-NL63 NPA were detected, represented 3.7% among all viral pathogens. One, three and one case occurred in August, October and February, respectively. All cases were male and two of them had underlying morbidity. The age of patients ranged from 8 month to 2-year-10-month. Other respiratory pathogens were co-infected in 3 cases, which was respiratory syncytial virus, adenovirus and *Mycoplasma pneumoniae*, and human metapneumovirus, respectively. The most common symptoms/signs of HCoV-NL63 infection among children admitted were cough (100%, ranged from 3 to 13 days), fever (71.4%, average 2 days) and stridor (71.4%). The most common diagnosis of HCoV-NL63 infection among children admitted were croup (71.4%), pneumonia (28.6%) and tonsillitis (28.6%), which was different from those reported in the literature. The admission duration was ranged from 2 to 5 days and all cases were discharged smoothly. In our study, HCoV-NL63 was the most predominant pathogen in children with diagnosis of croup (5/34), which was followed by parainfluenza type 3 , influenza B and parainfluenza type 1. Amplicon of nucleocapsid gene of three positive samples were sequenced and those were very similar to other strains in the literature.

Conclusion: HCoV-NL63 was an important respiratory pathogens in Taiwan and the disease spectrum and seasonal distribution were different from those in temperate areas. It may be an important pathogen of croup in our study. Further serology study for this virus was necessary.

Key words: human coronavirus NL63 , respiratory tract disease, real time reverse-transcript polymerase chain reaction , croup , Taiwan

Background: Human coronavirus NL63 (HCoV-NL63) is an important global respiratory pathogen among infants and young children. We evaluate the epidemics and diseases spectrum about the HCoV-NL63 infection in children in Taiwan.

Material and methods: Children with respiratory diseases who admitted to NTUH were enrolled in this study from May 2004 to Apr 2005. Real-time RT-PCR designed for nucleocapsid gene of HCoV-NL63 was used to screen the nasopharyngeal aspirate (NPA) samples and 1b gene primers were used for reconfirmation. Other respiratory virus pathogens were detected by virus culture, antigen test, serology and RT-PCR. The NC gene of positive samples were sequenced and compared to those reported in the literature.

Results: 539 NPA samples from children with respiratory diseases was enrolled in one year and at least one viral pathogen was detected in 187 samples. Seven cases (1.3%) of positive HCoV-NL63 NPA were detected, represented 3.7% among all viral pathogens. One, three and one case occurred in August, October and February, respectively. All cases were male and two of them had underlying morbidity. The age of patients ranged from 8 month to 2-year-10-month. Other respiratory pathogens were co-infected in 3 cases, which was respiratory syncytial virus, adenovirus and *Mycoplasma pneumoniae*, and human metapneumovirus, respectively. The most common symptoms/signs of HCoV-NL63 infection among children admitted were cough (100%, ranged from 3 to 13 days), fever (71.4%, average 2 days) and stridor (71.4%). The most common diagnosis of HCoV-NL63 infection among children admitted were croup (71.4%), pneumonia (28.6%) and tonsillitis (28.6%), which was different from those reported in the literature. The admission duration was ranged from 2 to 5 days and all cases were discharged smoothly. In our study, HCoV-NL63 was the most predominant pathogen in children with diagnosis of croup (5/34), which was followed by parainfluenza type 3, influenza B and parainfluenza type 1. Amplicon of nucleocapsid gene of three positive samples were sequenced and those were very similar to other strains in the literature.

Conclusion: HCoV-NL63 was an important respiratory pathogens in Taiwan and the disease spectrum and seasonal distribution were different from those in temperate areas. It may be an important pathogen of croup in our study. Further serology study for this virus was necessary.

Key words: human coronavirus NL63, respiratory tract disease, real time reverse-transcript polymerase chain reaction, croup, Taiwan