

## Editorial

# Emerging Respiratory Viral Infections

Infectious diseases are the second leading cause of death and the leading cause of disability-adjusted life years<sup>1</sup>. Despite earlier predictions to the contrary, infectious diseases remain a dominant feature of domestic and international public health considerations for the 21st century. In fact, the continual evolution of emerging and reemerging diseases will heighten the global impact of infectious diseases. At the dawn of the 21st century, the future of infectious diseases and its impact on societies throughout the world is strikingly apparent. The successful diagnosis, prevention, and treatment of a wide array of infectious diseases have altered the very fabric of society, providing important social, economic and political benefits. Like pandemic influenza, which has had an extraordinary impact on global health, there is a continual evolution of a wide range of emerging and reemerging infectious diseases with varying potentials for global spread.

Respiratory infections are among the most common causes of morbidity and mortality worldwide. These infections present a special challenge to physicians for several reasons, including the recent disasters caused by severe acute respiratory syndrome (SARS) and bird and swine influenza. In the developing world, respiratory infections are also a major cause of childhood death, although the contribution of viruses to such deaths is unclear<sup>2</sup>. Recently, a newly identified human respiratory virus, human metapneumovirus (hMPV), was reported by investigators in Netherlands. Human metapneumovirus is a respiratory virus belonging to the family paramyxoviridae<sup>3,4</sup> and its clinical significance is yet to be defined. After its initial discovery in the Netherlands, hMPV has been detected in respiratory specimens from patients of all ages in a number of countries.

Human Meta pneumo virus (hMPV) may be the cause of a significant proportion of both upper and lower respiratory tract infection in infants, children, and adults. The results of several studies suggest that hMPV may account for about 10% of respiratory tract infections in which a common respiratory virus, such as respiratory syncytial virus, or influenza or parainfluenza viruses, could not be detected. hMPV has been detected in patients with either upper or lower respiratory tract disease, or both. Symptoms associated with hMPV include cough, dyspnea, wheeze, and hypoxia. Epidemiological findings suggest that it may circulate worldwide and may have a seasonal distribution. So far this infection is not reported in tropical and subtropical countries.

hMPV infection was associated with clinical diagnoses of pneumonia (36%), asthma exacerbation (23%), or acute bronchiolitis (10%). When compared to those with respiratory syncytial virus infection, children with hMPV infection were older, and wheezing was more likely to represent asthma exacerbation rather than acute bronchiolitis. hMPV viral activity peaked during the spring-summer period. hMPV contributed to 441.6 hospital admissions

per 100,000 population <6 years of age., Approximately one third of patients with hMPV infection were clinically diagnosed to have pneumonia. Over half of the patients with hMPV had influenza like illness reported in one or more of their family contacts (all ages), while 26% reported an adult family member with influenza like illness. Seroepidemiologic data in Netherlands showed that all children are seropositive for hMPV antibody by 10 years of age<sup>3</sup>. Recurrent infection has been documented in a few children, and the virus has also been detected in adults<sup>3,5,6,7,8</sup>. hMPV is only found in a very small number of patients with AE-COPD. However it should be considered as a further possible viral trigger of AE-COPD because asymptomatic carriage is unlikely.

Human bocavirus (HBoV) is another worldwide-distributed respiratory pathogen which is highly diverse, dispersed, recombination prone, and prevalent in enteric infections. Human bocavirus 1 (HBoV1), a member of the parvovirus family, was first identified as a potential human pathogen in the year 2005. HBoV1 is found associated with lower respiratory infections in young children. Recently human bocavirus 2-4 has also been discovered associated mainly with gastroenteritis. HBoV infection is associated with a variety of signs and symptoms which include rhinitis, pharyngitis, cough, dyspnea, wheezing, pneumonia, acute otitis media, fever, nausea, vomiting, and diarrhea. HBoV1 is fairly prevalent in children presenting with acute wheezing. In a particular study, serologic specimen obtained from the patients with acute wheezing were found to be positive for human bocavirus DNA, representing systemic infection.

A new strain of Corona virus has emerged this year in Saudi Arabia. This virus aggressively attacks the lower respiratory system, leading to fever, pneumonia and even death. So far, 17 cases of Corona virus infection have been confirmed by the World Health Organization. Though the number of people affected is less, it has killed 65% of its known hosts and raises concern among health workers.

Viral cause of pediatric respiratory illness is identifiable in up to 95% of cases, but the detection rates decrease steadily by age, to 30-40% in the elderly<sup>9</sup>. The new viruses cause respiratory illnesses such as common cold, bronchitis, bronchiolitis, exacerbations of asthma and chronic obstructive pulmonary disease and pneumonia. Rarely acute respiratory failure may occur. The clinical role of other new viruses, KI and WU polyoma viruses and the torque teno virus, as respiratory pathogens is not clear.

## Reference

1. Anthony S. Fauci, Nancy A. Touchette, Gregory K. Folkers. Emerging Infectious Diseases: a 10-Year Perspective From the National Institute of Allergy and Infectious Diseases. *Emerging Infectious Diseases*. 2005;11(4):519-525.
2. Berman S. Epidemiology of acute respiratory infection in children in developing countries. *Rev Infect Dis*. 1991;13:S454-62.
3. Van Den Hoogen BG, De Jong JC, Groen J, Kuiken T, De Groot R, Fouchier RAM, et al. A newly discovered human pneumovirus isolated from young children with respiratory tract disease. *Nat Med*. 2001; 7:719-24.
4. Van Den Hoogen BG, Bestebroer TM, Osterhaus ADME, Fouchier RAM. Analysis of the genomic sequence of a human metapneumovirus. *Virology*. 2002;295:119-32.

5. Peret TCT, Boivin G, Li Y, Gouillard M, Humphrey C, Osterhaus ADME, et al. Characterization of human metapneumovirus isolated from patients in North America. *J Infect Dis.* 2002;185:1660-3.
6. Stockton J, Stephenson I, Fleming D, Zambon M. Human Metapneumovirus as a cause of community-acquired respiratory disease. *Emerg Infect Dis.* 2002;8:897-901.
7. Pelletier G, Dery P, Abed Y, Boivin G. Respiratory tract reinfections by the new human metapneumovirus in an immunocompromised child. *Emerg Infect Dis.* 2002;8:976-7.
8. Boivin G, Abed Y, Pelletier G, Ruel L, Moisan D, Cote S, et al. Virological features and clinical manifestations associated with human metapneumovirus: a new paramyxovirus responsible for acute respiratory tract infections in all age groups. *J Infect Dis.* 2002;186:1330-4.
9. Jartti T, Jartti L, Ruuskanen O, Söderlund-Venermo M. New respiratory viral infections. *Curr Opin Pulm Med.* 2012 May;18(3):271-8.