Novel and Re-Emerging Human Respiratory Viruses

Essay Submitted for Complete Fulfillment of Master Degree in Medical Microbiology & Immunology

By

Manal Mohammed Sulaiman HallalMBBCh.

Supervisors

Prof. Dr. Nagwa Abdel-Rahman Sedky

Professor of Medical Microbiology & Immunology Faculty of Medicine – Cairo University

Ass. Prof. Dr. Eman Ahmed El-Seidi

Assistant Professor of Medical Microbiology & Immunology Faculty of Medicine – Cairo University

> Faculty of Medicine Cairo University 2008

ABSTREACT

Respiratory infections are major causes of morbidity and mortality worldwide. Viruses are considered an important cause of respiratory disease in both the community and hospital settings and are associated with infection at all levels of the respiratory tract. Respiratory viruses have been grouped into six distinct families including the *Paramyxoviridae*, *Orthomyxoviridae*, *Picornaviridae*, *oronaviridae*, *Adenoviridae* and *Herpesviridae*. However, this list of pathogens was extended with the discovery of novel respiratory viruses. The recent advances in molecular technology have enabled the detection of several new viral agents in specimens collected from the human respiratory tract.

The hMPV was first described in 2001, and is considered a significant respiratory pathogen, particularly of children. The most closely related human virus is the hRSV, with similar epidemiological and clinical characteristics. However on the basis of morphological, biochemical and genetic analyses, hMPV seemed to be closely related to aMPV-C, thus it was classified in the same genus *Metapneumovirus*.

Key Word

Novel and Re-Emerging Human Respiratory Viruses

CONTENTS

Acknowledgment	
List of Common Abbreviations	II
List of Figures	IV
List of Tables	VI
General Overview	1
Viral Respiratory Pathogens	5
Paramyxoviridae	5
Orthomyxoviridae	15
Picornaviridae	22
Coronaviridae	26
Adenoviridae	34
Herpesviridae	40
Human Metapneumovirus	44
Discovery and Classification	44
Structure and Characteristics	47
Genomic Organization	51
Infection of Experimental Animal Models	59
Pathogenesis and Host Response	60
 Infection and Pathogenesis 	60
• Immune Response	64
Epidemiology	69
Clinical Manifestations	79
Diagnosis	89
Treatment and Prevention	95

1. Live attenuated vaccines	97
A. Vectored vaccines	98
B. Deletion mutants	99
C. Chimeric viruses	100
2. Subunit vaccines	101
Infection Control Measures	102
Human Bocavirus	103
Discovery and Classification	103
Structure and Characteristics	105
Genomic Organization	107
Pathogenesis	109
Epidemiology	111
Clinical Manifestations	114
Diagnosis	118
Infection Control Measures	121
Emerging Human Coronaviruses	125
SARS Coronavirus	125
Human coronaviruses NL63 and HKU1	128
Avian Influenza viruses	131
Other Novel Respiratory Viruses	135
KI and WU Polyomaviruses	135
Mimivirus	138
Summary	145
References	147
Arabic Summary	

ACKNOWLEDGEMENT

"First and Foremost, Thanks to Allah, The Beneficent and Merciful of all"

I would like to express my profound thanks and deepest gratitude to **Prof. Dr. Nagwa Abdel Rahman Sedky**, Professor of Medical Microbiology and Immunology, Faculty of Medicine, Cairo University, for her valuable guidance and her continuous support.

My heartful thanks and deep appreciation must go to Ass. Prof. Dr. Eman Ahmed El-Seidi, Assistant Professor of Medical Microbiology and Immunology, Faculty of Medicine, Cairo University, for her clear advices, valuable remarks and her endless cooperation and guidance throughout the preparation of this essay.

I am much obliged to all my colleagues in our Medical Microbiology and Immunology Department for their sincere guidance, generous attitudes and continuous encouragement.

Finally, I would like to address my family and thank them deeply for their patience, unlimited support, enthusiasm and care.

LIST OF COMMON ABBREVIATIONS*

aMPV Avian metapneumovirus

aMPV-C Avian metapneumovirus serotype C

ARTI Acute respiratory tract infection

CoV(s) Coronavirus(es)

E protein Envelope protein

F protein Fusion protein

G protein Attachment glycoprotein

HA Haemagglutinin

HBoV Human bocavirus

hMPV Human metapneumovirus

HPAI Highly pathogenic avian influenza viruses

hRSV Human respiratory syncytial virus

KIV KI polyomavirus

L protein Large polymerase protein

LRTI(s) Lower respiratory tract infection(s)

M protein Membrane protein or Matrix protein

MAbs Monoclonal antibodies

^{*}Abbreviations that have been mentioned more than ten times.

N protein Nucleocapsid protein

NA Neuraminidase

NS protein Non-structural protein

OC Organ culture

ORF(s) Open reading frame(s)

P protein Phosphoprotein

PCR Polymerase chain reaction

PIV(s) Parainfluenza virus(es)

PIV3 Parainfluenza virus type 3

RT-PCR Reverse transcription -polymerase chain

reaction

S protein Spike glycoprotein

SARS Severe acute respiratory syndrome

SH protein Small hydrophobic protein

URTI Upper respiratory tract infection

VP1 and VP2 Virus proteins 1, 2

WUV WU polyomavirus

^{*}Abbreviations that have been mentioned more than ten times.

LIST OF FIGURES

Fig. no.	Title	
1.	The structure of a paramyxovirus.	7
2.	Comparison of gene maps of members belonging to the <i>Pneumovirinae</i> and <i>Paramyxovirinae</i> subfamilies of nonsegmented negative-strand RNA viruses.	9
3.	Influenza A virus visualized by transmission electron microscopy.	16
4.	The structure of an influenza virus.	17
5.	An electron micrograph of a picornavirus particle 30 nm in diameter and displaying a hexagonal profile.	22
6.	Schematic representation of coronavirus virion structure showing the locations of the structural proteins.	28
7.	Structure of adenovirus.	35
8.	The structure of a <i>Herpesviridae</i> virion.	41
9.	A negative-stained electron micrograph of human metapneumovirus.	47
10.	Negative-stain electron micrographs of human metapneumovirus.	48
11.	Schematic representation of the genomic organization of members of the <i>Pneumovirus</i> genus.	51
12.	Phylogenetic relationships among metapneumoviruses, following alignment of nucleotide coding sequences for the N, P, M, F and $M2$ genes.	53

Fig. no.	Title	Page no.
13.	Pathologic findings of lung tissue sections after human metapneumovirus infection.	63
14A.	Epidemiologic pattern of upper respiratory tract infection with human metapneumovirus and other virus infections in the Vanderbilt Vaccine Clinic, California, USA.	75
14B.	Cumulative monthly rates of human metapneumovirus and other virus infections from 1982 to 2001 in the Vanderbilt Vaccine Clinic, California, USA.	76
15A.	Early cytopathic effect of human metapneumovirus in rhesus monkey kidney (LLC-MK2) cell monolayers.	91
15B.	Late cytopathic effect of human metapneumovirus in rhesus monkey kidney (LLC-MK2) cell monolayers.	91
16.	Combination approach of conventional virus isolation and molecular techniques to detect human metapneumovirus infection.	92
17.	Electron micrographs of human bocavirus in three different samples.	105
18.	Electron micrograph of a coronavirus.	123
19.	Influenza A virus reservoir.	129
20.	Acanthamoeba polyphaga Mimivirus (formerly called "the Bradford coccus") as observed under light microscopy after Gram staining.	136
21.	Electron micrographs of Mimivirus.	137
22.	Cryo-electron microscopy images of Mimivirus.	138

LIST OF TABLES

Table no.	Title	Page no.
1.	Oral and respiratory diseases caused by viruses.	3
2.	Genera and representative species of the family <i>Paramyxoviridae</i> .	6
3.	The Picornaviridae.	24
4.	Coronaviruses and Toroviruses.	27
5.	Antigenic groups of Coronaviridae.	31
6.	Subgrouping of human adenoviruses: hemagglutination and oncogenicity.	36
7.	Classification of human herpesviruses.	42
8.	General properties of the genera of the subfamily <i>Pneumovirinae</i> .	49
9.	Amino acid sequence relatedness (% identity) between the proteins of human respiratory syncytial virus subgroup A or human metapneumovirus subgroup A and the indicated viruses.	56
10.	Incidence of human metapneumovirus infection in several studies.	70
11.	Clinical characteristics and outcomes among children seen for acute respiratory infection in an emergency department, grouped by virus RNA detection.	80

Table no.	Title	Page no.
12.	Symptoms and signs of human metapneumovirus infection compared with human respiratory syncytial virus infection in hospitalized children from cited published studies.	82
13.	Clinical findings in 28 human metapneumovirus-infected Canadian subjects, by age group.	84
14.	Clinical and socio-economic impact of different virus infections among the household contacts of the children in whom a single infectious agent was demonstrated.	88
15.	Application of Koch's postulates to Mimivirus as a pathogen.	142
16.	Summary of the novel and re-emerging human respiratory viruses.	145

GENERAL OVERVIEW

Respiratory infections are major causes of morbidity and mortality worldwide. In children younger than five years old, acute respiratory tract infection (ARTI) is the leading cause of death (Bryce et al., 2005). The burden of respiratory tract infections is not limited to the pediatric population. Pneumonia, influenza and influenza-like illnesses are the sixth leading cause of death for all age groups (Barlett et al., 2000).

Although the clinical features of respiratory tract infections are easily recognized, the etiology of a large proportion of disease remains undetermined. For community-acquired pneumonia, the infectious agent responsible for disease is identified in only 50% of cases, despite the sensitivity of diagnostic tests such as polymerase chain reaction (PCR) and serological methods (**Ruiz** *et al.*, 1999; **Zambon** *et al.*, 2001).

Viruses are an important cause of respiratory diseases in both the community and hospital settings. They are associated with infections at all levels of the respiratory tract. Viruses are responsible for a significant number of cases with upper respiratory tract symptoms as well as laryngotracheobronchitis (croup), bronchiolitis and pneumonia. They are a well-recognized cause of severe and lifethreatening infections in the immunocompromised, the elderly, neonates and individuals with compromised cardiac or pulmonary systems. Moreover, they are responsible for more 'trivial' asymptomatic infections also and mild symptomatology in a community setting. Seasonal outbreaks of respiratory virus infections account for a considerable proportion of medical consultations (Hibbitts and Fox, 2002).

The importance of viral respiratory tract infections (VRTIs) is immense. There are considerable costs associated with VRTIs in terms of decreased productivity and time lost from work or school, visits to healthcare providers and amount of drugs prescribed. Another important factor contributing to the impact of VRTIs is the inappropriate use of antibiotics; this significantly adds to the cost of management and to the increasing prevalence of antibiotic resistant bacteria (**File**, **2003a**).

Viruses spread in respiratory droplets, aerosols and saliva by close contact and on hands. Similar respiratory symptoms can be caused by several different viruses, as seen in Table 1 (Murray 2005a).

Table 1: Oral and respiratory diseases caused by viruses.

Disease	Etiologic Agent
Common cold	Rhinovirus*
(including	Coronavirus*
pharyngitis)	Influenza viruses
	Parainfluenza viruses
	Respiratory syncytial virus
	Metapneumovirus
	Adenovirus
	Enterovirus
Pharyngitis	Herpes simplex virus
	Ebstein-Barr virus
	Adenovirus*
	Coxsackie A virus* (herpangina, hand-foot-and-mouth disease) and other
	enteroviruses.
Croup, tonsillitis,	Parainfluenza virus 1*
laryngitis and	Parainfluenza virus 2
bronchitis (children	Influenza virus
younger than two	Adenovirus
years)	Ebstein-Barr virus
Bronchiolitis	Respiratory syncytial virus* (infants)
	Metapneumovirus
	Parainfluenza virus 3* (infants and children)
	Parainfluenza viruses 1 and 2
Pneumonia	Respiratory syncytial virus* (infants)
	Metapneumovirus
	Parainfluenza virus* (infants)
	Influenza virus*
	Adenovirus
	Varicella-zoster virus (primary infection of adults or immunocompromised hosts)
	Cytomegalovirus (infection of immunocompromised hosts)
	Measles

^{*}Most common causal agents.

(Murray, 2005a)

Although the etiology of the majority of lower respiratory tract infections (LRTIs) is thought to be viral, yet in only 40% of cases can a viral agent be identified, even with the use of genomic amplification methods (File, 2003b; Louie *et al.*, 2005). In children, human respiratory syncytial virus (hRSV), parainfluenza viruses (PIVs) and influenza viruses are known as the major causes of bronchiolitis and pneumonia. However, in up to a third of these cases, an infectious agent cannot be identified, thus suggesting that previously unidentified viruses may be circulating (Kahn, 2007).

Following the boom in respiratory virology in the 1960s, species of rhinoviruses, coronaviruses (CoVs), enteroviruses (EVs), adenoviruses, PIVs and hRSV were added to influenza and measles viruses as causes of respiratory tract infections. In restricted patient groups, such as the immunocompromised, members of the family of herpesviruses including herpes simplex (HSV), cytomegalovirus (CMV), varicella-zoster virus (VZV), Epstein-Barr virus (EBV) and human herpes virus 6 (HHV-6) have also been associated with respiratory disease. More than 200 antigenically distinct viruses have been documented as causes of sporadic or epidemic respiratory infections in infants, children and adults. However, this varied and diverse group can be divided among six distinct families: *Paramyxoviridae*, *Orthomyxoviridae*, *Picornaviridae*, *Coronaviridae*, *Adenoviridae* and *Herpesviridae* (Mackie, 2003).

Recent advances in molecular technology have enabled the detection of several new viral agents in specimens collected from the human respiratory tract and thus this list of pathogens was extended with the discovery of novel viruses such as human metapneumovirus (hMPV), human bocavirus (HBoV), the NL63 and HKU1 CoVs, KI and WU polyomaviruses and the giant mimivirus (**Sloots** *et al.*, **2008**).