600,000 of those deaths. Eighty-five percent of these deaths occur in sub-Saharan Africa and southeast Asia. **OBJECTIVE:** We aimed to review rotavirus prevalence studies of children in Africa from 1975 to 2006. **METHODS:** Three multilingual Medline searches (limited to humans) were performed: “RV,” country/Africa, and epidemiology/diarrhea. Additional inclusion criteria included children <5 years of age, conducted over >3 months, and including >50 children. Data were analyzed in 4 periods. **RESULTS:** Of the initial 189 studies identified, 75 in 18 countries met the additional inclusion criteria (Table 1). More than half of the studies were hospital based. In all studies the most common serotypes were G1 (25%), G4 (16%), G2 (13%), G3 (12%), P[8] (37%), P[6] (35%), and P[4] (11%). From 1996 to 2006 the common serotypes were G1 (22%), G4 (17%), G2 (13%), G3 (13%), P[6] (37%), P[8] (35%), and P[4] (11%). **TABLE 1. Results of 75 Studies on Rotavirus Prevalence in Children <5 Years Old in Africa**

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<tbody>
<tr>
<td>Total No of studies</td>
<td>75</td>
<td>12</td>
<td>39</td>
</tr>
<tr>
<td>Duration, mo</td>
<td>12 (10–15.5)</td>
<td>12 (10–12.5)</td>
<td>12 (12–12.5)</td>
</tr>
<tr>
<td>Rotavirus-positive, %</td>
<td>26</td>
<td>25</td>
<td>25</td>
</tr>
<tr>
<td>Studies with serotyping</td>
<td>18</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>Rotavirus-positive with serotyping, %</td>
<td>24</td>
<td>—</td>
<td>5</td>
</tr>
</tbody>
</table>

— indicates that data were not available.

**CONCLUSIONS:** The current prevalence rate is 30% (range: 17%–38%). Present serotypes include G1 through G4, G8, G9, P[8], P[6], and P[4]. Rotavirus diarrhea represents a significant disease burden. Current rotavirus prevalence studies are important, because there are effective rotavirus vaccines available to prevent mortality and severe disease.

**ASSOCIATION OF CYTOKINE-RELATED GENE EXPRESSION WITH DENGUE INFECTION SEVERITY**

Submitted by Woraman Waidab
Woraman Waidab, Kanya Suphapeetiporn, Chalurumphon Srichomthong, Sirapraka Tongkobpetch, Chitsanu Pancharoen, Vorasuk Shotelersuk, Usa Thisyakorn
King Chulalongkorn Memorial Hospital, Bangkok, Thailand

**INTRODUCTION:** Dengue is the most prevalent mosquito-borne viral disease and one of the most serious infectious diseases worldwide. Infection by any of the serotypes of dengue viruses (DEN-1–DEN-4) may result in different severities ranging from a relatively benign fever, called dengue fever (DF), to fatal dengue shock syndrome. The pathogenesis of dengue hemorrhagic fever (DHF) and dengue shock syndrome is thought to be mediated by various host factors. Previous reports have suggested an involvement of immune response mediators as well as apoptosis-related molecules in the severity of dengue infection. **OBJECTIVE:** Our aim was to elucidate the cellular gene responses to dengue viral infection at the transcriptional level and to correlate expression levels with disease activity and/or clinical manifestation. **METHODS:** Expression levels of interleukin 8 (IL-8), IL-1β, matrix metalloproteinase 9 (MMP-9), and Fas in peripheral blood cells were assayed for 10 children with DF, 10 children with DHF, and 5 healthy controls by using real-time reverse-transcription quantitative polymerase chain reaction. **RESULTS:** Expression levels of IL-8, IL-1β, MMP-9, and Fas were higher in children who developed DHF than in those with DF. **CONCLUSIONS:** The messenger RNA expression levels of IL-8, IL-1β, MMP-9, and Fas were significantly elevated in children with DHF, which suggests that these mediators are involved in the pathogenesis. The messenger RNA expression level might serve as a predictor of dengue disease activity. Reverse-transcription polymerase chain reaction has a potential to be another rapid and useful tool in assessing disease severity, leading to a proper therapeutic plan.

**HIGH SEROPREVALENCE OF HUMAN METAPNEUMOVIRUS INFECTION IN CHILDREN IN THE CHONGQING, CHINA, AREA**

Submitted by Xiaodong Zhao
Xiaodong Zhao, Zhang Qin
Division of Immunology, Children’s Hospital, Chongqing Medical University, Chongqing, China

**INTRODUCTION:** Human metapneumovirus (hMPV), first isolated in 2001 in the Netherlands, was identified as a respiratory etiologic agent in a variety of regions. A number of reports have described evidence of hMPV infection on mainland China. However, the description of the seroepidemiology of hMPV infection remains limited. **OBJECTIVE:** We aimed to define the seropositivity of hMPV immunoglobulin G (IgG) antibodies in different age groups of children in Chongqing, China. **METHODS:** The specificity of the enzyme-linked immunosorbent assay was first validated by using respiratory syncytial virus (RSV)-infected cell lysates subtracted sera and Western blotting based on anti-hMPV animal serum. This assay was subsequently used to determine the presence of IgG antibodies to hMPV and RSV in 325 serum samples from children aged 0 to 6 years. **RESULTS:** There was no cross-reaction between the hMPV and RSV enzyme-linked immunosorbent assays observed in our system. Seropositivity of anti-hMPV IgG antibodies in children aged 0 to 5 months was 74.5%,
64% for children aged 6 to 11 months, 72.7% for children aged 12 to 23 months, 87.1% for children aged 24 to 35 months, and 90.3% for children 3 to 6 years old, respectively. The seropositivity of hMPV and RSV was considerably similar in almost all age groups.

**CONCLUSIONS:** hMPV seems to be a common and important respiratory pathogen in Chongqing’s children. Almost all individuals had been exposed to hMPV by the age of 6 years.

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**DETECTION OF HUMAN BOCAVIRUS IN CHINESE CHILDREN WITH RESPIRATORY TRACT INFECTION**

Submitted by Xiaodong Zhao  
Xiaodong Zhao  
Division of Immunology, Children’s Hospital, Chongqing Medical University, Chongqing, China

**INTRODUCTION:** Human bocavirus (HBoV), a parvovirus discovered in 2005, was identified as a respiratory pathogen in a proportion of respiratory tract diseases with an unknown causative agent.

**OBJECTIVE:** Our goal was to investigate the role of HBoV in acute lower respiratory tract infection in Chinese children.

**METHODS:** Two hundred forty-five nasopharyngeal aspirates collected from January to December 2006 from hospitalized children with acute lower respiratory tract infection were tested for the presence of HBoV DNA by using polymerase chain reaction (PCR) that targeted the NP-1 gene. Bulk PCR products were subjected to nucleotide sequence analysis. Medical charts were reviewed for clinical features of HBoV infection.

**RESULTS:** HBoV DNA was detected in 11 (4.5%) of the 245 nasopharyngeal aspirates. HBoV infection occurred year-round and peaked in winter. The age range of the children was from 48 days to 18 months. Coinfections of HBoV and respiratory syncytial virus were found in 2 (18.2%) of 11 samples. Nucleotide sequence of the NP-1 gene PCR products showed considerably high identity (99%). Clinical symptoms included cough and wheezing.

**CONCLUSIONS:** HBoV seems to be one of the respiratory pathogens for acute respiratory tract infection in the Chongqing area, particularly in young children. Understanding of the clinical relevance of HBoV infection will require additional studies.

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**COMBINATION OF ARTESUNATE-AMODIAQUINE AS A TREATMENT FOR UNCOMPPLICATED FALCIPARUM MALARIA IN CHILDREN**

Submitted by Syahril Pasaribu  
Pasaribu Syahril, Pasaribu Ayodhia Pitaloka, Lubis Chairuddin Panusunan  
Department of Pediatrics, Medical School, University of Sumatera Utara, Medan, Indonesia

**INTRODUCTION:** Resistance of falciparum malaria to both chloroquine and pyrimethamine-sulfadoxine has been reported from Indonesia and other countries. Since the end of 2004, we have changed the standard treatment of uncomplicated falciparum malaria to use a combination of artesunate and amodiaquine.

**OBJECTIVE:** Our aim was to evaluate the efficacy and adverse reactions of artesunate-amodiaquine as a treatment for uncomplicated falciparum malaria in children.

**METHODS:** We conducted a cross-sectional study at Panyabungan, Mandailing Natal Regency, North Sumatera Province, Indonesia, from August to September 2006. The sample was school-aged children between 5 and 18 years old. The sample received an oral dose of artesunate (4 mg/kg body weight) combined with an oral dose of amodiaquine (10 mg/kg body weight) for 3 days. Parasitemia was assessed at days 0, 2, 7, and 28.

**RESULTS:** Peripheral blood smears were performed for 376 school-aged children; 135 of them tested positive for falciparum malaria. At the end of the study (28 days), 121 cases completed a full course of study. From the peripheral blood smears on days 2, 7, and 28, we found a 100% cure rate. Adverse reactions included 20 children (16.5%) with headache, 10 (8.3%) with vomiting, and 1 (0.8%) with tinnitus.

**CONCLUSIONS:** A combination of artesunate and amodiaquine can be used as treatment for uncomplicated falciparum malaria in children with the caution of headache as an adverse reaction of the drug combination.

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**INTERLEUKIN 18 GENE POLYMORPHISM AS A POTENTIAL HOST-SUSCEPTIBILITY FACTOR IN TUBERCULOSIS IN CHONGQING, CHINA**

Submitted by Li-Ping Jiang  
Li-Ping Jiang  
Children’s Hospital, Chongqing Medical University, Chongqing, China

**INTRODUCTION:** Interleukin 18 (IL-18), which is an important interferon γ inducer, regulates the expression of the proinflammatory cytokine interferon γ and the antituberculosis response.

**OBJECTIVE:** Our goal was to investigate polymorphisms of the IL-18 gene promoter and determine whether polymorphism of the IL-18 gene promoter is a
**HIGH SEROPREVALENCE OF HUMAN METAPNEUMOVIRUS INFECTION IN CHILDREN IN THE CHONGQING, CHINA, AREA**

Xiaodong Zhao and Zhang Qin

*Pediatrics* 2008;121;S132

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