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.

DETECTION OF HUMAN BOCAVIRUS IN CHINESE CHILDREN WITH RESPIRATORY TRACT INFECTION

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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.

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

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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.

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

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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

potential host-susceptibility factor in tuberculosis in Chongqing, China.

METHODS: A total of 123 patients (including 91 children and 32 adults) with tuberculosis and 249 normal controls (including 167 children and 82 adults) were selected randomly. The polymorphisms at positions -607A/C and -137G/C in promoter of the *IL-18* gene were analyzed by using polymerase chain reaction with sequence-specific primers.

RESULTS: The allele and genotype frequencies of IL-18/-607 gene polymorphisms were similar in patients with tuberculosis and in controls. However, frequencies of the -137GG, GC, and CC genotypes were 67.9%, 28.5%, and 3.6%, respectively, in controls and 78.9%, 19.5%, and 1.6%, respectively, in those with tuberculosis. Frequency of the -137GG genotype in tuberculosis was significantly higher than that in controls ($\chi^2 = 4.881$; $P = .027 < .05$). The frequency of allele G at position -137 in patients with severe tuberculosis was significantly higher than that in patients with pulmonary tuberculosis ($\chi^2 = 4.336$; $P = .037 < .05$).

CONCLUSIONS: Polymorphism of the IL-18 gene promoter at position -137 is a potential host-susceptibility factor in tuberculosis in Chongqing. The people with allele C at position -137 in the promoter of the *IL-18* gene may be protected against mycobacterium tuberculosis infection. The polymorphisms at position -137 of the *IL-18* gene may be associated with a severe degree of tuberculosis.

ASSOCIATION OF POLYMORPHISMS OF THE INTERLEUKIN 18 RECEPTOR: A GENE WITH SUSCEPTIBILITY TO TUBERCULOSIS IN CHONGQING, CHINA

Submitted by Li-Ping Jiang

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INTRODUCTION: The interleukin 18 (IL-18) receptor complex is a heterodimer consisting of IL-18Rα and IL-18β. Both chains are required for IL-18 signaling transduction in T cells and natural killer cells.

OBJECTIVE: We aimed to determine whether polymorphisms of the IL-18Rα gene promoter were associated with susceptibility to tuberculosis in Chongqing, China.

METHODS: In 123 patients (91 children and 32 adults) with tuberculosis and 249 normal controls (167 children and 82 adults) in Chongqing, we analyzed the polymorphisms at positions -69T/C and -638T/C in the promoter of IL-18Rα by using polymerase chain reaction with sequence-specific primers.

RESULTS: Allele and genotype frequencies at position -638 of the IL-18Rα gene polymorphisms were similar in patients with tuberculosis and normal controls ($P > .05$). However, the frequency of -69/CC was significantly lower in patients with tuberculosis than in controls ($\chi^2 = 8.484$; $P = .004 < .05$). The frequency of -69/TT was significantly higher in patients with tuberculosis than in controls ($\chi^2 = 4.027$; $P = .045 < .05$). The frequency of allele C at position -69 in tuberculosis was significantly lower that than in controls ($\chi^2 = 9.816$; $P = .002 < .05$). The frequency of allele C at position -69 in patients with severe tuberculosis was significantly lower than that in patients with pulmonary tuberculosis ($\chi^2 = 4.664$; $P = .031 < .05$).

CONCLUSIONS: Polymorphisms of the IL-18Rα gene at position -69 were associated with susceptibility to tuberculosis in Chongqing. The people with allele C at position -69 may be protected against mycobacterium tuberculosis infection. Moreover, the position -69 of IL-18Rα may be associated with a severe degree of tuberculosis.

PLACENTAL ADENOVIRAL GENOME: POLYMERASE CHAIN REACTION DETECTION AND PLACENTAL HISTOLOGY IN PRETERM AND TERM INFANTS

Submitted by Eufrosini Tsekoura

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INTRODUCTION: Intrauterine infection is an important cause of spontaneous preterm birth. However, evidence-based etiology for the causative role of viral infection is still lacking. Intervillous trophoblasts express adenovirus receptor. Infection of trophoblast cells in vitro by adenovirus early in pregnancy has shown increased apoptosis. Adenovirus early in pregnancy may cause placental dysfunction. Mature syncytiotrophoblasts do not express adenovirus receptor.

OBJECTIVE: The aim of this study was to test the hypothesis that detection of adenovirus in placental tissue is associated with preterm birth and correlates with placental histopathological findings that are suggestive of infection.

METHODS: Placentas were prospectively collected from consecutive deliveries. Detection of the adenovirus genome was tested by polymerase chain reaction assay. Placental histology and immunohistochemistry studies with monoclonal antibody CD45 were evaluated for

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