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**INTRODUCTION:** Human bocavirus (family *Parvoviridae*) was recently identified in children with respiratory tract infection (RTI), first in Sweden, and subsequently in different parts of the world.

**OBJECTIVE:** The aim of our study was to gain insight into the epidemiology of bocavirus in children with RTI in Greece.

**METHODS:** One hundred ten throat-swab samples were collected during the autumn and winter months of 2006–2007 from previously healthy children (aged 1 month to 13 years) who were hospitalized for RTI. DNA was extracted from the samples, and polymerase chain reaction was performed to amplify the *NS1* gene of the bocavirus genome. Polymerase chain reaction products were sequenced and compared with respective bocavirus sequences.

**RESULTS:** Bocavirus DNA was detected in 10 samples (9%). Comparison with previously identified bocavirus sequences showed a high degree of identity. Mean age of the children was 1.8 years (range: 2 months to 4 years). The most common symptoms were fever, cough, and various degrees of respiratory distress. A majority of the children (9 of 10) were clinically diagnosed as having lower RTI, mainly acute bronchiolitis and pneumonia.

**CONCLUSIONS:** This is the first report of human bocavirus infection in Greece, which suggests that the virus is spread worldwide, and it is associated with RTI in infants and young children.

## GENETIC CHARACTERIZATION OF THE F PROTEIN OF RESPIRATORY SYNCYTIAL VIRUS STRAINS ISOLATED IN THE BEIJING, CHINA, AREA

Submitted by Qi Lu

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**INTRODUCTION:** Respiratory syncytial virus (RSV) is the most common viral pathogen for lower respiratory tract infection among young children. However, pathogenic mechanisms and molecular characteristics of RSV are still not completely understood, so the development

of an effective vaccine has been hindered. F protein has been shown to be a potential RSV subunit vaccine candidate, so the study on genetic characteristics of F protein may be important for further investigation.

**OBJECTIVE:** Our goal was to determine the genetic characteristics of the F protein.

**METHODS:** Seventy-six strains of human RSV were isolated from 2001 to 2004 in Beijing, China, of which 6 representative strains were chosen.

**RESULTS:** Among the 6 Beijing isolates, 4 belonged to subgroup A. The F gene of the isolates shared 97.0% to 97.4% nucleotide sequence identity and 92.1% to 93.0% amino acid sequence identity. They were highly homologous with GenBank Nos. AY198175, AY198176, and AY198177 (China Hebei). The other 2 isolates belonged to subgroup B, and 97.3% and 98.2% sequence identity was seen at nucleotide and amino acid levels, respectively. The nucleotide sequences of subgroup B showed the highest identities with GenBank Nos. NC001781 and AF013254. Phylogenetic analysis of nucleotide sequences revealed that those 4 within group A were monophyletic and closely related to each other, but those 2 within group B were distributed in 2 distinct clusters. AA200-225 and AA259-278 on the F gene are conservative between subgroups A and B.

**CONCLUSIONS:** Subgroup A and B strains cocirculated, which indicates that there were different transmission chains in Beijing from 2001 to 2004. AA200-225 and AA259-278 are potential segments to develop an effective vaccine in Beijing or even in China.

## SEROEPIDEMIOLOGY OF HEPATITIS A IN GREEK CHILDREN

Submitted by Vassiliki Papaevangelou

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**INTRODUCTION:** Hepatitis A is a vaccine-preventable disease with epidemiology that has changed over the past decades. In Greece, the vaccine has been available and recommended, but no universal mass vaccination has been implemented as yet.

**OBJECTIVE:** We sought to study the seroepidemiology of hepatitis A in Greek children.

**METHODS:** The seroepidemiology of hepatitis A in children 0 to 14 years of age living in Greece was studied. We collected 100 sera per year of age, stratified by geographic region. Demographic data and documented

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