

Miri, in the north of Sarawak in 2007. Stool samples collected from these two isolated outbreaks were tested for rotavirus, which is a primary etiological agent of gastroenteritis. This study aimed to characterize the G (VP7) and P (VP4) genotypes of group A human rotavirus circulating in these two outbreaks. The G and P types of the rotavirus-positive faecal specimens were determined by reverse-transcription PCR and sequencing.

**Methods:** Faecal specimens were resuspended in PBS and were subjected to nucleic acid extraction by using the Chemagic Viral Extraction Kit (Chemagen, Germany). Rotavirus was detected by RT-PCR using published primers specific for VP4 and VP7. Positive samples were subjected to DNA sequencing and partial sequences of the G and P gene were analysed using Lasergene (DNASTAR, Madison WI, USA) software and phylogenetic tree analysis using a neighbour-joining method.

**Results:** A total of 272 samples were tested for rotavirus and of these 75 (72%) and 68 (40%) in Serian and Miri respectively, were positive for group A human rotavirus. A total of 105 sequences were obtained, and five different G-P combinations were identified. In both outbreaks, G1[P8] were the most common strains found which constituted of 87.6% of all the rotavirus typed. Other genotypes include the emergent strains G9[P8] (7.6%), G2[P4] (3.8%) and a rare G3[P9] (1%). Out of the 5 combinations only G1[P8] and G9[P8] strains were identified in the 2001 outbreak in Serian while G1[P8], G2[P4] and G3[P9] were found circulating in the 2007 outbreak in Miri.

**Conclusion:** Given variations observed in circulating rotavirus strains, continued monitoring of genotypes is essential to identify emerging strains, track common strains and evaluate impact of rotavirus vaccines.

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16.020

#### Phylogenetic Analysis of the VP1 Gene of Human Echovirus 30 Isolates from Sarawak Reveals An Emerging Genotype

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**Background:** Human enteroviruses are the leading cause of aseptic meningitis (ASM) worldwide. Human echovirus 30 (E30), together with E9 and E11, are the enteroviruses most frequently implicated in community outbreaks of ASM. In Sarawak, in 2001 and 2004, we have isolated E30 from a number of patients during a prospective study of central nervous system infection.

**Methods:** The complete nucleotide sequences of the VP1 gene for 23 E30 isolates from Sarawak were determined by RT-PCR and sequencing using published and in-house designed primer sets. The relationship between the 23 Sarawakian E30 VP1 sequences and an additional 470 E30 VP1 sequences obtained from the GenBank database were investigated by phylogenetic analysis using a maximum likelihood approach.

**Results:** The phylogenetic analysis of all 493 E30 VP1 sequences revealed 3 separate genotype groups which included two previously published genotypes (I and II) and a previously undescribed genotype that we have designated as genotype III. The Sarawak strains belonged to two separate genotypes (II and III). Strains isolated in 2001 belonged to genotype II whereas strains isolated in 2004 were from genotypes II and III. A global comparison of E30 VP1 sequences revealed that multiple lineages (within or in separate genotype groups) of E30 strains may circulate at any one time. This is in contrast to previously published reports that a single virus lineage appear to circulate at a time and that temporal displacement of the lineage occurs with time. Our results also showed that E30 strains can be divided geographically into 'continental' and 'cosmopolitan' types.

**Conclusions:** Increased capacity for virus diagnostics has improved our appreciation for the disease burden of E30. This has led to the description of an emerging genotype (III) and a better understanding of the molecular epidemiology of E30.

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#### Surveillance of Acute Hepatitis B in Taiwan

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**Backgrounds and Purpose:** In Taiwan, hepatitis B virus (HBV) infection is the leading cause of acute viral hepatitis. An effective universal HBV vaccination program was launched since 1984. We assessed the impact of vaccination on acute hepatitis B in terms of incidence and risk factors.

**Methods:** Cases definition of acute hepatitis B meets the clinical and laboratory criteria. HBsAg existed less than 6 months and IgM-anti-HBc positive are necessary. From 1994 to 2007, reported cases to Taiwan CDC via the National Notifiable Diseases Surveillance System were enrolled. The incidence of birth cohorts who were born between 1974 and 1993 (10 years after or before vaccine introduction) was further analyzed. Risk factors were recorded.

**Results:** Totally, 4255 patients (gender: 1326F/2929M; birth years: 1902–2007) were diagnosed as acute hepatitis B, representing 52% of all acute viral hepatitis patients in 14 years. The median age of onset was 31 years (range, 0–94 years), and the overall incidence was 1.43/100,000 (range, 1.01–1.88/100,000). For people's birth years between 1974 and 1983 ( $n=1388$ ), the incidence of acute hepatitis B was 34.59/100,000 (range, 9.65–44.46/100,000). It decreased to 4.06/100,000 (range, 0.62–12.13/100,000) for those birth years between 1984 and 1993 ( $n=131$ ) and their HBV vaccine coverage was 86.19% (range, 75.70–92.05%). Possible risk factors were investigated for cases reported during 2006 and 2007. The occurrence of acute hepatitis B may be related to people who had recent surgery (22.9%), lived with family members of HBV carriers (12.5%), or had HCV infection (7.6%). Sharing razors or toothbrushes (6.9%), acupuncture