

newly introduced RV vaccines, RotaTeq® which contains G1, G2, G3, G4, and P1A viruses (Merck) and Rotarix™ which contains a G1P1A[8] virus (GlaxoSmithKline).

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#### 16.017

### Study on the Circulation of HEV71 on Selected Communities in Sarawak

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**Background:** Human enterovirus 71 (HEV71) is a common aetiology of hand-foot-and-mouth-disease (HFMD) where it occasionally causes CNS illnesses. In 1997, Sarawak experienced a HEV71-associated HFMD outbreak with 34 deaths reported. Following the outbreak, a prospective HFMD surveillance study showed that HEV71-associated HFMD outbreaks occurred in Sarawak every three years, each caused predominantly by different genogroups of HEV71; genogroup-B3 in 1997, genogroup-B4 in 2000, and genogroup-B5 in 2003. This study attempts to investigate the circulation of HEV71 in between the three-year cycle outbreaks before an expected outbreak in 2006 in Sarawak.

**Methods:** Three communities, Villages-A, B and C, were selected based on their locations with reference to the Rajang river, the epicenter of the 1997 outbreak. Stool samples were collected through 2 visits; the first collection in mid-2005 and the second in February 2006. Filter-sterilized samples were inoculated into rhabdomyosarcoma and QB1-293A cells. Virus cultures were observed for cytopathic effect (CPE) daily for 14-days. Upon blind-passage, cultures without CPE were considered negative. Reverse-transcription-polymerase-chain-reaction (RT-PCR) on positive cultures was done using primers for partial VP1 previously described by Oberste *et al.* RT-PCR positive products were subjected to DNA sequencing and molecular analysis.

**Results:** During the first collection, 106 samples were collected from Village-A, 428 from Village-B and 183 from Village-C. The second collection yielded 88 samples from Village-A, 410 from Village-B and 177 from Village-C. While, no virus was isolated from the first collection of Village-A, 4% of samples from Village-B and 6% of samples from Village-C yielded enteroviruses respectively. From the second collection, 8% of samples from Village-A, 6.8% from Village-B and 4.5% from Village-C, yielded enteroviruses. The viruses isolated were identified mostly as echovirus-6 (E6), E7, E19, coxsackievirus-A (CA) 20, CA21, CA24 and coxsackievirus-B (CB) 4.

**Conclusion:** HEV71 was not circulating in sampled villages but enteroviruses species B and C were.

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#### 16.018

### HCV Genotypes in Haemodialysis Units: A Preliminary Study

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**Introduction:** Serological verification among haemodialysis patients in Kuantan, Pahang, an East Coast town in Peninsular Malaysia is routinely updated for every 3 months by Ministry of Health. However, the determination of the HCV genotypes for each infected patient has not yet been attempted. This study aims at the determination of HCV genotypes among infected haemodialysis patients.

**Methodology:** 22 seropositive patients out of 208 (10.5%) from 4 haemodialysis units (HDUs) were enrolled in this study during the period from March to August 2007. Detection of HCV RNA from serum was done by using RT-PCR technique targeting 212 bp of the 5'UTR region. Meanwhile, the base sequences of the above regions were deduced using the same primers as for the RT-PCR. The nucleotide sequences data were analyzed with Bioedit software and classification of the genotypes was done using neighbor-joining method together with known sequences obtained from NCBI homepage.

**Result:** Out of 21 samples (male=57%), 2 are negatives. The 19 positive HCV-RNA samples were subjected for sequencing analysis. The analysis showed that 63.2% (12/19) were of genotype 3, 26.3% (5/19) of genotype 1 followed by 5.3% (1/19) of genotype 4 and 1 isolate (5.3%) is undetermined. Furthermore, the genotype distribution showed discrete clustering among units. Sequence comparisons revealed that 4 strains from one HDU have a G insertion (-208) which is not detected in other strains including ones that were retrieved from NCBI sequence database.

**Conclusion:** Genotype 3 is the most prevalent genotype found among haemodialysis patients in Kuantan which is in concordance with previously published HCV genotype prevalence in Malaysia. Furthermore, genotype clustering suggests a nosocomial and blood transfusion infection which requires further subtyping test. Meanwhile, nucleotide sequence analysis suggested that HCV adaptation to certain environment may lead to mutations in the well conserved region (5'UTR).

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#### 16.019

### Molecular Characterization of Rotavirus A Associated with Outbreaks of Acute Gastroenteritis in Sarawak in 2001 and 2007

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**Background:** An unusual increase in the burden of gastroenteritis cases was noted in Serian, in the south of Sarawak in 2001. A similar occurrence was also observed in