

**Objectives:** We sought to analyze the predominant genotype responsible for the most severe and largest outbreak of DHF that hit Karachi in 2006.

**Study Design:** Retrospective analysis of stored serum samples for dengue virus genotype by multiplex RT-PCR, anti dengue IgM, IgG and review of clinical charts of patients admitted to Aga Khan University Hospital.

**Results:** Viral RNA detection of 250 patients, revealed positive results in 185 (74.0%) samples. DEN-2 was predominant genotype ( $n=104$ , 56.2%) and accounted for 53.6% of primary cases (total 81). Within secondary cases 63.2% were due to DEN-2 (total 57), rest were positive for DEN-3. DHF ( $p=0.064$ ) and abdominal pain ( $p=0.059$ ) were frequently associated with DEN-2 as compared to DEN-3. None of the samples were positive for DEN-1 and DEN-4

**Conclusion:** Co-circulation of DEN-2 and DEN-3 was responsible for the 2006 outbreak in Karachi. Primary and secondary cases were seen in both groups. Cases with DHF showed marginal association with DEN-2. Introduction of new serotype (DEN-3) and or genotypic shift of endemic serotype (DEN-2) are the probable factors for the recent outbreak of DHF in this region.

doi:10.1016/j.ijid.2008.05.266

## Antibiotics - Gram negative (Poster Presentation)

17.001

### Rapid Molecular Assay for the Diagnosis of Clarithromycin Resistant *Helicobacter pylori* Directly from Human Gastric Biopsies - An Approach to Design Antibiotic Regimen

S.K. Tiwari\*, G. Manoj, G. Sivaram, K.S. Ahmed, M.D. Aejaz Habeeb, A.A. Khan, C.M. Habibullah

Center for Liver Research and Diagnostics, Deccan College of Medical Sciences, Hyderabad, India

**Background:** *Helicobacter pylori* has been a major cause for an array of gastrointestinal diseases. Though the outcome of infection is largely dependent on the complex interplay of bacterial and host factors, the most important concern of a physician is to diagnose and treat the infection effectively. Most of the current regimens available for eradicating *H. pylori* include Clarithromycin. Bacterial resistance of *H. pylori* to clarithromycin is related to the structural change of 23S rRNA. This structural change of 23S rRNA is caused by the single nucleotide polymorphism (SNP) of the 23S rRNA gene, at the position of 2142 or 2143 respectively. Therefore we aimed to develop an inexpensive and reliable high-throughput method to diagnose *H. pylori* infection and score such SNP's of the 23S rRNA which would aid in determining the treatment strategy for *H. pylori* eradication.

**Methods:** Thirty-eight dyspeptic subjects were included from whom five gastric biopsies were obtained. Biopsies were used for culturing, DNA isolation and for histopathology. DNA extracted was subjected to amplification using specific oligonucleotide primers targeting the 16SrRNA and the 23SrRNA gene of *H. pylori*. The results were compared with minimum inhibitory concentrations for CAM.

**Results:** 32 (84.2%) of 38 subjects were *H. pylori* positive, 24 (75%) were infected with wild (wt) *H. pylori* strains, 6

(18.75%) were infected with A2143G mutant strains, 1 (3.1%) was infected with both wt. & A2143G mutant strains, and only one was infected with the strain with the A2142G mutation. The median of MIC values for CAM in the wt strains was  $<0.015 \mu\text{g/mL}$  and those with A2143G or A2142G mutations was  $>1.0-2.0 \mu\text{g/mL}$ .

**Conclusion:** This method can therefore be used prior initiating treatment and design optimal treatment strategy other than those based on clarithromycin. Further the assay is also helpful to identify subjects infected with multiple strains of *H. pylori*.

doi:10.1016/j.ijid.2008.05.267

17.002

### Carbapenem Resistance (CARB-R) among *Pseudomonas aeruginosa* (PSA) Isolates in Indian Medical Centers: A Preliminary Report From the Surveillance of Antimicrobial Resistance in India (SARI) Study

A. Manoharan\*, S. Chatterjee, D. Mathai,

SARI Study Group

Christian Medical College, Vellore, India

**Background:** High prevalence of co-resistance to betalactam, aminoglycoside and quinolone classes of antimicrobials among Enterobacteriaceae has necessitated the use of carbapenems in the treatment of serious infections among hospitalized patients. We monitored CARB-R rates among PSA isolates at seven Indian medical centers.

**Methods:** Among 176 PSA isolates collected during Jan 2005-June 2006, antimicrobial susceptibility testing was performed on 61 isolates (minimum of 5 from each medical center) by Kirby Bauer method using ceftazidime (CAZ), imipenem (IMP), meropenem (MEM), piperacillin (PIP), amikacin (AMK) and ciprofloxacin (CIP). CARB-R isolates (resistant to either IMP/MER) were screened for Metallo-Beta-Lactamase (MBL) by Double Disk Diffusion Test (DDDT) using EDTA as the inhibitor for IMP, MER and CAZ (CLSI guidelines). Those screened DDDT positive were confirmed by IMP+EDTA Etest strips.

**Results:** CARB-R was found to be 44.3% (overall resistance rates at these centers ranged from 28%–53%. Among them 13 (48.1%) were MBL. Resistance among MBL strains to CIP and PIP was 100% while for AMK and CAZ it was 92%. Non-MBL resistance to these antimicrobials ranged between AMK 50% to CIP 58.3%. Specificity and sensitivity of IMP+EDTA DDDT used for screening MBL was 87.9% and 84.4% respectively when compared to the confirmatory test. Specificity to MER and CAZ Etest was  $<50\%$ .

**Conclusion:** CARB-R among PSA is high and is widely prevalent in Indian medical centers. MBL production is the major mechanism of CARB-R among PSA. MBL production among PSA can be screened using the less expensive DDDT using IMP+EDTA. High rates of resistance ( $>50\%$ ) to other antipseudomonal classes of drugs renders their choice ineffective in the treatment of PSA. Carbapenem use should be judicious to minimize further emergence of MBL among PSA. Clonality of MBL genes need to be done.

doi:10.1016/j.ijid.2008.05.268