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 Session: Antibiotics
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Activity of cefaperazone-sulbactam against gram negative bacilli

R. Gurung*, N. Poudyal, R. Baral, N.R. Bhattarai, B. Khanal, S.K. Bhattacharya

BP Koirala Institute of Health Sciences, Dharan, Nepal

Background: Background

Sulbactam irreversibly inhibits the hydrolytic activity of beta-lactamases. This compound is commercially available in combination with either ampicillin or cefoperazone. In each instance, the activity of the partner antibiotic against beta-lactamase producing bacteria is restored. In this context the present study was aimed to find out the antimicrobial susceptibility pattern of GNB against cefaperazone-sulbactam and to correlate its activity against commonly used antimicrobials for treatment of GNB.

Methods: All Gram negative bacilli isolated from different clinical samples during a period of three months were tested against cefaperazone-sulbactam, meropenem, ceftazidime, cefotaxime, ceftriaxone, chloramphenicol, cotrimoxazole, ampicillin, amikacin, gentamycin, nalidixic acid, ciprofloxacin, ofloxacin, norfloxacin, nitrofurantoin, aztreonam, carbenicillin, piperacillin and tobramycin using standard Kirby-Bauer disc diffusion antimicrobial susceptibility testing method. The susceptibility was recorded as susceptible, intermediate susceptible and resistant by measuring the zone of inhibition they showed. The data were recorded in Microsoft excel sheet and analyzed in terms of percentage.

Results: A total of 406 Gram negative bacilli were isolated from different clinical samples. Majority of samples were from females (59.4%). The mean age of patient's was 34.85. Out of 15 different species of GNB, *Escherichia coli* was the frequent isolate (56.4%), followed by *Acinetobacter anitratus* (17.5%), *Klebsiella pneumoniae* (9.1%) and *Pseudomonas aeruginosa* (5.9%). Almost all were isolated from urine (66.7%), pus (19.2%) and blood (7.9%). Ten percent of isolates were resistant to meropenem, which was the least resistant drug, followed by cefaperazone-sulbactam (14.7%) followed by amikacin (26.25%), chloramphenicol (38.46%). Isolates showed high degree of resistance against cephalosporins ranging from 73% to 96%.

Conclusion: Gram negative bacilli showed high level of susceptibility towards cefaperazone-sulbactam combination. It can be considered as a cheap alternative in treatment of severe infections caused by gram negative bacilli in our setting which would reduce the cost of other expensive antimicrobials agents.

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Characterization of carbapenemase producing Enterobacteriaceae

B. Harish*, R. Srinivasan

Jawaharlal Institute of Medical Education & Research (JIPMER), Pondicherry, India

Background: The increase in antibiotic resistance among gram-negative bacteria is a notable example of how bacteria can procure, maintain and express new genetic information that can confer resistance to one or several antibiotics. An increasing number of organisms are resistant to a number of antimicrobial agents. The present study was undertaken to phenotypically characterize the carbapenemase producing Enterobacteriaceae. To isolate and identify carbapenemase producing clinical isolates, determine the antibiotic susceptibility patterns by MIC and characterize the carbapenemase production phenotypically and genotypically.

Methods: The study was carried out in the Department of Microbiology, JIPMER, Puducherry, India, with 50 Meropenem resistant Enterobacteriaceae isolates from patients with different illnesses. Identification, antibiogram, Minimum Inhibitory Concentration, Metallo beta-lactamase assay, Modified Hodge's Test were performed according to CLSI guidelines. Multiplex Polymerase chain reaction was carried out for blaVIM, blaIMP, blaNDM, blaKPC. The amplified DNA was analyzed by electrophoresis on a 1% agarose gel.

Results: Out of 50 Meropenem resistant isolates belonging to the family Enterobacteriaceae 54% were *Klebsiella pneumoniae* and 48% of specimens were wound swabs, followed by tracheal aspirates (20%). 68% of the isolates were from males. 40% of our isolates were from patients of age group 30 to 50 years. By MIC, 90% of them conferred high resistance to meropenem (4 to >128 µg/ml). 92% of the isolates were MBL positive and 58% were modified Hodge's test positive. The presence of blaNDM and blaVIM were confirmed by Agarose gel electrophoresis.

Conclusion: Our finding emphasizes the increasing carbapenem resistance and possible ramifications of their spread to other similar bacteria. There is need to monitor the use of these high end antibiotics both in hospital setup and general practice level.

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Comparison of nasal carriage of *Staphylococcus aureus* and its antimicrobial resistance in various grades of medical students

S.H. Hashemi*, M.-Y. Alikhani, M.-A. Seif-Rabiee, S. Ahmadi

Hamedan University of Medical Sciences, Hamedan, Iran, Islamic Republic of

Background: *Staphylococcus aureus* has been known as one of the most common nosocomial pathogens worldwide. Methicillin-

resistant *S.aureus* is one of the most important nosocomial pathogens with increasing global prevalence in recent 3 decades. Regarding to being carrier, medical students can be considered as one of the infection sources. The aim of this study was to assess the prevalence of nasal carriage of this organism in medical students.

Methods: In a cross-sectional study nasal swabs were collected from 466 medical students including 216 preclinical, 179 clinical students and 71 residents. Samples were cultured on blood agar. *S. aureus* isolates were further analyzed for antibiotic resistance. Each person was questioned for sex, grade, recent disease and drug history and family members' employment in hospital.

Results: Of 466 students, 109 (23.4%) were nasal carrier of *S. aureus*. According to the educational categories, 52 (94.1%) pre-clinical students, 39 (21.7%) clinical students, and 18 (25.3%) residents were carrier. No significant association was observed between nasal carrier rates and educational categories. Most isolates were resistant to penicillin (97.2%), and 53.2% were methicillin-resistant. Most methicillin-resistant strains were isolated from clinical students (76.3%, $p < 0/001$), and most vancomycin-resistant isolates were found in residents (41.2%, $p < 0/001$).

Conclusion: The rate of nasal carriage of *S.aureus* in medical students was similar to general population and hospital personnel, but the rates of MRSA and vancomycin-resistant *S. aureus* carriers are higher in medical students.

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Trend of penicillin-resistant *Streptococcus pneumoniae* in a tertiary teaching hospital in Malaysia

S.A. Hassan*, I. Nabilah, M. Zeehaida, H. Habsah

Universiti Sains Malaysia, Kota Bharu, Malaysia

Background: Antimicrobial resistance is a worldwide health-care problem. Geographic variations in the resistance of various bacterial pathogens are notable in Asia. Regarding *Streptococcus pneumoniae*, the Asian Network for Surveillance of Resistant Pathogens (ANSORP) study demonstrated that Asians had the world's highest level of antimicrobial resistance. Increasing prevalence rates of β -lactam- and macrolide-resistant *S. pneumoniae* strains have been observed in many countries. The aim of the survey was to determine the prevalence of Penicillin-resistant *Streptococcus pneumoniae* (PRSP) in our hospital

Methods: Retrospective laboratory based analysis of bacterial isolates from clinical specimens in Hospital Universiti Sains Malaysia (HUSM) from January 2001 to December 2011 was done. Antimicrobial susceptibility was determined using disc diffusion method and the minimum inhibitory concentration against penicillin was determined by Etest. The susceptibility was interpreted according to the Clinical and Laboratory Standards Institute (CLSI). Data were analyzed and presented as descriptive statistic.

Results: A total of 686 *Streptococcus pneumoniae* were isolated. Twenty isolates (2.9%) were PRSP. Majority of PRSP were isolated from sputum ($n=9$) followed by tracheal aspirates ($n=6$), swab ($n=3$), and eye ($n=1$). There was only one case of invasive PRSP. There were 16 isolates of *Streptococcus pneumoniae*

from cerebrospinal fluid however none of them were resistant to penicillin. Yearly analysis revealed that the highest PRSP isolation was in 2009 ($n=7$). The resistant rate of PRSP to trimethoprim-sulfamethoxazole was 63.2%, erythromycin 65.0%, cefotaxime 8.3%, and chloramphenicol 25%. However, 100% sensitivity was observed in ceftriaxone, ceftazidime, cefuroxime, amoxicillin-clavulanic acid and vancomycin.

Conclusion: Cases of PRSP were low in our hospital as compared to other Asian country. Periodic surveillance of resistance patterns is crucial to control cases of PRSN and establish guidelines for the administration of appropriate antimicrobial agents against this pathogen. Implementation and adherence to infection control measures by every health care provider is crucial to control the transmission of this pathogen.

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Multilocus sequence typing of clinical ESBL- producing *E. coli* strains

W.S. Ho^{1,*}, K.-L. Thong², C.C. Yeo³

¹ University of Malaya, Kuala Lumpur, Malaysia

² Institute of Biological Sciences, Laboratory of Biomedical Science and Molecular Microbiology, University of Malaya, Kuala Lumpur, Malaysia

³ Universiti Sultan Zainal Abidin, Kuala Terengganu, Malaysia

Background: Extended-spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae* is now a major problem in many hospitals in Malaysia especially in the critical care settings and *E. coli* is one of the most common organisms associated with ESBL production. Currently, CTX-M is the most common type of ESBLs with CTX-M-15 being the most prevalent genotype found in many parts of the world except for Asia. The wide distribution of CTX-M-15-producing *E. coli* strains globally has been partially contributed by the dissemination of the *E. coli* O25-ST131 clone. Therefore, the objective of this study was to detect the presence and prevalence of the *E. coli* O25-ST131 clone in our Malaysian strains and to determine the sequence types of CTX-M positive strains via MLST analysis.

Methods: PCR was used to detect and further subgroup the CTX-M genes of 20 ESBL-producing *E. coli* clinical isolates using established published primers. Specific detection of *E. coli* O25-ST131 clone targeting the specific *pabB* gene was carried out. For CTX-M producing-isolates that did not yield positive amplification for *pabB* gene, MLST was carried out using 7 housekeeping genes to determine their sequence types.

Results: Among the 20 ESBL-producing *E. coli* isolates, 17 harbored CTX-M-15 genes and 2 harboured CTX-M-14. Four ESBL-producing *E. coli* were positive for *pabB* gene indicating the presence of *E. coli* O25-ST131 clone. Using MLST, another common sequence type was observed for the ESBL-producing *E. coli*: ST354 ($n=3$). Three O25-ST131 clones were CTX-M-15 positive while another ST131 clone carried CTX-M-14. All three ST354 were CTX-M-15 positive. Other sequence types such as ST10, ST46, ST57, ST117, ST224, ST349, ST405, ST533, ST602 and ST617 ($n=1$) were also identified.