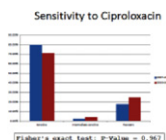


Sensitivity to Meropenem



Conclusion: The use of Levofloxacin as a prophylactic agent had not resulted in a statistically significant increase of resistance among the common Gram negative pathogens. However, close monitoring is warranted as a trend towards increase in the proportion of resistance was noted.

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Type: Poster Presentation

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 Time: 12:45-14:15
 Room: Hall 3 (Posters & Exhibition)

Prevalence and antibiotic sensitivity profiles of bacteria causing community acquired pneumonia



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Background: Despite the availability of potent new antimicrobial agents and vaccines, Community Acquired Pneumonia (CAP) remains a common and serious illness. The microbial etiologies and their resistant patterns vary widely. Frequent, irrational and unnecessary use of antibiotics, changes in environment, changes in lifestyle and increased mobility of the people have contributed to changes in the patterns of microbial profiles and their resistant patterns in the Community. Unfortunately, there have been very few studies done regarding etiology of CAP, prevalence of causative organisms and their resistance pattern in Nepal. Thus it was quite crucial to detect them in our context

Methods & Materials: A descriptive cross-sectional study conducted over a period of six months (March 2011–August 2011) at Bacteriology laboratory of Tribhuvan University and Teaching Hospital (TUTH) among 600 clinically diagnosed CAP patients visiting TUTH-OPD. Sputum samples that met the acceptance criteria of ASM were further processed according to the standard methodology.

Results: Bacterial etiologies could be identified only in 25.5% of cases of CAP. *Haemophilus influenzae* (26.9%), *Streptococcus pneumoniae* (20.0%) and *Pseudomonas aeruginosa* (19.4%) were the commonest bacterial etiologies. Twenty-six percent of *H. influenzae* isolates were MDR. The prevalence of MDR bacteria in CAP patients was 41.25%. Among gram-negative bacterial isolates, the highest number of MDR was seen in *Pseudomonas aeruginosa*, followed by *Klebsiella pneumoniae*, *E. coli* and *Acinetobacter* spp.

The prevalence of ESBL, AmpC and MBL producing gram-negative bacteria were **10.1%** (more common among *Klebsiella*

Conclusion: Different bacteria are responsible for CAP in our setting. MDR, ESBL, MBL and AmpC producing bacterial strains are present in our Community also. Thus it has demanded to take special care during treatment of patients with community acquired infections also and also sought for other similar type of extensive studies on large number of community isolates to characterize their genetic relatedness and resistant patterns so that appropriate measures can be applied.

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Antibiotic resistance pattern of HA-MRSA strains isolated from leukemia patients in Baghdad, Iraq



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Background: *Staphylococcus aureus* (*S. aureus*) is an important pathogen for hospital-associated infections, and it is especially difficult to treat because of emerging resistance to many antimicrobial drugs. Methicillin-resistant *S. aureus* (MRSA) have emerged as a clinically relevant human pathogen. Intracellular destruction of invading *S. aureus* is mainly mediated by phagocytosis, and this phagocytic process is crucial to the host innate defense against Staphylococci, so, disorders of phagocytic cells- as in cases of leukemia- cause frequency of infections at epithelial surfaces and the frequency of dissemination. The aim of study is to evaluate MRSA strains isolated from leukemia patients admitted to hospitals in regard to drug resistance.

Methods & Materials: A cross-sectional study was conducted at the Hematology center/Al-Mustansiriya University- Baghdad, from November 2013 to March 2014, where 48 known leukemia patients aged from 15 to 81 years have been enrolled for the detection of MRSA in their blood. Blood culture and conventional methods were used for the isolation and identification of pathogenic bacteria, along with the phenotypic and genotypic methods (i.e. detection of "PBP2a") for the identification of MRSA. Antibiotic susceptibility testing and vancomycin minimum inhibitory concentration (MIC) were also performed for all *S. aureus* isolates.

Results: Positive blood culture results were detected in 34 (71%) of patients. Among them, *S. aureus* was accounted for 11 (26.8%) of isolates. Antibiotics susceptibility tests for *S. aureus* isolates showed that 9 (82%) strains isolated from patients in current study were of MRSA variety. All of the *S. aureus* strains (100%) in current study were susceptible to Carbapenems. Intermediate resistance to vancomycin was noticed in 4 (36.4%) *S. aureus* isolates (i.e.

VISA strains), with no totally vancomycin-resistant (VRSA) strains. All of phenotypic MRSA isolates, except of one, were positive for PBP2a.

Conclusion: The study concludes that *S. aureus* is the most prevalent pathogen causing bacteremia in leukemia patients, with MRSA variety comprising the majority of these strains. Also, phenotypic method for MRSA detection can be performed using either of Methicillin, Oxacillin, or Cefoxitin with same results, with a non-significant statistical difference between the phenotypic method and the genotypic method- via the PBP2a detection.

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Prevalence and risk factors for intestinal colonization with vancomycin resistant enterococci among patients admitted to intensive care units of a large teaching hospital in Southern India



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Background: Vancomycin Resistant Enterococci (VRE) emerged as one of the major nosocomial pathogen across the globe. Gut colonisation rate with VRE is higher in patients admitted to ICUs due to high antibiotic pressure. VRE colonisation increases the risk of developing infection up to 5-10 folds. The aim of this study was to determine the rates of VRE colonization among patients admitted in two of the ICUs i.e. Medical Intensive Care Unit (MICU) and Pediatric Intensive Care Unit (PICU) and to assess the various risk factors which are associated with VRE colonization.

Methods & Materials: Rectal swabs were collected after 48 hours of ICU admission from a total of 302 and 198 patients from MICU and PICU respectively. Additionally samples were collected every 48 hours from 32 patients admitted in MICU and 19 patients in PICU whose initial VRE colonization was negative. The samples were inoculated on to Bile Esculin Sodium azide Agar (BEA) with 6 mg/ml of vancomycin. Growth on this medium were identified by standard biochemical test and Minimum Inhibitory Concentration (MIC) of vancomycin and teicoplanin was detected by Agar dilution method. Resistance genes for vancomycin were detected by PCR. Risk factors were assessed by logistic regression analysis. The patients were followed up to determine VRE infection rates

Results: The rates of VRE colonization in patients admitted to MICU was significantly higher (29%) than those in PICU (19%). Majority of the isolates were *Enterococcus faecalis* (62.6%) followed by *Enterococcus faecium* (38.4%). All the VRE isolates were positive for *vanA* gene. Younger age, increased duration of hospital stay, consumption of ceftriaxone and vancomycin were found to be significantly associated with VRE colonization in MICU, while in PICU,

only vancomycin usage was the significant risk factor. Among VRE colonized patients, six (4.7%) acquired VRE infection.

Conclusion: The VRE colonization rates in our ICUs were comparable to other hospitals worldwide. Strict adherence to hand hygiene and education of health care workers is necessary to minimize the nosocomial transmission of this organism.

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A study of 24 patients with colistin resistant gram negative isolates in a tertiary care hospital in South India



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Background: As the use of colistin to treat carbapenem resistant gram negative infections increases, colistin resistance is being increasingly reported in Indian hospitals.

Methods & Materials: Retrospective chart review of clinical data from patients with colistin resistant isolates (MIC > 2). Clinical profile, outcome and antibiotic combinations that were used to treat colistin resistant infection were analysed.

Results: Twenty four colistin resistant isolates were reported over 18 months (Jan 2014–June 2015). The mean age of the patients was 58.33; average length of stay was 36.37 days. Previous hospitalisation within 3 months was noted in all 24 patients. An invasive device was used in 22(91.67%) patients. Urine was the commonest site of infection=8(33%), followed by blood= 6(25%), respiratory=5(20.8%), pus=4(16.67%) and other (CSF)=1(4.17%). Commonest organism was Klebsiella, n=21(87.5%). Antibiotics that were used in their current admission prior to isolating a colistin resistant organism were: colistin in 15 patients(62.5%), carbapenem in 19(79.17%), BL-BLI in 9(37.5%), tigecycline in 12(50%). 16(66.6%) were considered to have true infection while 8 (33.3%) were considered as colonisation and were not treated. Sensitivity of these isolates to other drugs tested were – tigecycline 18/24(75%), chloramphenicol 15/24(62.5%), amikacin 7/24(29.17%), cotrimoxazole 3/24(12.5%). Fosfomycin was tested in 4 isolates only and was sensitive in all. Antibiotic that were used for treatment were combinations of tigecycline, chloramphenicol, fosfomycin, amikacin, ciprofloxacin, cotrimoxazole and sulbactam. Among 16 patients with true infection, 4(25%) improved, 9(56.25%) expired and 3(18.75%) were transferred to other centers in poor condition at patient's request. Among 8 patients who were considered to have colonisation, there were no deaths and 7(87.5%) improved. Among the 6 bacteremic cases, 5 patients expired and 1 improved. Among the non-bacteremic patients with true infections 4/10(40%) expired. Bacteremic patients had a significantly higher risk of death compared to all non-bacteremic patients (p=0.014) though not significantly in non-bacteremic infections after exclusion of colonization (p=0.145).

Conclusion: Colistin resistance among Gram negative bacteria, especially Klebsiella, is emerging in Indian hospitals and carries a