Comparison of efficacy of definitive therapy of beta-lactams versus vancomycin for methicillin-susceptible *Staphylococcus aureus* bacteremia: a systematic review and meta-analysis

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Background/Purpose: Vancomycin is commonly started empirically for staphylococcal bacteremia. However, when culture results show methicillin-susceptible *Staphylococcus aureus* (MSSA), some clinicians still continue vancomycin, particularly if patients were improving, and sometimes the busy clincians might just forget to de-escalate. The purpose of this study is to compare the efficacy of beta-lactams versus vancomycin as definitive therapy for MSSA bacteremia.

Methods: Two authors independently searched the PubMed, EMBASE and International Pharmaceutical Abstracts through Nov 01, 2018. Any study comparing efficacy of definitive therapy with cefazolin or antistaphylococcal penicillins versus vancomycin was considered for inclusion. Studies missing one of these criteria were excluded. We estimated the relative risk (RR) with 95% confidence intervals (CIs) using random-effects model and evaluated heterogeneity (I^2).

Results: Six observational studies (total of 920 patients) were included. A significantly lower all-cause mortality was found with beta-lactams compared to vancomycin (RR, 0.473; 95% CI, 0.253 to 0.885; P-value = 0.019; $I^2 = 0\%$). The relapse occurred less significantly with beta-lactams compared to vancomycin (RR, 0.386; 95% CI, 0.155 to 0.963; P-value = 041; $I^2 = 0\%$). With regard to persistent bacteremia more than 3 days, it was also lower with beta-lactams (RR, 0.135; 95% CI, 0.022 to 0.812; P-value = 0.029; $I^2 = 0\%$).

Conclusion: This meta-analysis provides support for the higher efficacy of beta-lactams over vancomycin as definitive therapy. Clinicians should ensure that empiric vancomycin is de-escalated to beta-lactams once culture results confirm that the causative pathogen for bacteremia is MSSA.

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Knowledge and attitude about antibiotics usage among mothers at nursery center of Princess Nourah University

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Introduction: An estimated 159 million antibiotics are unnecessary prescribed per year which led to antibiotic abuse. Unnecessary exposure to antibiotic reduces its effectiveness over time, which will cause a resistance to antibacterial agents. Since the mother's knowledge and attitude toward antibiotics which leads to antibioticts misuse might influence the children general health by causing a weakness in their immune system, this study purpose was to assess the knowledge and attitude of the mothers who have children about the antibiotics usage and their relation to some demographic characteristics.

Method: a cross-sectional study was conducted among 149 mothers who have children in nursery center at Princess Noura University. Participants were recruited through purposive sampling technique. Data was collected by a questionnaire about knowledge and attitude regarding antibiotic use that consisted of 25 questions. Data was statistically analyzed using computerized software statistical package SPSS version 23. Chi square was used to examine the association between knowledge, attitude and some demographic variables.

Result: 55% of the participants had good knowledge about antibiotics and 58% had good attitude towards proper use of antibiotics. The level of knowledge among the participants was significantly associated with having a family member in health field ($p = .04$). On the other hand, the total level of attitude was shown to be associated with age and education level ($p = .02$), ($p = .03$) respectively. However, knowledge had no significant association (> 0.05) with the attitude of the mothers toward antibiotics use.

Conclusion: Targeted antibiotics awareness campaigns are necessary to educate the mothers about the hazards of antibiotics abuse in an attempt to decrease .antibiotics resistance among children.

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Quantitative proteomics identified unique protein signatures in the context of overlap of HIV subtypes

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Human immunodeficiency virus-1 (HIV-1) mainly relies on host factors to complete its life cycle. Hence, it is very important to identify HIV-regulated host proteins for better understanding of the virus life cycle and pathogenesis. In addition, understanding these proteins may possibly identifying core target molecules as diagnostic and prognostic markers. The discovery of targets for potential therapeutic intervention will improve the management of these patients.

Our study population is uniquely comprised of three different HIV infected groups: 1) patients with HIV type 1 (HIV-1), known to be both highly prevalent and virulent. 2) HIV-1 elite controllers (HIV-EC), rare proportion of HIV-1 infected persons with undetectable HIV-1 viremia without Antiviral therapy (ART), a model for successful immune activity against HIV-1. 3) Last group, are those infected by HIV type 2, rare, yet a unique and understudied model of 'natural' attenuated lentivirus infection, with an overrepresented group of infected patients who progress to AIDS slowly and effectively control viral replication.

Quantitative gene expression analyses platforms such as Proteomics are capable of discovery disease related or specific biomolecules for the diagnosis and treatment monitoring of HIV infection in addition to other related infectious diseases. This study aimed at discovery of implicating biomarkers of HIV-induced diseases and elucidating the molecular mechanisms involved in

HIV infections. Peripheral blood plasma (PBP) samples from different HIV infected patients and negative control from healthy donors were subjected to expression proteomics using label-free quantitative liquid chromatography tandem mass spectrometry (LC-MS/MS). Over 314 unique PBP protein species were identified from all the samples of which 100 were significantly differentially expressed (≥ 2 to ∞ - fold change & $p < 0.05$) between HIV-1, HIV-2 and HIV-1 EC control subjects. Majority of these proteins shares similar expression changes between HIV-1, and HIV-2 versus HIV-1 EC. Two of the identified proteins XRCC5 and PSME1 were implicated in the early phase of the pathway network for HIV life cycle. Other identified proteins were involved in infectious disease and disease of signal transduction. Among them were MAP2K1, RPL23A, RPS3, RPS8, CALR, PRDX1, SOD2, LMNB1, LMNA, PHB, FGA, and FGB. Interestingly; despite high degree of similarity in protein profiles of HIV-1 and HIV-2, we identified only six proteins with significant expressing changes ($P < 0.05$). These include ETFB, PHB2, S100A9, LMO2, PPP3R1 and Vif, a fragment of Virion infectivity factor of the immunodeficiency virus type 1. In conclusion, we have identified HIV-related protein expression changes and these proteins once validated in large sample cohort might potentially be capable of early diagnosis and prognosis of HIV diseases.

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Optimizing efficiency of testing, reporting and utilization of Antimicrobials in diagnostic Microbiology

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Background: Antimicrobial susceptibility testing is performed using various techniques in a Microbiology laboratory. Implementation of interpretive standards like CLSI (Clinical laboratory Standards Institute) can optimize antibiotic usage and avoid indiscriminate testing and reporting.

Methods: CLSI 2017 interpretive standards for antimicrobial testing were implemented at Microbiology section, KFSHRC, Jeddah. All testing panels were revised accordingly and some of the obsolete tests were removed from the panels. Surrogate testing was implemented for certain drugs on appropriate specimen types. Susceptibility reports were released with additional comments whenever deemed necessary. Direct susceptibility testing from blood cultures were performed traditionally for gram positive and gram negative isolates and reported to physicians. Upon receiving MIC from automated susceptibility testing machine, these direct susceptibility results were suppressed. Considering the recommendations from Infectious Diseases department that MIC results are more reliable for gram negative isolates, direct testing by disc diffusion on positive blood cultures was discontinued.

Results: Retrospective analysis after implementation showed a 43% reduction in annual material cost for antibiotic discs compared to the previous year. Surrogate testing using cefazolin and Ampicillin could predict the susceptibility to few other drugs thus providing alternative drug choices available for treating certain conditions like uncomplicated UTI (Urinary tract Infection). Quality control for antimicrobials could be streamlined by omitting unnecessary weekly testing with infrequently reported antimicrobials. Effective manpower utilization was also possible after optimizing the workflow by eliminating non value added tasks.

Conclusions: Judicious means of testing and reporting of antimicrobials can prevent overuse and assist in antibiotic stewardship. Besides this, cost savings can be achieved by optimizing antimicrobial testing and effective manpower utilization.

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Phenotypic and genotypic characterization of carbapenem-resistant *Enterobacteriaceae* in Bahrain and Saudi Arabia

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Background: Carbapenem resistant *Enterobacteriaceae* (CRE) is a worldwide emerging public health threat. These gram-negative rods are predominantly associated with nosocomial and systemic infections which are difficult to treat and control since they are resistant to numerous antibiotic agents. Carbapenemase production is presently the most important mechanism of carbapenem resistance in *Enterobacteriaceae* and believed to be primarily responsible for the increasing spread of CRE. Different genotypic and phenotypic methods exist to detect carbapenemases; however, each has a limitation. Recently, the CLSI guidelines suggest utilizing mCIM assay.

Purpose: We aim to evaluate the performance of mCIM test in detection of carbapenemase activity in *Enterobacteriaceae* in reference to molecular methods and to determine the common carbapenemase genes at King Fahad Specialist hospital (Saudi Arabia) and Salmaniya medical complex (Bahrain).

Methods: A total of 110 non-duplicate clinical isolates of *Enterobacteriaceae*, were tested by mCIM assay and the performance was compared with multiplex PCR designed to detect the five common carbapenemase genes (KPC, VIM, IMP, NDM and OXA-48).

Results: *All of the isolates* had one of the common carbapenemase genes. The sensitivity of the mCIM is 97.3% with 95% CI of (0.916–0.992). Only 3 of the isolates were mCIM false negative. The results indicate that in Bahrain and Saudi Arabia, OXA-48 is the dominant carbapenemases among *Enterobacteriaceae* followed by NDM, with low prevalence of VIM.

Conclusions: Our results confirm that mCIM test is a simple tool for the reliable confirmation of carbapenemase activity in *Enterobacteriaceae*, especially in clinical microbiological laboratories with limited resources.

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Platelet abnormalities with piperacillin compared to other beta-lactams: A meta-analysis of randomized controlled trials

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Background/Purpose: Prolonged use of some β-lactams can lead to hematological side effects, particularly thrombocytopenia. Piperacillin/tazobactam can cause thrombocytopenia as an adverse drug reaction according to the statement of the manufacturer's package insert of the drug.

The aim of this study is to compare the rate of serum platelets abnormalities between piperacillin/tazobactam and other β-lactams.