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 over-represented 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