

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.