resistant genes. All 7 carried blaVIM resistant P.aeruginosa isolates were found to be MBL producers by MHT and MICs methods. This indicates that the incidence of genes responsible for carbapenemase production in P.aeruginosa is of concern and further molecular investigations are required.

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Bioinformatics Analysis pipeline of Whole-Genome Sequence Data to Investigate Antimicrobial Resistance

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Background: Next generation sequencing (NGS) is rapidly becoming the technique of choice for the investigation and prediction of antimicrobial resistance (AMR) at an unprecedented scale. Whole-genome sequence data enables the analysis of the genetic information of AMR genes and the assessment of virulence and relatedness among the pathogens carrying these genes. Currently, there is a paucity of microbial genomics and bioinformatics-based research to improve understanding of AMR challenges in the Gulf Health Council (GHC) countries. Here we present the bioinformatics pipeline in development at KAIMRC to identify molecular mechanisms of AMR from genomes sequenced using Illumina platforms.

Methods: The bioinformatics pipeline includes i) read quality assessment and trimming ii) read mapping to reference sequences to detect multi-locus sequence types (MLST), virulence and AMR genes iii) assembly and annotation iv) single-nucleotide polymorphism (SNP) detection and phylogenetic analysis. It was developed using publicly available and open source software and in-house scripts for automation and data management. The pipeline was evaluated on 22 genomes from multidrug-resistant klebsiella pneumoniae isolates recovered from patients at King Abdulaziz Medical city, Riyadh, sequenced locally using Illumina Miseq.

Results: The pipeline showed that the K. pneumoniae isolates comprised of eighteen ST14, two ST147, one ST231 and one ST278. Comparative analysis and phylogenetic tree using SNP identified relatedness among the isolates belonging to ST14. Resistance genes detected including NDM-1, OXA-48, OXA-9, OXA-1, mph(A) and msr(E) using the pipeline correlated with the phenotypic resistance profiles.

Conclusions: The validation of our pipeline showed its potential to accurately detect AMR genes and assess relatedness amongst isolates during outbreaks. It is suitable for the study of any bacterial pathogen although further development is required for the full automation.

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A Snapshot about the Mobile Colistin Resistance (mcr) in The Middle East and North Africa Region

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Background and Purpose: The emergence of colistin resistance among GNB is overwhelming. The recent reporting of the novel plasmid mediated colistin resistance genes (mcr-) is a serious concern and intimidating to accelerate the spread of pandrug resistant bacteria. To date, eight different mcr- genes were described. A number of studies have confirmed the worldwide dissemination of the mcr-1, and other MDR genes in several Enterobacteriaceae, including E.coli, Klebsiella pneumoniae and Salmonella spp. Yet, few data are available on the dissemination of mcr-genes other than mcr-1in human samples, in the MENA Region.

Methods: A multiplex PCR assay was used to screen for the presence of mcr-1 to mcr-5 in large collections of >1,000 GNB of human origin. The isolates were collected from the GCC countries, Egypt and Jordan, for surveillance purposes of MDR GNB. Pooling of the isolates were prepared to expedite the screening process. Positive controls of mcr-2, mcr-4 and mcr-5 genes were synthesized using

Equine Herpes Virus-1 as a template, to amplify the designated gene products.

Results: The mcr-1 gene was detected in one pool belongs to E.coli isolates from Qatar, and in one pool consist of E.coli and K.pnemoniae from Jordon. The results also detected the presence of mcr-5 gene in a pool indicated E.coli isolates from Saudi Arabia.

Conclusion: This is the first detection of mcr-1 in Jordon, and mcr-5 in the Saudi Arabia in samples derived from human isolates. Further studies will be conducted to confirm the source of these isolates. Also, the full characterization of the bacteria carrying the mcr-1 and mcr-5 will be confirmed by next generation WGS using illumine MiniSeq platform to further identify other MDR genes, sequences types and plasmids harboring mcr genes. This finding should stimulate active surveillance programs to monitor the emergence and spread of MDR in the MENA region.

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Direct Physician Engagement as a Stewardship Modality to Curtail the Overuse of Antimicrobials in the Intensive Care Units at a Tertiary Care Hospital in Saudi Arabia

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Background: Antimicrobial Resistance (AMR) is a major healthcare threat worldwide. As bacteria have become resistant to almost all available antimicrobials, previously treatable healthcare infections have now become life threatening. Antimicrobial misuse by treating physicians is believed to be a major contributor to this problem.

Methods: As part of the infection prevention and control departmental activities, the Antimicrobial Stewardship Program (ASP) team conducted a prospective audit in the adult and trauma ICUs at King Abdulaziz Medical City-Riyadh (KAMC-R) between September and December 2017. The ASP team consists of an ID consultant and 2 infection control practitioners. Targeted antimicrobials were reviewed by the ASP team and treating physicians to determine the appropriateness given the available clinical and laboratory information. Interventions were recommended by the ASP team, who also checked the implementation of these interventions by treating team.

Results: A total of 401 antimicrobial prescriptions were reviewed during the audit period. Frequently prescribed antimicrobials included piperacillin/tazobactam (20.2%), meropenem (19.7%), and vancomycin (10.5%). Empiric therapy represented 68% of all prescriptions, followed by therapeutic (29%), and prophylactic (3%) ones. Cultures were available for 384 (96%) prescriptions and the results were positive for 37% of them. Of the 401 antimicrobials reviewed, 314 (78.3%) were appropriately prescribed (Figure 1). Corrective interventions were suggested by the ASP team in 86 (21.6%) of the prescriptions. The most common intervention suggested was discontinuation of the antimicrobial (63%), followed by change the type of antimicrobial or its dose (50%), de-escalation (9%), and IV to oral (1%). Overall 54 (63%) of the 86 interventions recommended by the ASP were carried out by the treating team.

Conclusion: Direct engagement of an infectious disease physician of the ASP team with treating physicians in ICU setting can led to improvement of the appropriateness of antimicrobial use. The concept of direct physician engagement holds promise as an effective stewardship modality.

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Risk Factors And Outcomes For Clostridium Difficile Infection In King Abdulaziz Medical City (KAMC), Riyadh. A Case Control Study

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Keywords: Clostridium difficile; Risk factors; Outcomes; Case control; Infection Control

Background: Clostridium difficile infection (CDI) incidence and severity has been substantially increasing over the past few years. Nevertheless, there is almost lack of local data describing the risk factors associated with CDI among hospitalized patients. The aim of the current study was to determine the risk factors for CDI development and complications at tertiary care setting.

Methods: A case-control design was performed through chart review of adult patients who have been tested for the C. difficile using PCR test at King Abdulaziz Medical City (KAMC, Riyadh, Saudi Arabia) during the study (2013 and 2014). Data on potential risk factors, medications, and outcome were collected by infection control staff using a structured data collection form. Two controls were recruited for each case while ensuring group matching on age (within 5 years), gender, year, and hospital location (ICU, ward, ER). Inclusions included testing for the C. difficile using PCR test on unformed stool samples irrespective of the patient symptoms. Both gender and all hospital locations were eligible to be included. Exclusions included testing on formed stool, duplicate samples, age under 18 years, and children.

Results: A total of 321 total 310 patients were included in the study; 103 cases and 207 controls. they included 159 (51.2%) males and 151 (48.8%) females, with no difference between groups (p = 0.97). The average age was in 62 ± 22 years in cases and 60 ± 20 years in controls (p = 0.61). the source of admission was emergency department in 94.2% of the cases and 88.8% of the control (p = 0.11). CDI cases were mainly healthcare-acquired (62.1%). In univariate analysis, cases were significantly associated with age, immunosuppression, malnutrition, cancer chemotherapy, number of antimicrobials used, and the number of antimicrobial days. In multivariate analysis, cases were independently associated with malnutrition (OR = 1.66, CI: 0.10–0.58, p = 0.001) and the number of antimicrobial use (OR = 1.26, 95% CI: 1.02–1.55, p = 0.020). Cases had significantly frequent complications (14.6% versus 0.5%, p < 0.001) but generally similar mortality (24.3% versus 31.2%, p = 0.205). After an adjustment for several confounders, mortality was independently associated with age (OR = 1.04, 95% CI: 1.02–1.05), ICU stay (OR = 3.37, 95% CI: 1.74–6.49), higher number of antimicrobial days (OR = 1.05, 95% CI: 1.02–1.08), renal diseases (OR = 2.60, 95% CI: 1.37– 4.89), and immunosuppression (OR = 3.09, 95% CI: 1.60–5.99).

Conclusion: The study outlined a number of comorbid and healthcare-related risk factors for developing CDI and associated mortality among admitted patients at tertiary care setting. The finding may help healthcare providers in targeting patients at higher risk of CDI with more preventive and infection control measures.

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