

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-1 in 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

