## PP032

### Emergence of mobile colistin resistance genes mcr-1 and mcr-8 in Saudi Arabia

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**a. Background and Purpose:** Colistin represents the last-resort antibiotics used for treating carbapenem-resistant Enterobacteriaceae related infections. Colistin resistance has been reported in Saudi Arabia in Gram-negative bacteria (up to 40%). Nevertheless, only a handful of cases were identified to be mcr-linked due to the current clinical microbiology techniques, which do not utilize Whole-Genome Sequencing (WGS). In this study, we surveyed mcr-types from Multiple-Drug resistant (MDR) Klebsiella pnumoniea clinical isolate using WGS.

**b. Methodology:** The Klebsiella pnumoniea isolates sequenced as part of an effort to sequence Gram-negative bacteria pathogens isolates in the MDR organism surveillance depository (n = 1633) for the period 2014-2018 (unpublished data). The isolate carrying mcr-8 (NGKP-54) was cultured from the sputum of a female patient in her late-60s who were treated from Non-Small-Cell Lung Carcinoma in the western of Saudi Arabia in 2015.

**c. Results and Discussions:** In silico multilocus sequence typing (MLST) allocated NGKP-54 to a novel sequence type (ST3513) that is a single-locus variant of ST-1425, frequently accompanying the production of many carbapenemases in the Middle East. The NGKP-54 was resistant to aminoglycoside, colistin, cephalosporin, and fluoroquinolone. The isolate was resistant to colistin by broth microdilution, confirmed by genome analysis revealed multiple colistin-resistant genes. The MIC of colistin were determined to be 16 μg/ml. WGS of old surveillance Kp isolates identified colistin-resistant genes mcr-1, mcr-8, and partial mcr-8. Each gene was cloned and tested for colistin resistance contribution. The Strain NGKP-54 contains two and partial colistin genes all contributing to its colistin resistance.

**d. Conclusions:** Thus far, this is the first report of mcr-8 in colistin non-susceptible Kp in Saudi Arabia and the first global report of the combined resistance of multiple mcr genes. This requires a further investigation especially that Saudi Arabia is a hub for annual mass-gathering events.

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## PP033

### Prevalence of Molecular Mechanisms of Carbapenem Resistance in Pseudomonas aeruginosa clinical isolates from Saudi Arabia

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Background/Purpose: Pseudomonas aeruginosa is one of the most successful emerging multidrug-resistant causative pathogen in hospital acquired infections leading to high morbidity and mortality rates. It is intrinsically resistant to some commonly used antibiotics, and it is capable of acquiring resistance to multiple classes of antibiotics. Carbapenemase-producing isolates are becoming more common worldwide and here we evaluated the prevalence of carbapenemase-encoding genes in P. aeruginosa clinical isolates collected from different hospitals in Saudi Arabia through the National Guard-Health Affairs (NGHA) Antimicrobial resistance (AMR) Surveillance program.

**Methods:** P. aeruginosa isolates (n = 635) were collected between March 2018 and March 2019 from five hospitals located in the east, west and center of Saudi Arabia. Identification was confirmed using species-specific PCR targeting the oprL gene. Susceptibility testing was performed using the Vitek II system. Carbapenemase (IMP, VIM, NDM, KPC, GES, OXA48) and Extended-Spectrum β-lactamase (VEB, PER and BEL) genes were screened by PCR.

**Results/Discussion:** Susceptibility testing showed that isolates were mostly resistant to imipenem (28.2%) followed by meropenem (23.0%), ciprofloxacin (20.8%), ceftazidime (17.8%), piperacillin-tazobactam (16.9%), cefepime (13.2%), amikacin (8.5%), gentamicin (8.3%), colistin (2.4%). In total, 18.7% (119/635) P. aeruginosa isolates were resistant to meropenem and imipenem (MIC $\geq$ 8 mg/L). PCR detected the presence of genes encoding blaGES (n = 16), blaVIM (n = 6), blaNDM (n = 1) or blaOXA48 (n = 1) carbapenemases in only 20.1% (24/119) of these isolates; three of the six VIM producers harboured also genes encoding PER (n = 2) and VEB (n = 1). Four isolates 3.4% (4/119) isolates carried only blaPER (n = 2) or blaVEB (n = 2) whereas resistance profiles in the remaining isolates suggest that the upregulation of efflux and/or changes in the composition of outer membrane porins are at the origin of resistance to carbapenems.

In conclusion, our study identified various molecular mechanisms contributing to carbapenem resistance among P. aeruginosa isolates in Saudi Arabia.

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