

**EV0350**

**ePoster Viewing**

**Resistance surveillance & epidemiology: Gram-negatives**

**Outbreak of CTX-M-15 and SHV-12 extended-spectrum beta-lactamase (ESBL) co-producing *Klebsiella pneumoniae* in a neonatal intensive care unit (NICU), in Ha'il, Saudi Arabia**

Mushtaq Khan<sup>1</sup>, Mohammed Almogbel\*<sup>1</sup>, Ibraheem Ashankyty<sup>1</sup>, Khalid Al-Mutier<sup>1</sup>, Ahmed Altheban<sup>2</sup>, Musa Alenezi<sup>3</sup>, Sahar Hammam<sup>4</sup>, Afaq Gowhar<sup>1</sup>, Mohamed Tharwat<sup>5</sup>, Rayan Alahmadi<sup>6</sup>, John P. Hays<sup>7</sup>, Godfred Menezes<sup>1</sup>

<sup>1</sup>*Molecular Diagnostic and Personalized Therapeutic Unit, College of Applied Medical Sciences, University of Ha'il, Ha'il, Saudi Arabia*

<sup>2</sup>*Training Department, Nursing College, University of Ha'il, Ha'il, Saudi Arabia*

<sup>3</sup>*Maternity Hospital, Ha'il, Ha'il, Saudi Arabia*

<sup>4</sup>*Pathology Department, Maternity Hospital, Ha'il, Ha'il, Saudi Arabia*

<sup>5</sup>*Molecular Diagnostics and Personalised Therapeutics Unit (Mdptu); College of Public Health & Health Informatics, University of Ha'il, Ha'il, Saudi Arabia., Ha'il, Saudi Arabia*

<sup>6</sup>*Molecular Diagnostics and Personalised Therapeutics Unit (Mdptu); College of Applied Medical Sciences, University of Ha'il, Ha'il, Saudi Arabia., Ha'il, Saudi Arabia*

<sup>7</sup>*Erasmus MC, Medical Microbiology & Infectious Diseases, Rotterdam, Netherlands*

**Background:** Neonates are at a very high risk of developing life-threatening bacterial infections in intensive care settings. In the majority of cases these healthcare-associated infections are associated with *Klebsiella pneumoniae* and *Escherichia coli* and require the administration of antibiotic therapy. However, there has been a rapid and global dissemination of extended-spectrum- $\beta$ -lactamase (ESBL) producing *Klebsiella pneumoniae* and *Escherichia coli* in the hospital setting, which complicates and limits current antibiotic treatment options. This increase has been mainly due to the successful dissemination of CTX-M-15 gene-carrying bacterial isolates via mobile genetic elements. The aim of this study was molecular characterization of antimicrobial resistance and clonality determination of the *Klebsiella pneumoniae* and *Escherichia coli* isolates from an outbreak in a neonatal intensive care unit (NICU), in Ha'il, Saudi Arabia.

**Material/methods:** During April 2014, an outbreak of 3rd generation cephalosporin resistant infections was reported within a neonatal intensive care ward in a maternity hospital at Ha'il, Saudi Arabia. A total of 821 samples were screened, including 407 patients and 414 others (comprised of health care workers, concerned staff and NICU environment). The bacteria cultured were identified by routine tests as well as MALDI-TOF mass spectrometry (Bruker). Antibiotic resistance testing was performed using VITEK 2 and Microscan. PCR-sequencing was performed to determine the presence of blaTEM,

blaSHV and blaCTX-M antibiotic resistance genes. Isolate genotyping was performed using pulsed field gel electrophoresis (PFGE) protocol adapted from PulseNet.

**Results:** A total of 41 *K. Pneumoniae* isolates were cultured from neonates with the majority of isolates (95.1%) being resistant to 3rd generation cephalosporins. Overall 90.2% of the *K. Pneumoniae* isolates were resistant to aminoglycosides. However all the *K. pneumoniae* were susceptible to ciprofloxacin, levofloxacin, carbapenems, colistin and tigecycline. A total of 87.8% (36/41) *K. pneumoniae* were co-producers of CTX-M-15 and SHV-12. Further, 4.8% were CTX-M-2 producers and 63.4% were positive for TEM-1.

A total of 19 *E. coli* isolates were cultured from neonates, with the majority of isolates (17/19) being resistant to 3rd generation cephalosporins. However, all the isolates were sensitive to aminoglycosides, ceftazidime, amikacin, nitrofurantoin, levofloxacin, piperacillin/ tazobactam, carbapenems, colistin, and tigecycline. A total of 21.0% were co-producers of CTX-M-15 and SHV-12. Further, 31.6% were positive for CTX-M-2 and 57.9% were TEM-1 positive. The majority (31/41) of *K. pneumoniae* isolates belonged to a single genotypic lineage at the 85% similarity level, while *E. coli* isolates grouped into 2 genetic clusters at 80% similarity (18/19 isolates).

**Conclusions:** This is the first report of CTX-M-15-positive *K. pneumoniae* and, *E. coli* isolates recovered from an outbreak in a NICU in Hail, Saudi Arabia. It is alarming to notice a high rate of outbreak isolates with simultaneous production of CTX-M-15 and SHV-12 conferring high level resistance to oxyimino-cephalosporins.