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Poster Session VI

Epidemiology with molecular typing

MLST AND PFGE TYPING OF *E. COLI* AND *K. PNEUMONIAE* STRAINS ISOLATED FROM BLOODSTREAM INFECTIONS FROM VERY-LOW BIRTH WEIGHT INFANTS IN POLAND.

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**Objectives**

Infections of the newborns, particularly with very low birth weight (VLBW) remain one of the most significant problems of the contemporary medicine.

The most important risk factors of bloodstream infection (BSI) are invasive devices and frequent use of antimicrobials. The aim of this study was typing the most isolated Gram-negative rods from BSI in VLBW newborns.

**Methods**

Data collection was made from 2009 to 2011 and included 5 neonatal intensive care units (NICUs).

A total of 55 Enterobacteriaceae bacteria from BSI were isolated. Among them were *Escherichia coli* (24), *Klebsiella pneumoniae* (16), *Enterobacter cloacae* (5), *Klebsiella oxytoca* (4), *Serratia marcescens* (4) and *Morganella morganii* (1) isolates.

Species was determined in the Vitek automatic system, drug resistance was determined by disc diffusion method (according to EUCAST guidelines). Extended –spectrum beta-lactamases (ESBLs) activity was detected with a modified double disk synergy test. Genotyping of *E. coli* and *K. pneumoniae* isolates was carried out using pulsed field gel electrophoresis (PFGE) and multi locus sequence typing (MLST) methods.

**Results**

Among the infections caused by *E. coli*, 20.8% of BSI was associated with central venous catheter (CVC) and 8.3% with peripheral venous catheter (PVC).

ESBLs activity was detected in 6 *E. coli* isolates, five of them carried the bla-CTX-M-15 gene and 1 had CTX-M-3 gene.

PFGE typing demonstrated that all *E. coli* isolates had unique pulsotypes.

MLST typing revealed 10 different sequence types: ST131 (7 isolates), ST69 (5), ST141 (3), ST998 (3), ST73 (1), ST75 (1), ST95 (1), ST543 (1), ST569 (1). One isolate was non-typeable.

Among the infections caused by *K. pneumoniae*, 43.75% was associated with CVC and 18.75% with PVC. ESBLs activity was detected in 9 *K. pneumoniae* isolates, 8 had bla-CTX-M-15 and 1 had CTX-M-3 gene.

PFGE typing showed 8 different pulsotypes. The most - 6- isolates - belonging to one clone. Additional three clones consisted of two isolates. Remaining 4 isolates had unique pulsotypes.

MLST typing revealed also 8 different sequence types: ST 336 (6 isolates), ST6 (3), ST 11 (2) ST17 (2), ST153(1), ST321 (1), ST 870 (1). PFGE main clone was compatible with ST 336.

**Conclusions**

Studied rods were still the most important Gram-negative bacteria in polish NICUs, but both had completely different epidemiology. They also require a different type of surveillance and infection control.

*E. coli* isolates showed very unlike pulsotypes, epidemic clones were not detected. Seven isolates belonging to high-virulent ST131. The success of the ST131 clone is explained by fluoroquinolone resistance and numerous virulence factors. ST-131 is responsible for the worldwide dissemination of CTX-M-15.

*K. pneumoniae* more often than *E. coli* causes clonal epidemics – strains belonging to main clone (and ST336) came from the same NICU and from the outbreak. Only two *K. pneumoniae* isolates belonging to major international hospital clone ST11 showing high-level resistance.

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