EV0100

ePoster Viewing

Antimicrobials: epidemiology of MDR Gram-negatives

Epidemiological comparison of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae from equine patients at the Finnish Veterinary Teaching Hospital in 2011-2014

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Objectives
Equine infections caused by Extended-Spectrum Beta-lactamase (ESBL) producing *Enterobacteriaceae* were observed at the end of 2011 at the Equine Veterinary Teaching Hospital of the University of Helsinki. Due to increasing number of infections in fall 2012 and spring 2013, enhanced surveillance, including contact patient screening, was initiated. Objectives of this work were to describe ESBL-producing isolates collected between 10/2011 – 05/2014 and to investigate their clonality.

Methods
Infection specimens were investigated with conventional methods. Screening specimens were plated onto selective agars (ESBL Brilliance, Oxoid). Identification of bacterial isolates was done with biochemical methods and susceptibility testing with the disk diffusion method (CLSI). ESBL phenotype was confirmed with the double disk method and ESBL/AmpC detection disks (MAST, UK). Clonality by species was investigated by a PFGE method (PulseNet, CDC) and analysed by UPGMA-cluster analysis with 0.5% optimization and 1% Dice band matching tolerance with $\geq$ 85 % similarity cut off value. ESBL genes (CTX-M, TEM, SHV) were investigated with multiplex PCR and sequencing.

Results
A total of 117 ESBL-isolates from infections (n=25 isolates) and screening specimens (n=92) were investigated. These originated from 83 horses. Twenty four (29%) horses had an infection.

Of the 117 ESBL isolates, 43 (37%) were *Klebsiella pneumoniae*. Nearly all (n=39) represented the same PFGE clone with minor differences and all but two were isolated during April – August 2013. The members of the major clone were also resistant to trimethoprim-sulfonamides, enrofloxacin, gentamicin and doxycycline. Thirteen representatives of the clone possessed the CTX-M-1 gene.

E. cloacae (n=32/117, 27%) distributed into 12 PFGE types with six clusters of two to nine isolates. *E. coli* (n=31/117, 26%) scattered into 21 pulsotypes, of which the largest one had seven members. The rest were divergent types with one to three isolates. Six *K. oxytoca* isolates formed two clusters. Regarding other species, two *E. aerogenes*, two *Citrobacter braakii* and one *C. freundii* were identified.

Of the ESBL isolates, 74/117 were resistant to trimethoprim-sulfonamides, enrofloxacin and gentamicin. No resistance to amikacin was observed. *Enterobacter* and *Citrobacter* spp. commonly showed both ESBL and AmpC phenotype whilst *Klebsiella* spp. and *E. coli* expressed ESBL phenotype.

Apart from isolates belonging to the major *K. pneumoniae* clone, no apparent time clusters were detected for clones of other species. However, during April – August 2013, many ESBL species with heterogeneous PFGE patterns were observed. These originated mainly from screening specimens. Numerous horses had more than one species.

Conclusion
The results indicate nosocomial spread of *K. pneumoniae* clone with temporal association. Concurrent, temporal clustering of heterogeneous ESBL species with the *K. pneumoniae* clone, as well as simultaneous presence of multiple species in the same horse may suggest plasmid transmission between bacterial genera.