VPH-PP-09

TITLE
ANTIBIOTIC RESISTANCE AND GENETIC PROFILE OF KLEBSIELLA PNEUMONIAE FROM CLINICALLY DISEASED PIGLETS

Jobke van Hout[1], Tom Duinhof[1], Linda Peeters[1], Rianne Buter[1], Annet Heuvelink[1], Manon Houben[1]

[1] *GD Animal Health, Deventer, The Netherlands*

CONTENT
Background and objectives
In 2015, the first cases of septicaemia and sudden death in 2-3 week old suckling piglets, resulting from Klebsiella pneumoniae subspecies pneumonia (KPP) infection, were found in the Netherlands. KPP is in human medicine notorious for carbapenemase production/multi-resistance and concomitant treatment difficulties. This project aimed to evaluate antibiotic resistance (ABR) and molecular profiles of KPP from diseased piglets.

Material & Methods
KPP isolates were cultured at GD Animal Health from diseased piglets submitted for post-mortem examination. Antibiotic susceptibility testing (broth microdilution) was carried out. Eight isolates (from 6 different farms) were screened for presence of ABR genes using a commercial micro-array for E. coli. Additionally, a modified MLST was applied using genes phoE, infB and tonB. After sequence analysis and alignment, concatenated sequences were used for constructing a maximum parsimony tree and sequence types (ST) were assigned.

Results
Phenotypically (n=22; 2015-2018), very low levels/absence of resistance was observed for colistin, enrofloxacin, cefotaxim, apramycin, neomycin, gentamicin, amoxicillin/clavulanic acid and TMP/S. High level resistance was observed for florfenicol, macrolides and tiamulin.
Only one out of 8 isolates harboured aminoglycoside, beta-lactam, sulfonamide, tetracyline and trimethoprim resistance genes in its profile.
KPP MLST showed that 7 KPP isolates (including 3 isolates from the same farm) were genetically identical, sharing a known ST (ST30). For the other isolate another ST (ST37) was found.

Discussion & Conclusion
The KPP isolates showed phenotypically (hardly) no resistance to antibiotics relevant for human cases of KPP. The one isolate harbouring different resistance genes (based on micro-array) was phenotypically susceptible for these antimicrobials and belonged to ST30. A similar ST was found in English and Australian KPP isolates from diseased piglets.
More KPP isolates from diseased piglets from different geographical areas need to be analysed to gain more insight into dissemination of clinically relevant KPP strains.