

Session: OS175 Origin, dissemination and impact of mcr genes

**Category: 3b. Resistance surveillance & epidemiology: Gram-negatives**

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**mcr-1 and mcr-2 variant genes identified in *Moraxella* spp. isolated from pigs**

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**Background:**

Colistin, regarded as an antibiotic of last resort, is active against a range of Gram-negative bacteria, including *Acinetobacter* species and *Klebsiella* species. The emergence of colistin resistance genes (*mcr-1* and *mcr-2*) on mobile genetic elements in *Escherichia coli* is of high therapeutic relevance. These genes have been identified in zoonotic pathogens and commensals from food producing animals which is of public health relevance as they may provide a source of infection to humans via the food chain. The aim of the study was to determine the occurrence of colistin resistance genes *mcr-1* and *mcr-2* in Gram-negative bacteria isolated from pig farms in Great Britain.

**Material/methods:**

Gram-negative bacteria (n = 657) were isolated from pooled caecal contents (10 pigs per farm) collected at slaughter from pigs from 57 pig farms in GB. Eighteen morphologically different colonies per farm were selected from Brilliance UTI agar (Oxoid Ltd) containing either 1µg/ml cefotaxime, 1µg/ml ciprofloxacin or no antibiotic. Bacterial identification was carried out by MALDI-TOF (Bruker, Coventry, UK) or 16S rRNA gene sequencing. Whole genome sequencing was performed on the 657 Gram-negative isolates and presence of colistin resistance genes, *mcr-1* or *mcr-2*, determined using SeqFinder. For positive isolates, sequences were assembled and annotated, and the minimum inhibitory concentration of colistin was determined using the agar dilution method.

## Results:

Variants of the transferable colistin resistance genes were identified in *Moraxella* spp. isolated from caecal contents of healthy pigs at slaughter collected from six farms in GB. An *M. porci*-like isolate harboured a MCR-1 variant with 98.7% identity and only 7 amino acid substitutions to MCR-1, and a *M. pluranimalium*-like isolate harboured a MCR-2 variant with 87.9% identity to MCR-2 from *E. coli*. However they both expressed relatively low phenotypic resistance to colistin compared to *mcr* harbouring *E. coli*. Six *M. osloensis* isolates were positive for EptA which shared 62-64.5% identity to MCR-1 and MCR-2, and expressed variable levels of colistin resistance (2-4 µg/ml). No other *mcr-1* or *mcr-2* harbouring bacteria, including *E. coli* were isolated from these pig caeca. The *M. porci*-like and *M. pluranimalium*-like isolates both harboured the *bla*<sub>BRO-1</sub> β-lactamase gene, but only the *M. pluranimalium*-like isolate possessed *tetL*, a tetracycline resistance gene. There were differences between the AMR genes identified in these *Moraxella* and type isolates from these bacterial species.

## Conclusions:

*Moraxella* are Gram-negative bacteria found in animals and humans as commensals, or are associated with a range of disease. We report the first detection of two closely related *Moraxella* species isolated from healthy pigs, harbouring different MCR variants. This study enriches the currently limited data published on *M. porci* and *M. pluranimalium* isolates, showing that these species identified from healthy pig caeca harbour two variant forms of plasmid mediated colistin resistance genes.