

**P1403 Genomic epidemiology of colistin-resistant *Enterobacteriaceae* from farmers, farm animals, and hospitalised patients in Thailand**

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**Background:** Resistance to colistin conferred by plasmid-mediated genes has been identified in bacterial strains isolated from food, animals, inpatients and asymptomatic human carriers worldwide. This wide spread of resistant strains has raised public health concerns, especially that zoonotic transmission might be occurring. Here, we provide information on the molecular epidemiology of colistin-resistant, *mcr*-positive *Escherichia coli* and *Klebsiella pneumoniae* in Thailand between 2014-2017.

**Materials/methods:** 190 samples were collected from stool specimens from farm workers, inpatients and rectal swabs of healthy pigs. Genomic DNA from *E.coli* and *K.pneumoniae* isolates was sequenced on the Illumina NextSeq® platform. Genomic analysis included identification of multi-locus sequence type, presence of antimicrobial resistance genes and associated mutations, and construction of a phylogenetic tree based on core SNPs to determine the relationship between strains.

**Results:** 30 out of 190 isolates were resistant to colistin based on phenotypic testing: 15 *E.coli* and 15 *K.pneumoniae*. Additionally, only 5 *K.pneumoniae* out of 30 isolates from inpatients were resistant to carbapenems. Interestingly, there were an additional 10 *E.coli* isolates (7 swine and 3 from farmers) that had the *mcr* gene but were reported as susceptible to colistin. All 40 isolates also contained ESBL genes of which CTX-M-55 was the most common. 6 of 30 colistin-resistant isolates did not carry the plasmid-mediated *mcr* gene. However, 5 of them contained chromosomal colistin resistant genes: *mgrB* mutations were found in 2 isolates, another 2 isolates contained a *pmrB* D150Y mutation and a *pmrA* pseudogene and another isolate had a *pmrA* E57G mutation. Furthermore, these 5 isolates were identified from inpatients and also carried OXA-232 and NDM-1. Phylogenetic analysis showed that *E.coli* and *K.pneumoniae* did not spread clonally; however, 7 out of 40 isolates from farmers and swine appeared to be clonal (i.e., members of the same clade).

**Conclusions:** These findings suggest that the pig farms in Thailand may contain antimicrobial resistance genes, especially ESBL genes and colistin resistant genes. Further analysis is on-going to investigate isolates that were carrying *mcr* genes but were susceptible to colistin. Comparative genome analysis revealed all *K.pneumoniae* from inpatients had only mutations in chromosomal genes.

