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# O1042 Whole-genome sequencing (WGS) analysis of phenotypically ESBL- and AmpC-beta-lactamase producing Escherichia coli recovered from healthy food animals across Europe (2013-2014)

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**Background:** In a pan-European surveillance (European Antimicrobial Susceptibility Surveillance in Animals (EASSA), 2993 *Escherichia coli* isolates have been recovered from randomly collected faecal samples of cattle, pigs and chickens in various abattoirs. One-hundred *E. coli* isolates (0.5% from cattle [n=4], 1.3% pigs [n=15], 8.0% chickens [n=81]) fulfilled the criteria for cefotaxime and ceftazidime non-wildtype according to EUCAST criteria. The purpose of this study was to characterize the resistance genes and phylogenetic diversity of these presumptive ESBL/AmpC-β-lactamase producing strains by WGS analysis.

**Materials/methods:** WGS data were analysed using services of the Genomic and Epidemiology Center (https://cge.cbs.dtu.dk/services) to identify resistance genes, plasmid incompatibility groups and multilocus sequence types (STs). MyDbFinder was used to assign phylogenetic groups based on the “Clermont” classification. Conjugation was done with filter mating using *E. coli* J53 $Azi^R$ as recipient.

**Results:** Ninety-nine successfully sequenced isolates comprised SHV-12 (31%), CTX-M-1 (23%), and CMY-2 (20%) as predominant ESBL/AmpC types, and two isolates harboured CMY-2+SHV-12 and CMY-2+CTX-M-1. Other types observed were SHV-2 (1.0%), CTX-M-2/-14/-15(1.0/6.1/1.0%), and TEM-52(5.1%). Seven of nine isolates tested negative for ESBL/AmpC-β-lactamase genes revealed AmpC-promoter mutations. Plasmid location of ESBL/AmpC-β-lactamase genes was verified for 30 isolates either based on successful transconjugation or the co-localization of resistance and plasmid incompatibility group genes on the same contig. Apart from IncI1 (>80%), we detected IncB/O/K/Z, IncX1, and IncN.

Besides β-lactamase genes, several gene-families were observed encoding resistance to aminoglycosides (64.6%), trimethoprim (38.4%), phenicols (30.3%), macrolides (12.1%), polymyxins (1.0%), and fluoroquinolones (65.6%) including *qnrS1*(10.1%).

The isolates were assigned to phylogroups A/C (15.2/26.3%), B1 (28.3%), B2 (2.0%), D/E (14.1/13.1%), and to *E.* clades (1.1%). With 42 known and 8 novel types, a wide variety of STs was found, including STs previously observed in human isolates, such as ST131 and ST648. Overall, ESBL/AmpC types or STs were rarely correlated with the geographic origin of the isolates or animal species.

**Conclusions:** This EU survey shows that prevalence of ESBL/AmpC in enteric *E. coli* varies from 0.6 to 8.0% per animal species and predominantly comprises SHV-12, CMY-2, and CTX-M-1. The high diversity of STs and phylogenetic groups provides hardly any hint for clonal spread of certain lineages.