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Identification of extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* isolates in diseased food-producing animals from GERM-Vet 2008-2015

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Background and objectives: Extended-spectrum β -lactamase (ESBL)-producing bacteria represent risks for public health. The aim of this study was to investigate ESBL-producing *Escherichia coli* isolates originating from diseased food-producing animals.

Materials and methods: A total of 7,810 *E. coli* collected from diseased cattle (n= 3,188), pigs (n= 1,834) or poultry (n= 2,788) in the GERM-Vet (2008-2015) were subjected to antimicrobial susceptibility testing and screened for ESBL phenotype. ESBL genes were investigated by PCR/sequencing. ESBL-producing isolates were further characterized by phylotyping.

Results: ESBL-producers were identified in 396 bovine, 95 swine and 24 avian isolates. The isolates were distributed among phylogenetic groups A (57.5%), D (23.7%), B1 (17.9%) and B2 (0.9%). The most common ESBL genes detected were: bla_{CTX-M-1} (68.1%), bla_{CTX-M-15} (15.0%) and bla_{CTX-M-14} (11.8%). Additional resistance to non- β -lactam antibiotics (especially sulphonamides/trimethoprim and tetracyclines) was seen in 488/515 of ESBL-producing isolates (94.8%) and 451/515 (87.6%) isolates were multidrug-resistant (resistant to at least three classes of antimicrobial agents).

Conclusion: The dominant ESBL gene among *E. coli* isolates from diseased food-producing animals over time is bla_{CTX-M-1}. Additional resistance to non- β -lactam antibiotics may play an important role in the persistence and dissemination of ESBL genes.