

Wide Dissemination of CTX-M-Type Extended-Spectrum β -Lactamases in Korean Swine Farms

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Abstract : Extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* from food animals are considered as a reservoir for transmission of ESBL genes to human. The aim of this study is to assess the prevalence and molecular epidemiology of ESBL-producing *E. coli* colonization in pigs, farm workers, and farm environments to elucidate the transmission of multidrug-resistant clones from animal to human. Nineteen pig farms were enrolled across the country in Korea from August to December 2017. ESBL-producing *E. coli* isolates were detected in 190 pigs, 38 farm workers, and 112 sites of farm environments using ChromID ESBL (bioMerieux, Marcy l'Etoile, France), directly (stool or perirectal swab) or after enrichment (sewage). Antimicrobial susceptibility tests were done with disk diffusion methods and blaTEM, blaSHV, and blaCTX-M were detected with PCR and sequencing. The genomes of the four CTX-M-55-producing *E. coli* isolates from various sources in one farm were entirely sequenced to assess the relatedness of the strains. Whole genome sequencing (WGS) was performed with PacBio RS II system (Pacific Biosciences, Menlo Park, CA, USA). ESBL genotypes were 85 CTX-M-1 group (one CTX-M-3, 23 CTX-M-15, one CTX-M-28, 59 CTX-M-55, one CTX-M-69) and 60 CTX-M-9 group (41 CTX-M-14, one CTX-M-17, one CTX-M-27, 13 CTX-M-65, 4 CTX-M-102) in total 145 isolates. The rectal colonization rates were 53.2% (101/190) in pigs and 39.5% (15/38) in farm workers. In WGS, sequence types (STs) were determined as ST69 (*E. coli* PJFH115 isolate from a human carrier), ST457 (two *E. coli* isolates PJFE101 recovered from a fence and PJFA1104 from a pig) and ST5899 (*E. coli* PJFA173 isolate from the other pig). The four plasmids encoding CTX-M-55 (88,456 to 149,674 base pair), whether it belonged to IncFIB or IncFIC-IncFIB type, shared IncF backbone furnishing the conjugal elements, suggesting of genes originated from same ancestor. In conclusion, the prevalence of ESBL-producing *E. coli* in swine farms was surprisingly high, and many of them shared common ESBL genotypes of clinical isolates such as CTX-M-14, 15, and 55 in Korea. It could spread by horizontal transfer between isolates from different reservoirs (human-animal-environment).

Keywords : *Escherichia coli*, extended-spectrum β -lactamase, prevalence, whole genome sequencing

Conference Title : ICASVM 2018 : International Conference on Animal Science and Veterinary Medicine

Conference Location : London, United Kingdom

Conference Dates : August 20-21, 2018