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Wide dissemination of CTX-M-type ESBLs-producing *Escherichia coli* in Korean swine farms and spread of bla*CTX*-M-55 by horizontal gene transfer

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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 cultured in 190 pigs, 38 farm workers and 112 sites of farm environments, directly (stool or perirectal swab) or after enrichment (sewage). Antimicrobial susceptibility tests and *blaTEM, blaSHV and blaCTX*-M were detected. 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 the 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 the 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).

Biography

Young Ah Kim has her expertise in research of antimicrobial resistance. She is performing 3 year-project ‘The distribution of resistant bacteria from livestock, surrounding environment and related workers’ supported by the Korean Center for Disease Control and Prevention. The purpose of this project is to understand the transmission model of antimicrobial resistance mechanism among human, environment and animals, the introduction of a monitoring system for surveillance and the effective strategy for the control of antimicrobial resistance.

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