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ePoster Viewing

Molecular epidemiology of multidrug-resistant Enterobacteriaceae

Characterization of ST 38 CTX-M-producing *Escherichia coli* isolated from urine at a tertiary hospital in Daejeon, Korea

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Objectives: Recently, CTX-M-producing *Escherichia coli* is the most important cause of nosocomial urinary tract infections in the world. In Korea, ST131 is known to be the most frequently found CTX-M-producing *E. coli*, however, ST38 is also commonly found in Daejeon, Korea. In this study, we aimed to characterize ST 38 CTX-M-producing *E. coli* isolates and to investigate the molecular epidemiology in comparison with other ST types at a tertiary hospital in Daejeon, South Korea.

Methods: A total of 76, non-duplicate extended spectrum β -lactamase (ESBL)-producing *E. coli* isolates were obtained from urine at a tertiary hospital in Daejeon, Korea from 2011 to 2014. Polymerase chain reaction (PCR) and direct sequencing were performed to characterize the CTX-M, integrons, and insertion sequence common regions (ISCRs). Multilocus sequence typing (MLST), pulsed field gel electrophoresis (PFGE), phylogenetic analysis, and repetitive extragenic palindromic sequence (REP)-PCR were performed for epidemiological typing.

Results: Among 76 ESBL-producing isolates, 43 isolates produced CTX-M-14, 30 isolates CTX-M-15, and 3 isolates both CTX-M-14 and CTX-M-15. The most prevalent sequence type (ST) was ST131 (n=31, 40.7 %) in MLST, followed by ST38 (n=20, 26.3 %), ST405 (n=8, 10.5 %), and ST69 (n=5, 6.57%). Only one of ST 131 isolates had ISCR1, while 5 ST38 isolates contained ISCRs, among which 2 had ISCR2 and 3 had ISCR14. Most of CTX-M producing *E. coli* isolates had class 1 integrons with identical gene cassette arrays of *dfrA17*–*aadA5* and *dfrA12*–*aadA2*. All of ST 131 isolates belonged to phylogenetic group B2 and showed identical rep-PCR pattern. All of ST 38, ST405, and ST 69 isolates belonged to phylogenetic group D, and all of ST 38 and ST405 isolates displayed the same REP-PCR pattern. According to the PFGE analysis, ST131 and ST38 isolates showed 20 and 12 distinct types respectively with 80% cut-off band pattern similarity.

Conclusions: The frequency of ST 38 clones producing CTX-M-14 was relatively high in Daejeon, Korea in comparison with in other countries and other areas of our country. ST 38 clone had more ISCRs than others. ST 38 strains showed significantly different phylogenetic pattern with ST 131. They contained class 1 integrons mostly. PFGE analysis showed that ST 131 and ST 38 isolates were not clonally related, and showed the genetic heterogeneity. In conclusion, ST131 clone CTX-M-producing *E. coli* but ST 38 also emerged as important clones spreading CTX-M type ESBLs in Daejeon, Korea.