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Abstract (poster session)

Emergence and genetic environment of CTX-M enzymes produced by clinical Escherichia coli isolates in Germany, 2005-2009

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Objectives: CTX-M type ESBLs are the predominant ESBL enzymes in Enterobacteriaceae isolates worldwide. The objective of this study was to evaluate the prevalence of CTX-M type ESBLs among German Escherichia coli (ECO) isolates between 2005 and 2009. Additionally, CTX-M producing isolates collected in 2005 were analysed regarding the transferability and the presence of ISEcp1 that have apparently involved in dissemination and expression of the enzymes. Methods: 300, 292 and 297 ECO recovered during three multicentre studies conducted in 2005, 2007 and 2009, respectively, were studied. ESBL-producing organisms were identified according to CLSI criteria and characterized by isoelectric focusing (IEF), amplification of blaCTX-M genes and sequencing. Conjugation experiments with CTX-M producing isolates collected in 2005 were done with ECO J53 as recipient strain. Transconjugants were selected using cefotaxime (4 mg/l) and sodium azide (200 mg/l). Plasmids of non-conjugative strains were transformed into competent ECO DH5-alpha cells by electroporation. Promotor regions of blaCTX-M genes were investigated by PCR and sequencing. Results: The percentage of CTX-M producing ECO was 4.7% (14/300) in 2005, 11.6% (34/292) in 2007 and 11.4% (34/297) in 2009. In 2005, 50% (7/14) of the CTX-M producing ECO harboured CTX-M-1, 35.7% (5/14) CTX-M-15 and 14.3% (2/14) CTX-M-14, while 26.5% (9/34), 58.8% (20/34), 11.8% (4/34), 2.9% (1/34) and 2.9% (1/34) of the CTX-M positive isolates produced CTX-M-1, -15, -14, -9 and -2, respectively, in 2007. In 2009, 44.1% (15/34), 50% (17/34) and 5.9% (2/34) of isolates expressed CTX-M-1, CTX-M-15 and CTX-M-14, respectively. 6 CTX-M-1 and 1 CTX-M-14 enzyme expressed by 7/14 CTX-M producing strains collected in 2005, were located on conjugative plasmids. CTX-M enzymes of the remaining 7 strains were not transferable. ISEcp1 was found in 6/7 strains (1 expressed CTX-M-1, 1 CTX-M-14 and 4 CTX-15) with non-transferable plasmids upstream the respective blaCTX-M gene as well as on conjugative plasmids of two strains expressing CTX-M-1 and -14, respectively. Conclusions: Our data suggest that the rate of CTX-M producing strains among ECO isolates doubled between 2005 and 2007, but remained unchanged between 2007 and 2009. CTX-M-1 was the primary CTX-M type in 2005, while CTX-M-15 predominated in 2007 and 2009. CTX-M-1 enzymes were mainly disseminated by conjugative plasmids whereas the spread of CTX-M-15 enzymes seems to be associated with ISEcp1.