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Title: Genotyping of extended spectrum- β -lactamases (ESBLs) detected cephalosporin-resistant *Escherichia coli* and *Klebsiella* species in Japan

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Body: Introduction: *Escherichia coli* and *Klebsiella* species are an opportunistic human pathogen. Outbreaks of these ESBL producers have occurred also in Japan, so cephalosporin-resistant strains were collected and analyzed for genotyping of their ESBLs. Methods: Fifty-six cefpodoxime-resistant (MIC, $>4 \mu\text{g/ml}$) strains collected from 6 hospital in Aichi and Gifu prefectures in Japan between Jan., 2010 and Dec., 2011. 32 *Escherichia coli*, 16 *Klebsiella pneumoniae* and 8 *K. oxytoca* were subjected to specific primer sets for detection of genetic determinants for TEM-1, SHV-, CTX-M-1 group, CTX-M-2 group, CTX-M-8 group, and CTX-M-9 group, extended spectrum β -lactamases (ESBLs), respectively. Each PCR amplicon was analyzed by direct sequencing. Results: Twenty-six(81.2%) of *E. coli* strains were found to carry genes for CTX-M-type ESBLs. Twenty *K. pneumoniae* carried CTX-M-type and SHV-type β -lactamases, respectively. However, no strain carrying genes for TEM-type, SHV-type or CTX-M-type β -lactamases was found in *K. oxytoca*. Most frequent variant types were CTX-M-3 and CTX-M-14, although this has been reported to be predominant in each group outside of Japan. Conclusion: These findings suggested that newly identified variants of ESBLs might well emerged and selected independently from those found in Europe by preferential use of carbapenems in Japanese clinical environments.