Analysis of the drug-resistant characteristics of *Klebsiella pneumoniae* isolated from the respiratory tract and *CTX-M ESBL* genes


Department of Clinical Laboratory, Sun Yat-sen Memorial Hospital, Sun Yat-sen University, Guangzhou, China

Corresponding author: H.Y. Li
E-mail: hongyuli0@126.com

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ABSTRACT. The main aim of this study was to understand the relationship between the drug-resistant characteristics of *Klebsiella pneumoniae* and CTX-M-type extended spectrum β-lactamases (ESBLs), and to detect the distributions of CTX-M-type ESBLs in clinically isolated strains. *CTX-M ESBL* genes isolated from the clinical samples were amplified by polymerase chain reaction and identified by sequence analysis; the antibiotic susceptibility of the samples was determined using the Kirby-Bauer disc-diffusion method. One hundred and five strains among the 246 isolated strains of *K. pneumoniae* tested positive for ESBL production (42.68%); 92 of these produced CTX-M ESBLs. Of the 92 CTX-M ESBL strains, 81 produced CTX-M-1 ESBLs and 11 produced CTX-M-25 ESBLs. Fifty-seven of the CTX-M-1 ESBL- and six of the CTX-M-25 ESBL-producing bacteria had *CTX-M ESBL* genes that coexisted in the plasmid and chromosome. The Kirby-Bauer antibiotic susceptibility method revealed that CTX-M ESBL-positive strains showed a higher rate of resistance to cefazolin, cefoxitin, cefuroxime, ceftazidime, cefotaxime, aztreonam, levofloxacin, and
coterimoxazole, compared to the CTX-M ESBL-negative strains (P < 0.05). The CTX-M ESBL genes were commonly observed in the K. pneumoniae isolated from respiratory tract samples; these were significantly associated with the drug-resistant characteristics of K. pneumoniae to β-lactam antibiotics.

**Key words:** Klebsiella pneumonia; CTX-M ESBLs; Drug resistance