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Title: The mutation characteristics of the bla_{CTX-M/SHV/TEM}-producing *Klebsiella pneumoniae* clinical isolates in multicenter in China

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Body: Objectives Due to the prevalence of CTX-M- and SHV-type extended-spectrum β -lactamase (ESBL)-producing Enterobacteriaceae in China, the base mutation characteristics of bla_{CTX-M/SHV/TEM}-producing *Klebsiella pneumoniae* were investigated. Methods From February 2010 to July 2011, 158 *K. pneumoniae* isolates from lower respiratory tract infection patients with positive double-disk synergy tests were collected from Beijing (69), Fujian (27), Anhui (22), Hebei (15), Liaoning (14), and Inner Mongolia (11). Ninety percent isolates were collected from common wards more than 48h after hospitalization. The bla_{CTX-M/SHV/TEM} genes were examined by PCR and sequencing. The nucleotide sequences were analysed via BLAST program. Results In total, 138 bla_{CTX-M} were detected, including 78 bla_{CTX-M-14}, 19 bla_{CTX-M-15}, 17 bla_{CTX-M-27}, 12 bla_{CTX-M-3}, 4 bla_{CTX-M-55}, 2 bla_{CTX-M-65}, 2 bla_{CTX-M-24}, 2 bla_{CTX-M-24a}, 1 bla_{CTX-M-38}, and 1 bla_{CTX-M-98}. 120 bla_{SHV} were detected, including 45 bla_{SHV-11}, 23 bla_{SHV-1}, 15 bla_{SHV-12}, 7 bla_{SHV-5}, 5 bla_{SHV-108}, 4 bla_{SHV-28}, 3 bla_{SHV-36}, 3 bla_{SHV2a}, 2 bla_{SHV-2}, 2 bla_{SHV-27}, 2 bla_{SHV-142}, 1 bla_{SHV-1a}, 1 bla_{SHV-26}, 1 bla_{SHV-32}, 1 bla_{SHV-33}, 1 bla_{SHV-38}, 1 bla_{SHV-60}, 1 bla_{SHV-103}, 1 bla_{LEN}, and 1 bla_{LEN-22}. Also, 91 bla_{TEM-1} and 1 bla_{TEM-135} were detected. 8 bla_{SHV} and 1 bla_{TEM-135} with the silent base mutations were detected, and none of the bla_{CTX-M}.

Conclusions The CTX-M-14, CTX-M-15, and CTX-M-27 were predominant ESBL genes in *K. pneumoniae* in China. The diversity of bla_{SHV} and bla_{CTX-M}, most silent mutations in bla_{SHV}, and only missense mutations in bla_{CTX-M} may be of significance contributing to epidemiological and clinical challenges.