

Multiple ambler class A ESBL genes among *Klebsiella pneumoniae* isolates in a Malaysian district hospital

ABSTRACT

Detailed reports regarding the distribution and activity of extended-spectrum beta-lactamase (ESBL)-producing *Klebsiella pneumoniae* isolates are currently not widely available in the Malaysian setting. This study was conducted to determine the ESBL genes distribution rate, phenotypic detection, and antimicrobial susceptibility patterns among beta-lactam resistant *Klebsiella pneumoniae* isolated from a Malaysian district hospital. *K. pneumoniae* isolates were collected from a microbiology laboratory at Hospital Pakar Sultanah Fatimah, Malaysia. Following exclusion and inclusion criteria, 141 isolates were selected for this study. *K. pneumoniae* was identified by phenotypic method, whilst antibiotics' susceptibility patterns were determined by the Kirby-Bauer method, as described in Clinical Laboratory Standard Institute (CLSI) guidelines (Oxoid, UK; Becton-Dickenson, USA). Detection of Ambler Group A ESBL gene (bla_{SHV} , bla_{TEM} , $bla_{CTX-M-1}$, $bla_{CTX-M-2}$, $bla_{CTX-M-8}$, $bla_{CTX-M-9}$, and $bla_{CTX-M-25}$) was done using polymerase chain reaction (PCR). ESBL genes were found in 85.8% of *K. pneumoniae* (121 of 141) isolates. Only bla_{SHV} , bla_{TEM} , $bla_{CTX-M-1}$, and $bla_{CTX-M-9}$ were detected among *K. pneumoniae* isolates with distribution rates of 75.2% (106 of 141), 41.1% (58 of 141), 44% (62 of 141), and 0.7% (1 of 141), respectively. There was no $bla_{CTX-M-2}$, $bla_{CTX-M-8}$, or $bla_{CTX-M-25}$ detected from any isolates in this study. Sequencing of representative amplicons revealed bla_{SHV} as SHV-12, bla_{TEM} as TEM-1, $bla_{CTX-M-1}$ as CTX-M-15, and $bla_{CTX-M-9}$ as CTX-M-18. The phenotypic detection rate of ESBL was 71.6% (101 of 141), whilst 9.2% (13 of 141) were positive for carbapenemase. AmpC beta-lactamase was detected in 22% (31 of 141) of all isolates. Antibiotic resistance was between 44.6% (netilmicin) and 97.2% (cefotaxime). Based on ESBL genes distribution, bla_{SHV} was a predominant gene found in one of Malaysian district hospitals, notwithstanding having bla_{TEM} , $bla_{CTX-M-1}$, and $bla_{CTX-M-9}$. Despite carrying multiple ESBL genes, some strains were positive for carbapenemase or AmpC beta-lactamase, which resulted in high antimicrobial resistance rates.

Keyword: Multiple ambler class; ESBL genes; *Klebsiella pneumoniae* isolates; Malaysia; Hospital