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# Molecular characterization of extended-spectrum-β-lactamases producing *Klebsiella pneumoniae* and *Escherichia coli* from hospitalized patients in Oman

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Extended-spectrum β-lactamases (ESBLs) are plasmid encoded enzymes that confer resistance to β-lactam antibiotics through the hydrolysis of the β-lactam ring. ESBLs are distributed worldwide with an increasing incidence and prevalence in the Middle East due to the misuse of antibiotics and lack of coherent antimicrobial surveillance studies. The aim of study is to analyze molecularly the antimicrobial resistance mechanisms of 50 *Escherichia coli* and *Klebsiella pneumoniae* isolates from nosocomial infections in hospitalized patients in Oman. Screening for antimicrobial resistance (AR) and ESBL production was carried out with the disk diffusion and E-test methods following CLSI guidelines. ESBL producers were screened for $bla_{\text{CTX-M}}$, $bla_{\text{SHV}}$, and $bla_{\text{TEM}}$ resistance markers via PCR using gene-specific primers. All amplified PCR fragments will be sequenced to determine their allelic variants. In order to demonstrate the overall genotypic variation, Pulsed-Field Gel Electrophoresis (PFGE) analyses were done separately among all *E. coli* and *K. pneumoniae* isolates. According to the AR analysis, 82% (41/50) of isolates were determined to be ESBL producing bacteria. The percentages of isolates with genetic markers for $bla_{\text{CTX-M}}$, $bla_{\text{SHV}}$, and $bla_{\text{TEM}}$ were 73%, 24%, and 68%, respectively. Preliminary PFGE analyses demonstrated high level of variation among ESBL isolates compared to non-ESBL producers. Further surveillance studies are needed to describe better the AR situation in these hospitals in Oman.