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Distribution of Drug Resistance Associated with AY-Lactamase Genes in *K. pneumoniae* Isolated from Outpatients

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Background & Hypothesis:
Extended-spectrum β-lactamases (ESBL) are enzymes produced by various bacterial species as a defence against β-lactam drugs, with the genes encoding those enzymes being mainly located on mobile genetic elements. The ESBL-producing *K. pneumoniae* is an important human pathogen that causes nosocomial infections. The aim of this study was to detect genes—markers of resistance to β-lactams drugs—*TEM* and *CTX-M* in *K. pneumoniae* isolated from outpatients.

Methods:
Thirty-six isolates of *K. pneumonia* used in this study were isolated from outpatients and tested for sensitivity to penicillin and cephalosporin using the disc diffusion method. We used isolates which were resistant to 1 or more antibiotics. PCR was used to detect β-lactamase genes *bla (TEM)* and *bla (CTX-M).*

Results:
The highest resistance of isolates of *K. pneumoniae* was to ampicillin (100%), and 58% were resistant to cefazolin and cefotaxime. These isolates harboured different β-lactamase genes. Among them, 28% were positive for *TEM* and 33% positive for *CTX-M*. Nineteen percent of isolates included *bla (TEM)* and *bla (CTX-M)* both.

Discussion & Conclusion:
Our data has revealed that multidrug resistance of the isolates *K. pneumoniae* is associated with β-lactamase genes and the presence of these genes in isolates from outpatients favour the spread of antimicrobial resistance in patients, the healthy population and environment. The study was supported by the Ministry of Education and Science of the Russian Federation, basic task number 1878 "Development of the fundamental aspects of molecular diagnosis of mitochondrial and pharmacology".