Evaluation of 16S rRNA methyltransferase gene in aminoglycosides resistant isolates of cancer patients

ABSTRACT

Aminoglycosides are used in empiric treatment of critically ill patients. Efficacy of aminoglycoside has been reduced due to dissemination of resistance. The aim of this study was to evaluate aminoglycoside resistance in cancer patients with pneumoniae. A total of 150 Bronchoalveolar lavage and Bronchial washing samples were collected from cancer patients. The samples were identified with standard microbiological procedures. Phenotypic susceptibility pattern of the isolates was determined against various groups of antibiotics such as Penicillins, Cephalosporins, Carbapenems, Monobactams, Aminoglycosides, Tetracyclins, Glycopeptides and Sulphonamides. The isolates with phenotypic resistant to aminoglycosides were further evaluated for the presence of armA gene. The strains of E. coli (12.5%), S. aureus (15.6%), Streptococcus (15.6%), Pseudomonas (18.7%) and K. pneumoniae (37.5%) were isolated. The phenotypic resistance profile showed highest resistance against aminoglycosides (Tobramycin, 53.1% Gentamicin and 50% Amikacin) followed by cephalosporins and sulfonamides group. The armA gene was detected in aminoglycoside resistant isolates. The overall genotypic resistance was evaluated as 21.8%. The armA gene was found in K.pneumoniae 23.5%, Pseudomonas 11.8% (4/24) and E. coli 5.9%. High level resistance to aminoglycosides raises therapeutic concern to health care professionals. These findings highlight the importance of effective monitoring and surveillance to the use of broad-spectrum antibiotics.