

Abstract

Nowadays, one of the major and significant problems of global hygiene (health) is the increasing prevalence of antibiotic-resistant pathogens (pathogens antibiotic resistance) in variety of human and animal population and this leads to the genesis and spread of resistant pathogens and resistance genes in them. One of this common diseases, are urinary tract infections that the main cause of it is *Escherichia coli*.

Tetracycline and beta-lactamase genes are the main plasmid genes in bacteria of Enterobacteriaceae family respectively that cause of more than 90% of *E.coli* strains resistant to β -lactamase drugs, and are an important cause of multiple drug resistance in nosocomial infections. With the emergence of drug resistance among pathogenic bacteria, the treatment of these kinds of diseases is much more difficult. B-Lactam antibiotics, long are considered the most common treatments for bacterial infections. Bacteria by producing β -Lactamase enzymes have become resistant to this class of antibiotics. β -Lactamase enzymes in bacteria are very diverse and in responding to antibiotic using, are constantly mutations in the active site of enzymes. So that, they have caused the appearance of new types of β -Lactamase in broad range. β -lactamase with broad ranges are enzymes that in addition to resistance to penicillin are considered as a range of broad resistance to Cephalosporins (third generation), such as Ceftazidime, Cefotaxime, Ceftriaxone and Munubaktams like Aztreonam.

In this study, the frequency of β -lactamase and tetracycline genes are evaluated in 100 clinical isolates and tried from these samples for the determination of resistance to β -lactams and tetracycline drugs, antibiotic sensitivity tests performed by disk diffusion method. With using of PCR method and specific primers for the beta-lactamase genes; *blaCTX-M*, *blaSHV* and *blaTEM* as well as *tetA* and *tetB* genes in tetracycline to be studied in desired stain. Furthermore, the role of classes one and two integronsin microbial multiple resistance to be evaluated in desired strain. Statistical analysis of the results is carried out with the SPSS statistical software.

Key words: Antibutic resistance, *E.coli*, ESBL genes, Beta lactamase, Plasmid mediated, Tetracycline genes



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Title:

Prevalence of extended-spectrum beta-lactamase, plasmid-mediated tetracycline genes and class 1 and class 2 integrons in *Escherichia coli* isolated from patients attending from teaching hospital in Zabol-Iran.

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