World Academy of Science, Engineering and Technology
International Journal of Biomedical and Biological Engineering
Vol:18, No:11, 2024

Real-time PCR to Determine Resistance Genes in ESBLEscherichia Coli Strains Stored in the Epidemic Diseases Laboratory of the National Institute of Hygiene (INH)

Authors : A. Qasmaoui, F. Ohmani, Z. Zaine, I. El Akrad, J. Hamamouchi, K. Halout, B. Belkadi, R. Charof

Abstract : The evolution of antibiotic resistance is a crucial aspect of the problem related to the intensive use of these substances in medicine for humans and animals. The production of ESBL extended spectrum β-lactamase enzymes is the main mechanism of resistance to β-lactam antibiotics in Escherichia coli. The objective of our work is to determine the resistance genes in E. coli strains.ESBL coli stored at the epidemic diseases laboratory of the National Institute of Hygiene. The strains were identified according to the classic bacteriological criteria. An antibiogram was performed on the strains isolated by the Mueller Hinton agar disc diffusion method. The production of ESBL in the strains was detected by the synergy assay technique and confirmed for the presence of the blaCTX-M1, blaCTX-M2, blaTEM, blaSHV, blaOXA-48 genes by gene amplification . Of the 27 observed strains of E.coli, 17 isolated strains present the phenotype of extended-spectrum Beta-lactamase with a percentage of 63%.. All 18 cefotaxime-resistant strains were analyzed for an ESBL phenotype. All strains were positive in the double-disc synergy assay. The fight against the emergence and spread of these multi-resistant antibiotic-resistant strains requires the reasonable use of antibiotics.

Keywords : E coli, BLSE, CTX, TEM, SHV, OXA, résistance aux antibiotique
Conference Title : ICAAR 2024 : International Conference on Antibiotics and Antibiotic Resistance
Conference Location : Jeddah, Saudi Arabia
Conference Dates : November 11-12, 2024