Frequency of Neonatal Blood Infections by E.coli, a Large-Scaled Beta-Lactamase in Some Hospitals of Rasht

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Abstract Introduction: Enterobacteriaceae family is one of the important human pathogens causing various infections. E. coli can be named of the most important bacteria of this family. These microorganisms can survive in water and its presence in water and food is due to contamination by feces. These microorganisms are commonly found in the digesting tract of humans and animals. E. coli infection can be treated by different antibiotics. The incidence of antibiotic resistance is one of the problems in the treatment of infections caused by these bacteria. The aim of this study was to evaluate the prevalence of newborn blood infections by E.coli bacteria -producing broad betalactamase in some hospitals in Rasht. Materials and Methods: After collecting 163 clinical samples over the therapeutic centers in Rasht, Escherichia coli isolations were identified by standard biochemical and laboratory methods. In order to determine antibiotic resistance, minimum inhibitory concentration (MIC) were analyzed by macrodilution method and presence of the coding genes for SHV and TEM antibiotic resistance were analyzed by PCR method. The aim of this study was to evaluate the prevalence of newborn blood infections by E.coli bacteria -producing broad betalactamase in some hospitals in Rasht. Results: The antibiogram results showed that all six strains were resistant. In the macrodilution method, 100% of the samples were resistant and the amount of MIC was equal to 500 micrograms per ml. And also the results of SHV gene sequencing for all strains and TEM for one strain were confirmed. Conclusion: Due to the difference in a series of results phenotype analysis, disk diffusion method, is not a reliable method for determining antibiotic resistance but it is just suitable for screening resistant strains. Final confirmation of this resistance by macrodilution and PCR methods must be done.

Keywords : Keywords: Escherichia coli, TEM, SHV, PCR