

**Prevalence of QnrA and QnrB resistance gene expression in *Excherichia coli* in Comparison To *Lactobacillus***

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Antibiotics support current medicines as their usage has decreased the mortality rate and improved life standards. Though the amount of infections produced by multidrug resistant (MDR) bacteria is growing worldwide and spectrum of terminal infections is becoming certain. Shocking rise in antibiotic resistance of some pathogenic strains of *Excherichia coli* has developed tangible public health hazards. Some of the genes determines antibiotic resistance amongst the bacteria. QnrA and QnrB are the moxifloxacin resistant genes in *Excherichia coli* that have shown resistance towards fluoroquinolones via different mechanism. *Lactobacillus* present in normal microbiota of human intestinal tract and plays a vital role as probiotic. *Lactobacillus* acts as a pool of gene resistance. *Lactobacillus* transmits resistant genes to *Excherichia coli* via horizontal gene transfer method. Clinical samples were collected from human patients and cultured on Eosin methylene blue agar and sensitivity assay was performed through disc method. Samples were subjected to isolation of gDNA and amplification of bacterial DNA through PCR. Gel electrophoresis was performed for separation and analysis of nucleic acids and gene expression was analyzed through qRT-PCR. The data was subjected to statistical analysis using one-way ANOVA and DMR by using graph pad prism version 6. Results of study have shown that QnrA and QnrB are resistant genes of *Excherichia coli* against fluoroquinolones and are highly expressed in this specie ( $P=0.015$ ) compared *Lactobacillus* ( $P=0.2$ ). It is concluded that moxifloxacin, a broad spectrum drug is highly resistant to *Excherichia coli*.

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