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Title: Molecular characterization of ESBL producing environmental bacterial strains and

their correlation with plasmid mediated quinolone resistance genes under environmental

stress.

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The current study was taken up to show the prevalence of ESBL'S and plasmid mediated

quinolone resistance among E. coli and K. pneumonia isolates in different water bodies in

South Delhi, India. An effort was made to work out on the molecular mechanisms

contributing enhancements in beta-lactamase and quinolone mediated resistance and co-

resistance to other class of antibiotics.

The study was carried out in which 150 samples of water were collected from the sewage of

Holy Family Hospital, Al-Shifa Hospital and different locations of Yamuna River.

E. coli and K. pneumonia isolates were identified by using specific media and biochemical testing. Antimicrobial sensitivity testing for isolates was done in which highest resistance was shown for Ampicillin and least was shown for Imipenem.

Phenotypic screening for ESBL production was done by preliminary and PDCT. Also in-vitro conjugation experiment was carried out on isolates isolated from Yamuna water and Hospital sewage water. Comparison between efficiency of conjugation in Yamuna water and hospital sewage water showed increase in gene transfer in Yamuna water than sewage which might be attributed to its greater temperature, turbidity, and greater pollution loads.

Following conjugation experiment, the antibiotic resistance gene transfer was identified by PCR based detection in the trans-conjugant which showed the positive result.

This may not divert out attention from the fact that less number of pharmaceutical industries and universities are working on discovering and probably designing new biomolecules to be used as future antimicrobials. The WHO or any other such global body should take all possible measures to motivate and incentivize the giant pharmaceutical industries to allocate more funds and a generous funding for research in the area by the universities should be encouraged govt. It is a challenge that must be met given more powerful techniques coupled with the online availability of huge nucleic acid and protein data bases and innumerable user friendly software. Emerging field of bioinformatics is an added aid that can be put to best use in this case.