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Preponderance of CTX-M type β -lactamases producing bacterial isolates in river Yamuna

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Antibiotic resistance has emerged as a great health care problem throughout the world. The β -lactam antibiotics act as life saving drugs for their large contribution to fight against bacterial infections. These antibiotics are no longer as effective due to escalating resistance problem. One of the most efficient mechanisms of resistance towards β -lactam antibiotics is the production of extended spectrum beta-lactamases (ESBLs). Among ESBLs, CTX-M type is most rapidly emerging and grievous groups. In aquatic environments bacteria from diverse origins are able to exchange their resistance genes through different genetic elements. In this present study, epidemiological survey of CTX-M type ESBL producing bacterial isolates from Delhi stretch of river Yamuna was carried out. Out of 402 isolates screened, 110 were found to be positive for ESBLs production through preliminary and PDCT analysis. Antibiotic susceptibility test against different class of antibiotics revealed a high level resistance among these isolates. The molecular analysis depicts the presence of *bla*_{CTX-M} gene in majority of isolates tested. Presence of resistance genes in the aquatic environment to such an extent indicates the seriousness and severity of the problem. It raises the concern for the awareness of society and advance research to prevent emergence and dissemination of drug resistance in natural habitats.

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Urban river environment as a repertoire of resistance genes: A novel variant of blaCTX-M identified from river Yamuna, India

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Infectious diseases caused by multidrug resistant pathogens are the world's greatest challenge posing a major threat to human health. In present day scenario, selection pressure has contributed much towards the acquisition and spread of resistance. A continual battle between humans and multitude of infectious organisms are well documented. As antimicrobial usage increased, so did the level and complexity of resistance mechanisms. An urban river water environment like Yamuna highly influenced by anthropogenic activities is a rich reservoir of diverse ESBLs-producing bacteria and ESBLs genes, in particular *bla*_{CTX-M}. Screening of water samples identified a novel variant of *bla*_{CTX-M} gene showing maximum homology to members of CTX-M-group-25 particularly *bla*_{CTX-M-78}. With positive amplification for *bla*_{TEM-116} and merP gene, the isolate was tolerant to high concentration of antibiotics with different mode of action and to heavy metals. Molecular modelling and docking with substrate cefotaxime revealed small catalytic pocket similar to classical TEM-1 and SHV-1 genes but well defined hydrolytic activity with high negative interaction energy possibly due to presence of substitutions leading to specific interactions may be accountable for high catalytic efficiency similar to CTX-M-9 that have broad active site. Ser237 and Arg276 responsible for high substrate specificity acting co-operatively to promote hydrolysis through structural alterations of active site and better accommodating the larger cefotaxime molecule was evident. The *bla*_{CTX-M-152} obtained from river Yamuna isolate of *Klebsiella georgiana* is believed to be progenitor of CTX-M-group-25 genes with residues having higher stability and broad spectrum hydrolytic efficacy. The studies of varied active sites giving information about the catalytic interactions are good templates for better wide range inhibitor discovery.

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