

## Preface

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Each year, we produce, protect and use more antibiotics than the previous year, because these drugs are saving millions of lives from infections. Although these drugs have protective roles against infectious bacteria, due to overuse of it pollution has been speeded in the environment. One of the most noted consequences of overuse or misuse of antibiotic pollution is the increased frequency of antibiotic-resistant bacteria in a different environment.

The river is the main places where bacteria can mingle in a diluted bisque of antibiotics and resistance genes are the recipe for transmitting resistance between different species and potentially converted into new multidrug-resistant (MDR), extensively drug-resistant (XDR) and pandrug-resistant (PDR) bacteria. Bacteria in the river water come from the city "wastewater treatment plants" (WWTPs) because WWTPs cannot remove all bacteria and from villages; and active antibiotic molecules, came from hospital waste, fish farms and pharmaceutical factories. That pollution has a huge potential for detrimental effects on the ecology of our rivers as well as on human and animal health. Therefore, we should monitor antibiotic and antibiotic resistance genes in our river water environment at a regular time interval and these steps will help us for dealing with the problem.

Rivers Mahananda and Karala flow through the middle of Siliguri and Jalpaiguri city respectively. Siliguri and Jalpaiguri are a city in the northeast Indian state of West Bengal and both cities sit in the foothills of the Himalayas. These both river basins sustain life and livelihoods of tea gardeners, fishermen and slum-dwellers. Tea gardeners consume the water resource for tea plantation and drain off the utilized excess water, which carries a variety of pesticides and fertilizers to those rivers. Slum-dwellers exploit the water resource for bathing, washing of clothes etc. Untreated waste water from city, garbage from the market and ash of cremation directly mix up with this river. As a result, the physicochemical and biological characteristics of the river water are gradually changing and producing the harmful effects on aquatic biota and thereby on human beings. Till date, no study has been done on the distribution of metallo- $\beta$ -lactamase amongst the eubacterial population, especially the members of *Enterobacteriaceae* of this river water system. Therefore it demands a thorough investigation of a riverine bacterial population.

The present study will therefore focus on two city river water environment for studying the prevalence and diversity of the metallo- $\beta$ -lactamase producers and will also try to forecast the risk associated with the dissemination of the metallo- $\beta$ -lactamase genes. This study has been undertaken to provide comprehensive descriptive information about the metallo- $\beta$ -lactamase producing eubacterial population and also to explore the phenotypic resistance pattern. Whole-genome sequencing of NDM-1 producing *Pseudomonas* sp. MR 02 bacteria correlate the genotypic and phenotypic characters and another more important objective of this work is to reveal the role of *bla*<sub>NDM-1</sub> genes in ampicillin catabolism.