PREFACE

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The river Torsa is the second largest river of Northern West Bengal and also an international river, intersecting three countries, China (Tibet), Bhutan and India. Concentrated urban developments, with increased human activity, in the nearby region of Torsa river basin have contributed to the degradation of water quality of this river. Human uses of water for almost all purposes result in the deterioration of water quality and generally limit the further potential use of water. Certain natural phenomena like torrential rainfall may also be the contributor for degrading water quality of a fresh water body. Such natural events may be frequent or occasional. Permanent factors like human activities may make water unfit for drinking or for specific uses and may serve as one of the major contributors for communicable diseases.

One periodic monitoring program was carried out to ascertain the physico-chemical characteristics of the Torsa river water as well as to determine the sanitary status by MPN determination. It was apprehended that microbiological examination should be carried out with the more definite objectives other than simply assessing the degree of fecal contamination. Therefore, another important aspect included was to explore the nature of microbial communities present in the river under study with special emphasis on the incidence and abundance of the antibiotic and metal resistant bacterial population.

Antibiotic resistant copiotrophic bacterial populations recovered from water samples of river Torsa exhibited very wide variations with large dispersion values. Significant differences in occurrence of different antibiotic resistant populations were recorded in various sampling months. Although antibiotics are needed to control bacterial infections, they can have broad, undesirable effects on microbial ecology. That is, they can produce long-lasting change in the kinds and proportions of bacteria – the mix of antibiotic susceptible types. On a large scale, antibiotic resistance that emerges in one place can often spread far and wide.

With this end in view, a further detailed study was needed that ultimately led to frame the presented research program. This study has been undertaken to provide detailed descriptive information about the antibiotic resistance patterns (ARPs) of the copiotrophic bacterial population and also to explore whether antibiotic resistance patterns among isolates from different sampling sites and seasons vary in a systematic manner or not. Isolation and molecular characterization of plasmids from the multiple-antibiotic-resistant (MAR) bacteria with an objective to evaluate their role in the horizontal transfer of resistance genes between bacteria of different species and genera have constituted another major area of this work.