

**Antibiotic Resistance Patterns of Selected Pathogenic
Bacteria Isolated from Water and Bottom Sediments
in the Iloilo Tidal Inlet (Iloilo River)**

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In PH 190: Special Studies and Research
Division of Biological Sciences
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ABSTRACT OF RESEARCH ENTITLED

Antibiotic Resistance Patterns of Selected Pathogenic Bacteria Isolated from Water and Bottom Sediments in the Iloilo Tidal Inlet (Iloilo River)

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In recent years, antibiotic resistance of pathogenic bacteria has become a public health concern. Although little is known of its environmental implications the presence of both potentially pathogenic bacteria and fecal coliform in rivers and other bodies of water raises the question of whether resistance transfer may actually occur in bodies of water. In relation, the Iloilo River for one has experienced changes in both ecological and sanitary conditions. With this threatening problem of both ecological and fecal pollution, the river could harbor microflora that could be of public health concern. Using the Kirby-Bauer Method, this study generally aims to determine the antibiotic resistance of pathogenic bacteria isolates (*E. coli*, *S. typhi* and *V. cholerae*) from water and bottom sediment samples from selected sampling areas in Iloilo River, Iloilo City. Stock cultures of bacterial isolates were obtained from the UPV-National Institute of Molecular Biology and Biotechnology (UPV-NIMBB) and were subjected to antibiotic resistance analysis using 12 different antibiotic classes. Results showed varying degrees of resistance in all of the sampling sites and species. Most isolates were highly resistant to penicillin and oxacillin and least resistant to ciprofloxacin. Multidrug-resistant isolates were also observed in all of the sampling sites and species. More isolates from bottom sediments were observed to be highly resistant than the isolates from water samples. Pearson correlation revealed that the antibiotic resistance patterns among the different species isolated from the different sources and sampling sites appeared to vary in a systematic manner indicative of a similar mechanism of antibiotic resistance development.