



Category: Metagenomics

Poster Prize Winner

# Molecular typing of antibiotic resistant bacteria isolated and identified as ESBL producers from polluted water reservoirs

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## Abstract

Anthropogenic polluted reservoirs are the mating hub for antibiotic resistant genes and multidrug resistant bacteria (MDR). The rapid emergence of this MDR is the consequence of mutations in the genes as well as the horizontal gene transfer of mobile elements carrying the resistant genes. Current study focuses on isolation and characterization of Extended spectrum  $\beta$ -lactamase (ESBL) producers from diverse water resources of Pune city and to understand the genetic modifications responsible for multidrug resistance using whole genome sequencing (Next Generation sequencing-Illumina sequencing). The identified isolates were *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterobacter cloacae* and *Stenotrophomonas maltophilia*. Mechanism of resistance developed by all isolates was efflux pump as per the genes (*adeL*, *macA*, *macB*, *ros B*) identified by Comprehensive Antibiotic Resistance Database. Primary phenotypic detection of isolates as ESBL producers and AmpC hyper producers was supportive as identified genes were resistant to all antibiotics including last resorts like carbapenems, peptide antibiotics. Rapid emergence of antibiotic resistance was seen in one isolate due to presence of additional 19 antibiotic resistant genes (*blaI*, *exo bet lactamase*, *PDC 9*, *CMY-83*, *mec I*, etc.). The investigation alarms the deadly pollution of reservoirs due to haphazard use of antibiotics which pressurizes rapid emergence and persistence of MDR.

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