# ANTIBIOGRAM AND GENOTYPING OF *PSEUDOMONAS AERUGINOSA* ISOLATED FROM HUMAN, ANIMAL, PLANT, WATER AND SOIL SOURCES IN NORTH INDIA

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**Abstract.** The present study was designed to determine antibiotic resistance rates and patterns and its correlation with enterobacterial repetitive intergenic consensus polymerase chain reaction (ERIC-PCR) whole genome analysis of *Pseudomonas aeruginosa* obtained from clinical and environmental sources. In order to determine the possibility of clonality in the bacteria and to track the resistance markers for a better understanding of the epidemiology of drug resistance. A total of 500 strains, 100 each from clinical, water, animal, plant and soil sources were subjected to antibiogram analysis by disc diffusion method. Seventy-five randomly selected strains, 15 each of the five sources were subjected to ERIC-PCR analysis. Clinical isolates were more resistant to combinations of very high numbers of drugs as compared to isolates from other sources. Weak clonality was observed in *P. aeruginosa* by ERIC-PCR method with 80% of the clinical strains belonging to only 3 clones. It could be concluded that it is the drug selection pressure in clinical environment that is causing the accumulation of drug resistance against many antimicrobials. Furthermore, *P. aeruginosa* does have clonal expansion. Further studies are warranted to confirm the results.

**Keyword:** *Pseudomonas aeruginosa*, MDR, ERIC- PCR, metallo β-lactamase, imipenem, India

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