RES-158

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Expansion of diverse 16S methyltransferase mediated aminoglycoside resistance in *Escherichia coli* from Clinical-Environmental Interface

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Background and Aim: Aminoglycosides are important antibiotics that are used as combination therapy. Wastewater and drainage systems, particularly those receiving effluents from hospitals, serve as critical convergence zones for resistant bacteria and resistance genes. Clinical-environmental interfaces support the survival and horizontal gene transfer among diverse microbial communities. These reservoirs have the potential to reintroduce resistance genes into clinical settings via contaminated water, food, or direct contact, posing serious threats to public health. Current investigation was aimed to characterize acquired 16S methyl transferase genes within isolates from Clinical-Environmental interface.

Materials and methods:

A total of 121 drainage samples were collected and isolated from different places near primary health care (PHCs) and tertiary referral hospital of Silchar, Assam

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Minimum inhibitory concentration (MICs) of isolates against aminoglycoside antibiotics were determined and disc diffusion method was also done for detection of susceptibility pattern towards cephalosporins and carbapenems

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PCR assay was performed targeting various 16S methyltransferase genes

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Horizontal transferability was determined by electroporation method and plasmid incompatibility typing was done for the transformants

Results: The isolates were screened for aminoglycoside resistance and a total of 79 (65.28%) were found to be resistant to atleast one of the aminoglycosides antibiotics viz; gentamicin, tobramycin, amikacin, netilmicin and kanamycin. Among 79 isolates it was observed that 45 (56.96%) were positive for 16S methyltransferase genes, viz; *rmtA* (n=14), *rmtB* (n=6), *rmtC* (n=9), *rmtD* (n=6), *armA* (n=4), *rmtF* (n=3), *npmA* (n=2), and *rmtH* (n=1). Majority of the isolates showed susceptibility towards imipenem. All the resistance genes were conjugatively transferable, and incompatibility typing showed multiple 16S methyltransferase genes were originated from diverse IncFIA, FIB and FIC group.

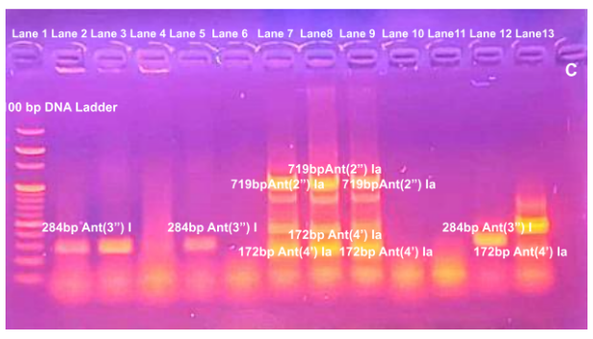

Figure 1: Gel image showing isolates harbouring AME genes

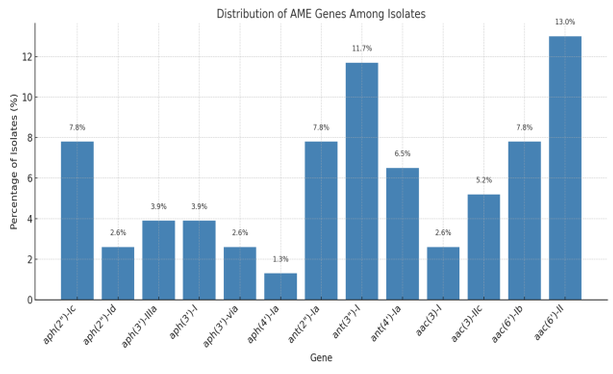

Figure 2: Graph showing distribution of AME genes

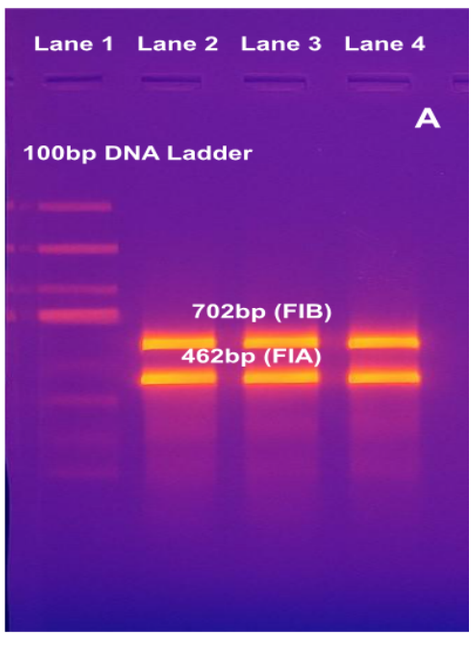

Figure 3: Gel image showing plasmid inc FIA &FIB types

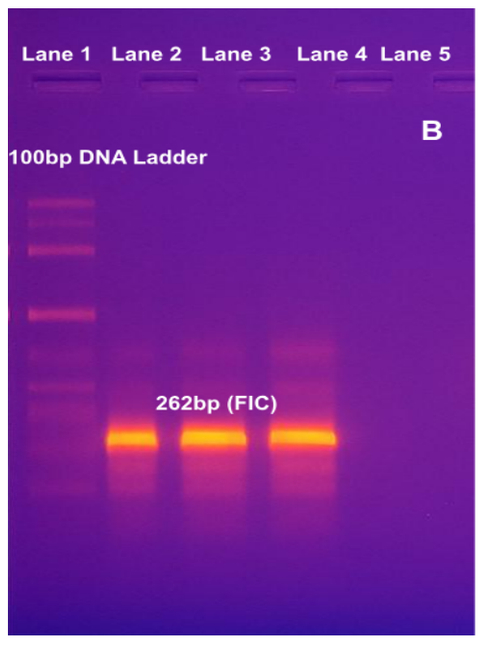

Figure 4: Gel image showing plasmid inc FIC type

Conclusion: The current study was able to highlight presence of diverse acquired 16S methyl transferases within this locality. The study is a starting point for investigation of transmission dynamics of resistance determinants from clinical to environmental setting and vice-versa.