sequence typing (MLST) of the *Salmonella* spp. were done based on the sequencing of seven housekeeping genes (*thrA*, *purE* , *sucA* , *hisD* , *aroC* , *hemD* and *dnaN*) to determine the circulatory sequence types (STs) of *Salmonella* spp. that are transmissible within the poultry farms. The data of this study showed a higher prevalence of *Salmonella* in broilers with interfarm transmission of common *Salmonella* STs and underscored the need for detail epidemiological investigation as well as strict hygienic practices in the poultry farms all over Bangladesh.

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Mechanism of carbapenem resistance in clinical *Pseudomonas* spp. in Bangladesh

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The aim of the present investigation was to explore Carbapenem resistance mechanism within *Pseudomonas* isolates from clinical origin. A total of 18 presumptive clinical *Pseudomonas* spp. were selected retrieved from diabetic, non-diabetic as well as UTI patients. Approximately seven clinical (39%) *Pseudomonas* spp. showed 100 % resistant to Imipenem, Meropenem and Doripenem. All of these Carbapenem resistant isolates showed resistance to 8 or more groups of antibiotics with 100% resistance to Ampicillin, Oxacillin, Nitrofurantoin, Vancomycin and Cephalosporin 1st to 4th generation antibiotics. The isolates showed significant resistance to other antibiotics such as 42.86% for Gentamycin, Amikacin, 57% for Tetracycline, 85.7% for Azithromycin, Doxycycline, Aztreonam and 85.7% for Floruroquinolone 1st to 3rd generation antibiotics. All Carbapenem resistant isolates were sensitive to Colistin. Amplified ribosomal DNA restriction analysis (ARDRA) and 16S rRNA gene sequence identified the *Pseudomonas* isolates within 3-genotypes such as *P. stutzeri* (ID: 40/D/Mac1, 40/D/Mac2, 40/D/Swab1, 40/D/CIP+Cefo1), *P. aeruginosa* (ID: 54/D/Mac3, 3C CIP+Cefo2) and *P. hibiscicola* (ID: 50/D/Swab1). Production of carbapenamase within the resistant isolates were confirmed by both blue carba test and combined disc assay and gene specific PCR of metallo-□-lactamase (MBL) (*bla*VIM-2, *bla*NDM-1and *bla*IMP-3 and *bla*IMP-4). The finds confirmed 4 clinical *P. stutzeri* isolates (ID: 40/D/Mac1, 40/D/Mac2, 40/D/Swab1, 40/D/CIP+Cefo1) as MBL producers and possessing *bla*VIM-2 gene encoded within an integron gene cassette *Int1*. All of the isolate contains Resistance-Nodulation-Division (RND)efflux pump *mexE* gene, but inhibition experiment using checkerboard method with specific RND efflux pump inhibitor, 1-(1-Naphthylmethyl)-piperazine had no significant effect on MICIMP(FIC index=1.0). This investigation concludes the emergence of *Int1* gene cassette mediated *bla*VIM-2Carbapenemresistant determinant in clinical *Pseudomonas* spp.

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Isolation and molecular profiling of arsenotrophic bacteria from groundwater and soils of aresnic prone areas in Bangladesh

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Arsenic (As) pollution in ground water and soil exerted one of the largest mass poisoning in the history of Bangladesh. About 35 to 77 million people incredibly exposed to high concentration of As (> 50 ppb) through drinking water and irrigation soil. Arsenotrophic bacteria and their functional genes contribute largely to the fate of arsenic compounds in the polluted environment. The present study aims to isolate arsenite metabolizing bacteria and to investigate their arsenotrophic genes (*aio, ars, arr*) from As contaminated ground water and soil. Nine ground water and seven soil samples were collected from arsenic prone area of Munshiganj and Bogura in Bangladesh. Total As contents was detected using Flame Atomic Absorption Spectrometry (FAAS). As contents of all groundwater samples were detected to be >50 ppb and those of soil samples was above 20ppm Exceeding the World health organization (WHO) standard for Bangladesh. A total of 80 heterotrophic and 62 autotrophic arsenite resistant bacteria were screened on respective minimal salt media (MSM) supplemented with 2 mM sodium arsenite. Phenotypic detection of arsenite oxidation was observed using $KMnO_4$ and $AgNO_3$ assays. Representative isolates were genotypically categorized by 16S rRNA PCR and amplified ribosomal DNA restriction analysis (ARDRA) followed by sequencing of representative genotypes. Presumed gene fragments for arsenite efflux pumps (*arsB*, *acr3P*), arsenite oxidase (*aio*) and arsenite respiratory reductase (*arr*) were amplified from each genotypes of the isolates. Five groundwater isolates belonging to *Burkholderia* spp. showed arsenite oxidation capacity and was positive for the presence of *aio* gene. Arsenotrophic bacteria found in this study could play a potential role in biogeocycling of aresnic and aerobic detoxification of highly toxic arsenite to less toxic arsenate in arsenic prone area.