



Category: Metagenomics

Poster Prize Winner

# Assessment of antibiotic resistance genes and integrons in commensal *Escherichia coli* from the Indian urban waste water: Implications and significance for public health

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## Abstract

Antibiotics like  $\beta$ -lactams, quinolones/fluoroquinolones, aminoglycosides and tetracycline constitute the major mainstay of treatment against most infectious diseases including *Escherichia coli*. Indiscriminate use of antibiotics for human and animal well-being has generated an enormous evolutionary pressure on bacteria especially *E.coli*, which has a highly plastic/evolving genome. Though, antibiotic resistance (AR) has been extensively studied in pathogenic *E.coli*, commensal strains have been studied less owing to lesser clinical significance. However, commensal strains pose a serious threat as reservoirs and transmitters of resistance genes to other bacteria. Therefore, the present study was undertaken to investigate the prevalence of resistance genes and integrons in commensal *E.coli* isolated from river Yamuna, Delhi, India, which receives plentiful urban waste water. Eighty three well-characterized *E.coli* strains of phylogroups A and B1 isolated from river Yamuna were investigated. Antimicrobial susceptibilities and minimal inhibitory concentrations (MICs) for  $\beta$ -lactams, aminoglycosides, tetracycline and quinolone/fluoroquinolone were determined by disk diffusion and Etest, according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Production of Extended spectrum  $\beta$ -lactamases (ESBL) and AmpC was investigated. Prevalence of antibiotic-resistance genes for  $\beta$ -lactams (*bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, *bla*<sub>CTX-M</sub>, *bla*<sub>OXA</sub>, *bla*<sub>CMY-42</sub>), aminoglycosides (*rmtA*, *rmtB*, *rmtC*, *armA*, *str*, *aacC2*), tetracycline (*tetA*, *tetR*, *tetM*, *tetW*), and plasmid-mediated quinolone resistance, PMQR (*qnrA*, *qnrB*, *qnrC*, *qnrD*, *qnrS*, *qep*, *aac*) were assessed. Integrons and gene-cassette arrays were characterized. Commensal *E.coli* strains showed a higher resistance to ampicillin (95%), less to cefazolin (45%) and still lesser to tetracycline (15%). About 19% of these strains showed multidrug resistant (three or more classes of antibiotics), of which 15% also produced ESBLs. None of the strains produced AmpC  $\beta$ -lactamases. About 6% of the strains were concurrently fluoroquinolone-resistant and ESBL producers. The *bla*<sub>TEM</sub> was present in most strains (95%), followed by *bla*<sub>CTX-M</sub> (15%). Aminoglycoside-resistance genes *viz.* *str* and *armA* were detected in 6% and 8% strains, respectively; tetracycline-resistance genes *viz.* *tetA* and *tetR* in 3% and 6% strains, respectively; and PMQR gene *viz.* *qnrS* in 15% of the strains. Class I integron was detected in 64% of the isolates, of which 7 strains had 3 different variable region gene-cassette arrays. *dfrA* and *aadA* gene families were widespread among the gene-cassettes identified.

**Citation:** Singh, N.S. and Viridi, J.S. Assessment of antibiotic resistance genes and integrons in commensal *Escherichia coli* from the Indian urban waste water: Implications and significance for public health [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 116. <https://doi.org/10.24870/cjb.2017-a102>