

First ‘One-Health’ study on genome-wide comparison of multidrug-resistant *Escherichia coli* from Human-Animal-Aquaculture-Environment continuum: a collective effort from six institutes of India

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Abstract

Summary: Antibiotic-resistant bacteria are emerging threat to the global public health. Estimates suggests >10 million deaths by 2050 due to AMR alone. Six Indian institute collaborated along with 4 UK universities to address the issue of antimicrobial resistance (AMR) through One Health approach under NEOSTAR project jointly funded by Department of Biotechnology (DBT), Government of India and UK Research and Innovation (UKRI), United Kingdom. To address a question “Dose AMR in livestock contributes to AMR in people? A pilot study was conducted which is a collaborative effort to collect archival microbial isolates of *Escherichia coli*, *Klebsiella* spp., *Staphylococcus aureus* and coagulase negative *S. aureus* (CoNS). The current study deals with *E. coli* isolates collected from ICAR-NIVEDI, ICAR-CIFT, ICAR-IVRI, ICAR-RCNEH, IIT-Delhi and GMCH and were subjected to QC analysis at ICAR-NIVEDI’s BSL2+ facility, these isolates were further segregated into 5 components viz., Animal origin (including aquaculture) (n=50) food of animal origin (n=30), Human (community settings) (n=3), Hospital origin (n=15) and Environment origin (n=14). A total of 112 *E. coli* isolates sequenced for whole genome through Illumina’s HiSeq 2500 platform at Sangers Institute, UK and paired end libraries were generated for all the 112 isolates were assembled and subjected to genome characterization and gene mining through various bioinformatics tools revealed the frequency of resistance, co-resistance, and resistant genes are high and similar across Human-Animal-Aquaculture-Environment continuum in India. This emphasizes the need to collaborate and mitigate antibiotic resistance with a ‘One Health’ approach.

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