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Molecular characterization of extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* in diverse food producing animals from eastern India

Samiran Bandyopadhyay¹, Debasish Kar, Debaraj Bhattacharyya, Bimalendu Mondal, Indranil Samanta², Achintya Mahanti², Premanshu Dandapat, Promod K Nanda, Arun K Das Tapan K Dutta³ and Subhasish Bandyopadhyay

¹Indian Veterinary Research Institute, India

²West Bengal University of Animal & Fishery Sciences, India

³Central Agricultural University, India

Emergence and dissemination of extended spectrum beta-lactamase (ESBL) producing *Escherichia coli* in both hospital and community infection is on the rise for last two decades, a considerable cause of concern for both medical and veterinary practitioners. The ESBL producing *E. coli* can inactivate beta-lactam antibiotics containing oxyimino group specially the third and fourth generation cephalosporins and monobactam. Food producing animals were implicated as a major reservoir of ESBL producers and contributing to further propagation of resistant strains to environment affecting community and public health. In order to determine the occurrence and further characterization of ESBL producing *E. coli* a total of 566 samples (milk and fecal) were collected from diverse food producing animals (cattle, goat, chicken, duck etc.) of eastern India. Of them 41 isolates were confirmed as ESBL producing *E. coli* using phenotypic confirmatory tests like standard combination disc method, ESBL E-test and detection of major ESBL genes blaCTX-M, blaTEM and blaSHV by PCR. The gene blaSHV was more frequently detected followed by blaCTX-M and blaTEM. Many of the isolates were positive for class I integron and sulphonamide resistance gene (sul-1). Added to this, few isolates also carried plasmid mediated quinolone resistance (PMQR) genes and virulence markers of extra-intestinal pathogenic *E. coli* (ExPEC). All the PCR amplified products were cloned and subjected to sequencing for homology analysis and data were submitted to gene bank. All the confirmed ESBL producers were resistant to ceftriaxone, ceftazidime, cefotaxime, aztreonam, cefpodoxime, and cefepirome. Resistance was also frequently noted to other antibiotics as well, like amoxicillin (94%), piperacillin+tazobactam (94%), cotrimoxazole (88%), ciprofloxacin (83%), tetracycline (77%), cefepime (66%) and chloramphenicol (61%). Phylogenetic analysis by ERIC PCR revealed genetic similarity among the ESBL strains isolated from different regions of eastern India. However, no specific trend was observed in respect to source of isolation, virulence or resistance gene profile. This is the first ever systemic study on ESBL producing *E. coli* in food producing animals from India. We also report for the first time ESBL producers carrying markers of ExPEC to the best of our knowledge.

samiranvet@gmail.com/sbandyo@ivri.res.in