

The First Identification of Multidrug Resistant Uropathogenic *Enterobacter hormaechei* Subsp. *Steigerwaltii* St93 from Sri Lanka

PDVM Perera^{1,2*}, S Gamage², HSM de Silva^{2,3}, SK Jayatileke³, N de Silva¹, A Aydin⁴, VI Enne⁴ and EM Corea²

¹Department of Microbiology, Faculty of Medicine, Sabaragamuwa University of Sri Lanka

²Department of Microbiology, Faculty of Medicine, University of Colombo, Sri Lanka

³Sri Jayewardenapura General Hospital, Nugegoda, Sri Lanka

⁴Centre for Clinical Microbiology, Division of Infection and Immunity, University College London, Royal Free Campus, Rowland Hill Street, London, UK

*v.perera@med.sab.ac.lk

The spread of multidrug resistant *Enterobacteriaceae* strains resulting in treatment failure and increased mortality has become a global health issue. Of these, members of *Enterobacter cloacae* complex are of major concern due to their association with transferable multidrug resistance and the establishment of successful clones. Such strains pose a potential threat to hospitals as they are known to cause hospital outbreaks. The data regarding antimicrobial resistance (AMR) and transmission in pathogenic bacteria are important to decide infection prevention and control measures locally and internationally. This paper describes the first identification of carbapenem-resistant *Enterobacter hormaechei* subsp. *steigerwaltii* ST93 in Sri Lanka. One *Enterobacter cloacae* strain (ECC) from a collection of ninety-four uropathogenic *Enterobacteriaceae* isolated from hospital-acquired urinary tract infections (HA-UTI) from Sri Jayewardenepura General Hospital, Sri Lanka was analysed using genomic sequencing and comparative genomics. Seventeen AMR genes that confer co-resistance for several antibiotic classes such as β -lactams, carbapenems, aminoglycosides, fosfomycins, macrolides, sulphonamides, trimethoprim, phenicols and tetracyclines were identified. Coexistence of two types of carbapenem resistance genes (*bla*_{NDM-4} and *bla*_{OXA-181}) was a significant finding. Virulence genes coding for several important functional proteins were identified. Some of these include *mrk* gene cluster that encodes type 2 fimbriae that are associated with biofilm formation and Type VI secretion systems loci (T6SS) which confers the ability to survive in a range of environments. The isolate did not carry any plasmids. However, several mobile genetic elements (*ISEcp1*, IS26-IS26 composite transposon and IS5) were identified flanking AMR genes such as *bla*_{CTX-M-15}, *bla*_{NDM-4} and *ble* gene cluster and *aac(6')-Ib-cr*, *bla*_{OXA-1}, *catB3* gene cluster that contribute to the horizontal transfer of these genes. This study provides important information on the development and dissemination of genes coding for antimicrobial resistance and adds to the currently scarce data on AMR in Sri Lanka.

Keywords: *Enterobacter Cloacae* Complex, Multi Drug Resistance, Antimicrobial Resistance Genes, Virulence Genes, Mobile Genetic Elements