WHOLE GENOME SEQUENCING OF EXTENDED-SPECTRUM BETA-LACTAMASE-PRODUCING *ESCHERICHIA COLI* ISOLATED FROM PATIENTS, FARM WASTE AND CANALS IN THAILAND

Chakkaphan Runcharoen[1], Kathy E. Raven[2], Sandra Reuter[2], Teemu Kallonen[4], Suporn Paksanont[1], Jeeranan Thammachote[3], Suthatip Anun[3], Beth Blane[2], Julian Parkhill[4], Sharon J. Peacock[1,2,4,5] and Narisara Chantratita[1]*

[1]Department of Microbiology and Immunology, Faculty of Tropical Medicine, Mahidol University, Bangkok 10400, Thailand; [2]Department of Medicine, Box 157 Addenbrooke's Hospital, University of Cambridge, Hills Road, Cambridge CB2 0QQ, United Kingdom; [3]Division of Clinical Microbiology, Medical Technology Department, Bhuddhasothon Hospital, Chachoengsao 24000, Thailand; [4]The Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, United Kingdom; [5]London School of Hygiene and Tropical Medicine, London, WC1E 7HT, United Kingdom Road, Cambridge CB2 0QQ, United Kingdom

Tackling multidrug-resistant *Escherichia coli* requires evidence from One Health studies, which capture a whole host of potential reservoirs in circumscribed geographic areas. We conducted a survey of extended-spectrum β-lactamase (ESBL)-producing *E. coli* isolated from patients, canals and livestock wastewater in Chachoengsao province, Thailand between 2014 and 2015, and analyzed the isolates using whole genome sequencing. The bacterial collection of 149 isolates contained 84 isolates from a single hospital and 65 from the hospital sewers, canals and farm waste water within a 20-km radius. *E. coli* ST131 predominated the clinical collection (29%), but was uncommon in the environment. Genome-based comparison of *E. coli* from infected patients and their immediate environment indicated low genetic similarity overall between the two, although three clinical-environmental isolate pairs differed by ≤5 single nucleotide polymorphisms. Thai *E. coli* isolates were dispersed throughout a phylogenetic tree containing a global *E. coli* collection. All Thai ESBL-positive *E. coli* isolates were multi-drug resistant, including high rates of resistance to amikacin (97%), tobramycin (77%), gentamicin (77%), ciprofloxacin (68%) and trimethoprim (68%). ESBL was encoded by six CTX-M elements and SHV-12. Three isolates from clinical samples (n = 2) or a hospital

*Corresponding author: E-mail: narisara@tropmedres.ac.th

One Health Operation Research under THOHUN Research Grants

sewer (n = 1) were resistant to the carbapenems (encoded by NDM-1, NDM-5 or GES-5), and three isolates [clinical (n = 1) and canal water (n = 2)] were resistant to colistin (encoded by *mcr-1*); no isolates were resistant to both drugs. Tackling these bacteria will be challenging based on their widespread distribution, but the low prevalence of resistance to the carbapenems and colistin suggests that efforts are now required to prevent these from becoming ubiquitous.