Prevalence and molecular characterization of multidrug-resistant ESKAPE pathogens isolated from patients at a Naval hospital in Thailand: 2016-2018

Sirigade Ruekit1, Apichai Srijan1, Katie R Margulieux1, Patrick McGann2, Oralak Serichantalergs1, Rosalin Kormanee3, Prawet Sukhchat1, John M Crawford1 and Brett E Swierczewski1

1Armed Forces Research Institute of Medical Sciences, Thailand
2Walter Reed Army Institute of Research, USA
3Queen Sirikit Naval Hospital, Thailand

Aim: ESKAPE pathogens, Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa and Enterobacter spp. (and E. coli in this study) are multidrug-resistant (MDR) bacteria with increasing challenges for healthcare institutions worldwide and recognized as one of the greatest threats to humans. This study report the prevalence of ESKAPE pathogens and molecular characterization of the resistant genes in these organisms.

Methods: 429 ESKAPE bacteria were isolated from clinical samples as part of active surveillance study in Queen Sirikit Naval Hospital, Chonburi, Thailand. Resistant strains reported through BD Phoenix System based on CLSI guidelines. Molecular characterizations of resistant genes were performed by PCR and Real-time PCR assays.

Results: Prevalence of MDR - E. faecium, S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa, Enterobacter spp., and E. coli were 1.2%, 4.0%, 24.9%, 22.6%, 4.7%, 42.4%, respectively. Percentage of vancomycin resistance Enterococcus (VRE) and methicillin resistance S. aureus (MRSA) were 83.3% and 76.5%, respectively. Carbapenem, ESBL, and colistin resistance in gram negative (GN)-ESKAPE pathogens were detected in 46.7%, 93.4%, and 3.0% respectively. The resistant genes detected in ESKAPE pathogens were as follows; vanA 100% in VRE; meca 100% in MRSA isolates. Carbapenem resistance in A. baumannii, K. pneumoniae, P. aeruginosa, Enterobacter and E. coli isolates were 49.5%, 35.3%, 7.9%, and 7.4%, respectively. Carbapenem resistant genes in GN-ESKAPE bacteria were; blaNDM 36.8%, blaOXA-48 family 27.4%, blaVIM 1.1% and blaKPC 0.5%, respectively. ESBL genes detected in this study were; blaSHV, blaOXA, blaCTX-M, blaDHA, blaCMY, blaPER and blaVER. Among 12 colistin resistant isolates, mcr-1 gene was detected in five E. coli and three K. pneumoniae isolates.

Conclusion: The continuous surveillance should be performed periodically in order to evaluate the prevalence of MDR-ESKAPE pathogens. The importance of this study is to prevent hospital-acquired infections, as well as greater antibiotic prescribing control in the hospital.

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Biography
Sirigade Ruekit is a Medical Research Technologist at the Armed Forces Research Institute of Medical Sciences. She is interested in multidrug resistance genes and molecular typing in enteric pathogens. For molecular typing, she performs and evaluate capsular typing of Campylobacter jejuni isolates by multiplex PCR and real-time PCR assays. For multidrug resistance studies, she perform and evaluate PCR and real-time PCR for extended spectrum of beta-lactamase resistance genes, carbapenemase genes, methicillin resistant gene and vancomycin resistance genes among enteric bacteria. She also performs DNA sequencing and analysis of DNA sequences to detect resistant gene mutation. For molecular training, she provides training to new technicians and/or visitors, update molecular technique to other technicians and provide training for co-laboratory. She is also responsible for preparing manuscript and generate publication.
sirigader@afrims.org