

JOINT EVENT

9th International Conference on **Emerging Infectious Diseases**

&

6th World Congress on**Control and Prevention of HIV/AIDS, STDs & STIs**

August 27-28, 2018 | Zurich, Switzerland

Prevalence and molecular characterization of multidrug-resistant ESKAPE pathogens isolated from patients at a Naval hospital in Thailand: 2016-2018Sirigade Ruekit¹, Apichai Srijan¹, Katie R Margulieux¹, Patrick McGann², Oralak Serichantalergs¹, Rosarin Kormanee³, Prawet Sukhchat³, John M Crawford¹ and Brett E Swierczewski¹¹Armed Forces Research Institute of Medical Sciences, Thailand²Walter Reed Army Institute of Research, USA³Queen 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; *bla*NDM 36.8%, *bla*OXA-48 family 27.4%, *bla*VIM 1.1% and *bla*KPC 0.5%, respectively. ESBL genes detected in this study were; *bla*SHV, *bla*OXA, *bla*CTX-M, *bla*DHA, *bla*CMY, *bla*PER and *bla*VER. 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.

Recent Publications:

1. Srijan A, Margulieux K R, Ruekit S, Snesrud E, Serichantalergs O, Kormanee R, Sukhchat P, Sriyabhaya J, Hinkle M, Crawford J M, McGann P and Swierczewski B E (2018) Genomic characterization of non-clonal *mcr-1*-positive multidrug-resistant *Klebsiella pneumoniae* from clinical samples in Thailand. *Microbial Drug Resistance* 24(4):403-410.
2. Serichantalergs O, Ruekit S, Pandey P, Anuras S, Mason C, Bodhidatta L and Swierczewski B (2017) Incidence of *Campylobacter concisus* and *C. ureolyticus* in traveler's diarrhea cases and asymptomatic controls in Nepal and Thailand. *Gut Pathogens* 9(47):1-7.
3. Serichantalergs O, Bodhidatta L, Nobthai P, Ruekit S, Supawat K, Swierczewski B E and Mason C J (2017) Distribution and Molecular Characterization of Enteroaggregative *Escherichia coli* Isolated from Children in A Case-control Study of Acute Diarrhea in Thailand. *Journal of Clinical Microbiology* 6(5):1-6.

4. Velasco J M, Valderama M T, Peacock T, Nirdnoy W, Nogrado K, Navarro F C, Chua D, Jr, Srijan A, Ruekit S, Macareo L R and Swierczewski B (2017) Carbapenemase-producing enterobacteriaceae and nonfermentative bacteria, the philippines, 2013–2016. *Emerging Infectious Diseases* 23(9):1597-1598.
5. Poramathikul K, Bodhidatta L, Chiek S, Oransathid W, Ruekit S, Nobthai P, Lurchachaiwong W, Serichantalergs O, Lon C and Swierczewski B (2016) Multidrug-resistant shigella infections in patients with diarrhoea, cambodia, 2014–2015. *Emerging Infectious Diseases* 22(9):1640-1643.

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.

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