guideline. The strains were also typed by random amplified polymorphic DNA (RAPD). The lipid A from resistance strains were extracted and subjected to the analysis using MALDI-TOF mass spectrometry.

Results: Sensitivity to colistin were determined when the MIC is $\leq$ 2 μg/ml according to CLSI guideline. Of the two hundred strains collected, twenty were found to have MIC ranging from 4 to 128 μg/ml. The RAPD grouped the resistance strains into five groups. The MALDI-TOF MS revealed that the basic structure of *A. buamannii* lipid A is the heptaacylated diphosphoryl lipid A (m/z 1910). The resistance strains exhibited the extra peaks at either m/z 2034, 2071 or 2194, which correspond to the additions of phosphoethanolamine, hexosamine or both to lipid A molecule, respectively. The addition of these residues takes place at the phosphate moieties of lipid A thus potentially cancelling the negative charges and may render *A. baumannii* the resistance to colistin.

Conclusion: The analysis of lipid A from Thai *A. baumannii* colistin resistance strains demonstrates the modification by which the negative charges were eliminated by the addition of small residues and may subsequently lead to the reduction of colistin target.

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Molecular epidemiology of *Acinetobacter baumannii* integrated with genomic resistance island

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Background: International clones of multi-drug resistant *Acinetobacter baumannii* integrated with Genomic Resistance Islands (GRI); AbaR1, AbaR2, AbaR3, AbaR5 have been identified. The objective of this study was to identify GRI harboring *A. baumannii* in Thailand and to establish its genetic linkage with international clones.

Methods: Thirty seven non-repetitive clinical isolates of carbapenem resistant *A. baumannii* were studied. Dot blot hybridization was performed to screen for class 1 integron element integrase gene (*IntI1*). Cassette characterization of class 1 integron element, GRI junctional typing, and amplification of class 1 integron borne resistance genes were performed by PCR. Real time multiplex-PCR (RT-MPCR) was performed to amplify integron and non-integron borne genes present in GRIs and resistant plasmid; AbaR1, AbaR2, AbaR3, AbaR5, and plasmid pACICU. Clonal evaluation was carried out by Multi-locus Sequence Typing (MLST) and eBurst analysis.

Results: Four GRI junctional types were identified, type I (n = 24, both 5′ and 3′ junctions present), type II (n = 3, 5′ junction only), type III (n = 7, 3′ junction only), and type IV (n = 3, no junction identified). The prevalence of class 1 integron element was 81.08% and this integron element harbored *bla*VEB-1 (n = 7), *arr-2* (n = 10), *cmlA* (n = 5), *bla*0XA-10 (n = 9), and *bla*TEM-1 (n = 15) genes. Cassette organization in *bla*VEB-1 containing 5.5 kb class 1 integron element was 5′CS-*aadB*-*bla*VEB-1-*arr-2*-*cmlA*-*aadA1*-*bla*OXA-10-3′CS. RT-MPCR identified a presence of *arsC* (n = 32), *aacA4* (n = 23), *aac3* (n = 15), and pACICU (n = 9). MLST typed 9 isolates into 6 STs; ST88 (n = 1), ST119 (n = 3), ST198-202 (one each). The isolates with similar junctional types had unique STs. The eBurst analysis for the first time identified the presence of pan-European clone I and II and Chinese clone ZS4 in Thailand.

Conclusion: The international clones of *A. baumannii* integrated with variants of GRI were prevalent in Thailand. Monitoring and surveillance of these multi-drug resistance clones is necessary to prevent further spread of these international multi-drug resistant clones in Thailand.

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The detection of the NDM-1 and other carbapenemase genes in multidrug resistant Gram negative bacilli (MDRGNB) in a Jamaican hospital

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Background: Resistance of clinically significant bacteria to carbapenem antibiotics, through the production of carbapenemases has become a global problem. This has serious implications as infections caused by these resistant organisms are difficult to manage.

Our aims were to determine if carbapenemases were a mechanism of resistance among MDRGNB isolated at the Microbiology Laboratory, University Hospital of the West Indies (UHWI), Jamaica, to identify specific carbapenemase genes and to determine the relatedness of the strains, so that policies regarding infection control and antibiotic therapy could be better informed.

Methods: At UHWI from May 2009 to March 2011, 105 MDRGNB (1*Klebsiella pneumoniae*, 3 *Escherichia coli*, 82 *Acinetobacter spp.* and 19 *Pseudomonas spp.*) were identified as potential carbapenemase producers during routine susceptibility testing of clinical isolates. Further phenotypic screening for carbapenemase production was performed using inhibitors and the modified Hodge test. Multiplex PCR for identifying OXA-23, 24, 51, 58 was performed on *Acinetobacter spp.* For the remaining isolates, multiplex PCRwas performed to detectNDM, KPC, VIM, GES, IMP and OXA-48 carbapenemase genes. PFGE was used to determine the relatedness of carbapenemase-positive isolates.

Results: Of 4 Enterobacteriacae tested, phenotypic screening and PCR identified the *Klebsiella pneumoniae* as the first isolate in Jamaica to possess the NDM-1 gene. Of the 82 *Acinetobacter spp*., all but 1 were positive for blaOXA 51, 12 had blaOXA 24, 2 blaOXA23, and 1 blaOXA58. One *P. aeruginosa*had the GES gene, but without sequencing, its carbapenemase activity is uncertain. *Acinetobacter spp. and Pseudomonas spp.* sharing similar genotypes were highly related, suggesting an endemic or outbreak strain.

Conclusion: Carbapenemase production is a cause of resistance amongst MDRGNB in Jamaica, some of which are related. Pheno-