ampicilin (56.3%), nalidixic acid (43.7%) and erythromycin (22.9%). No resistance was observed against ciprofloxacin or ceftriaxone. The isolates were found to have intermediate susceptibility toerythromycin (68.8%), nalidixic acid (56.3%) and ampicilin (33.3%).

Conclusion: Our findings showed that strains of *Vibrio cholerae* have become resistant to several antibiotics, and multidrug resistance is increasing. Hence, it is recommended that changing patterns of susceptibility to antimicrobials should be considered when responding to cholera outbreaks.

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Molecular analyses of metallo-β-lactamase genes in carbapenemresistant enterobacteriaceae isolated from three tertiary hospitals in the Philippines

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Background: Metallo-β-Lactamase (MBLs) has been reported to be carried by Carbapenem Resistant Enterobacteriaceae (CRE) in different countries worldwide.

Methods & Materials: In this study, 41 samples of carbapenem resistant Enterobacteriaceae were isolated from three tertiary institutions in the Philippines. These samples were either tested with Vitek® 2 antibiotic susceptibility cards or simple disk diffusion method and were found to be resistant to at least one carbapenem. Modified Hodge Test was used to detect carbapenem producers and Imipenem/Imipenem-EDTA combination was used to detect MBL producers. PCR amplification was done to detect MBL and other β-lactamase genes. Multilocus sequence typing (MLST) of samples was done to determine the clonality of MBL producing isolates.

Results: All samples were positive for carbapenemase production using Modified Hodge test while 31 samples were confirmed MBL producer based on Imipenem/Imipenem-EDTA combination disk method. Molecular analysis showed that NDM is the most common type of MBL in the samples with a prevalence of 58.5%, followed by IMP with 7.3% and VIM with 4.8%. Molecular analysis of the NDM sequences from NDM positive samples revealed amino acid substitutions at position 123 and 166 indicating that these could be new variants of NDM. MLST of NDM positive *E. coli* found that these samples belong to ST Complex 10, 69 and 398. MLST of *K. pneumoniae* isolates showed that most NDM positive *K. pneumoniae* belong to ST 147 which has been known internationally to harbour different carbapenemase genes.

Conclusion: MBLs, most importantly NDM is present in the Philippines at a high rate compared to other countries. This resistance mechanism was also found to be carried by different clones of Enterobacteriaceae. These findings suggest the need for a larger surveillance of this resistance mechanism in the country.

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Circulating clones and antibiotic resistance phenotypes of the S. Aureus strains in the Romanian hospitals

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Background: Panton–Valentine leukocidin (PVL)and enterotoxins (SEs) have been involved in the pathogenesis of staphylococcal infections. The expression of most virulence factors in *S. aureus* is controlled by the accessory gene regulator (*agr*). *S. aureus* (SA) strains can be divided into 4 major *agr* groups (I – IV). The genes encoding the enterotoxins are placed on the enterotoxin gene cluster *(egc*). Few data are about the enterotoxin gene profiles of the *S. aureus* strains in different geographical areas.

Methods & Materials: The purpose of the study was to determine the prevalence of the PVL, SEM & SEG genes, of the *agr* groups in the SAisolates from various hospitals and to investigate a possible relationship between the *agr* groups and the occurrence of the enterotoxin genes. In order to observe the significance of the presence of the genes in these strains the resistance pattern to antibiotics and the resistance phenotypes were determined.

Strains identification and the resistance profiles to antibiotics were performed by standard and automated methods (Vitek2Compact). The genes content of the clinical isolates were detected by PCR.

Results: The most abundant gene was the agr gene, present in 48,9% isolates, followed by the SEM&SEG (44,68%) and the PVL (19.1%) genes; 4 *agr* groups (I – IV) were detected in *S. aureus* isolates: the *agr* group III was the most predominant (27,7%) followed by the group I (10,6%) and the group *agr* II (6,4%). The group *agr* IV was less common (2,1%). All the arg positive strains are MRSA strains. The SEG gene was the least frequent SE gene in *S. aureus.* SA tested strains which own the agr, the SEM and the SEG genes, showed a high resistance to AB. The resistance phenotype was not influenced by the group of the agr gene (I or III) or by the association of the agr gene with the SEM and the SEG genes.

Conclusion: We draw attention upon the circulation in our geographic area of different clones carrying the agr genes alone or associated with the SEM, SEG and PVL genes, that originate from Europe and other parts of the world.

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