resistance to Erythromycin (37.5%), Clindamycin (33.3%), Gentamycin (35.4%), Ciprofloxacin (35.4%), Moxifloxacin (35.4%) and Rifampicin (35.4%). All the MRSA strains and the MSSA strains were susceptible to Linezolid, Trimethoprim-sulfamethoxazol, Fusidic Acid, Vancomycin, Teicoplanin and Tigecyclin. Of the MSSA strains 4.2% were resistant to Tetracycline and 2.1% were resistant to Eritromycin, but all the MSSA strains were susceptible to other AB. Of the *S. aureus* strains, 53.3% were MLSB strains, from which 13.3% presented inducible phenotypesand 40% showed constitutive phenotype.

Conclusion: Data from this study demonstrate the diversity of the *S. aureus* strains circulating in our geographical areas and the wide variability of the resistance phenotypes to various classes of antibiotics among the strains of *S. aureus*. It is observed that the percentage of the MRSA strains (41.7%) is higher to that reported by Romania in 2009 to the EARS-Net (35,6%). There exists also higher frequency of the MLSB (53.3%) strains compared to the MRSA (41.7%) strains isolated in our hospital. The prevalence of the MLSB type, shows an increasing trend among the strains of *S. aureus*, lately. The prevalence of the resistant strains is growing and creates difficulties in both treatment and prevention of the nosocomial infections.

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Antibiotic resistant patterns amongst clinical Vibrio cholerae O1 isolates from the Greater Accra Region, Ghana-2013

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Background: Cholera affects over 3.5 million people annually with between 100,000-130,000 deaths. One of the protocols in the treatment and control of cholera infection is antibiotic therapy. When sanitation, fluid replacement and antibiotic therapy standards are properly adhered to, Case Fatality Rates (CFR) are usually < 1%. However, in the absence of these measures, CFR could exceed 50%. Several studies report of increasing rates of antibiotic resistance amongst enteric bacteria including *Vibrio cholerae*, with integrons being mostly implicated as serving as genetic templates for the encoding and acquisition of antibiotic resistance. There has been no continuous surveillance on antibiotic susceptibility profiles for *Vibrio cholerae* O1 in Ghana. This study determined resistance patterns of *Vibrio cholerae* O1 to selected and commonly used antimicrobial agents, assessed differences in resistance patterns across year periods, and molecularly screened for the presence of Class 1 and 2 integrase genes.

Methods & Materials: We screened a cumulative total of 277 isolates archived between 2010 and 2012 from the Greater Accra Region-Ghana, using the disc diffusion method. Molecular screening was done for 89 isolates that were resistant to 6 or more antimicrobial agents. Univariate and multivariate analysis were done to express frequencies and compare categorical variables.

Results: Resistance patterns were high for co-trimoxazole 232/241 (96.3%), trimethoprim 265/276 (96.0%), erythromycin 255/270 (94.4%) and low for azithromycin 0/11 (0%), ciprofloxacin 1/274 (0.4%), doxycycline 40/235 (14.5%) and tetracycline 43/232 (15.6%). There was significant association between antibiotic susceptibility patterns over the period of years for doxycycline, chloramphenicol, co-trimoxazole, nalidixic acid, streptomycin and tetracycline ($P < 0.5$), except for ciprofloxacin, trimethoprim and erythromycin ($P > 0.05$). None of the tested isolates harboured Class 1 or 2 integron genes.

Conclusion: There are high levels of antibiotic resistance among the *Vibrio cholerae* O1isolates tested, though Class 1 and 2 integrons could not be implicated for this observation. The high rate of resistance to erythromycin is worrisome as it is the drug of choice for pregnant women and children because of the potential side effects from the use of the other available drugs. Nevertheless, azithromycin, ciprofloxacin, doxycycline and tetracycline can be relied upon in the treatment and control of cholera infections when not contra-indicated.

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Patterns of antimicrobial resistance in vibrio cholera strains isolated from patients with acute watery diarrhea during a cholera outbreak in southeast of Iran in summer 2013

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Background: Increasing antimicrobial resistance in potentially life-threatening enteric pathogens such as *Vibratos Cholera* is a growing global challenge in the treatment of patients. The objective of this study was to detect possible drug resistance in isolates collected from laboratory-confirmed cases of cholera during an outbreak that occurred between August and September 2013 in Sistan and Balouchestan province, southeast of Iran.

Methods & Materials: A total of 48 *vibrio cholera* isolates were obtained from patients with acute watery diarrhea. All patients were either Afghani nationals who newly crossed the border or Iranians that came in contact with Afghani patients. All strains isolated were of Inaba serotype. The samples were subjected to Antimicrobial Susceptibility Testing (AST) using the standard disk diffusion technique (Kirby-Bauer method). The disks were purchased from Iranian Padtan Teb Company. The antimicrobial content of different types of disks used for testing included: sulfamethoxazole -trimethoprime (5 μg), tetracycline (30 μg), nalidixic acid (30 μg), ciprofloxacin (5 μg), ampicilin (10 μg), ceftriaxone (30 μg) and erythromycin (15 μg). Using the criteria published by the Clinical and Laboratory Standards Institute (CLSI), the susceptibility of the isolates were determined as susceptible, intermediate, or resistant.

Results: The isolated strains showed resistance to sulfamethoxazole-trimethoprime (89.6%), tetracycline (60.4%),

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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