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antimicrobial agents were determined, according to guidelines of CLSI, by an agar dilution method. Molecular characterizations of β-lactamases were performed by PCR amplification, DNA sequencing, and Southern blot analysis. The $bla_{OXA-418}$ gene was expressed by a pET-30 system and the gene product was purified by His-Bind column and Mono S column. Steady-state kinetic constants of the purified enzyme were determined by fitting the initial rates directly to the Henri-Michaelis-Menten equation using nonlinear regression with the program DYNAFIT.
Among 38 isolates, one carbapenem-resistant *A. baumannii* harbored a novel variant ($bla_{OXA-418}$) of OXAs, which was encoded by the chromosome. The clinical isolate and its transformant showed resistance to carbapenems (especially to meropenem). Notable changes in MIC values were in line with the respective kinetic parameter differences. OXA-418 was most closely to OXA-228.
OXA-418 was derived from OXA-228 by the five substitutions (Val25Glu, Ser192Arg, Asp201Asn, Glu227Lys, and Asn257Asp; OXA numbering system). Among these substitutions, Asp201Asn and Glu227Lys are new sites for carbapenem resistance among OXA-228-like genes.

P1-GR56

Risk factors of MDR Gram negative bacteremia among hospitalized patients

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Background: Over the past decade, the numbers of bloodstream infections caused by multidrug-resistant (MDR) Gram-negative bacteria have risen sharply. MDR Gram-negative bacteremia increases not only mortality, but also patient morbidity, length of treatment and hospitalization costs. It is important to identify risk factors of MDR Gram-negative bacteremia among hospitalized patients to prevent these risk factors and to lower the incidence of MDR Gram-negative bacteremia.
Aim: To identify the risk factors of MDR Gram-negative bacteremia among hospitalized patients
Method: Risk factors were identified by a case-control study. Data was collected from inpatients medical record that had positive blood cultures of Gram negative bacteria from 2008-2013. The case group was subjects who had MDR Gram-negative bacteremia, and the control group was subjects who had non-MDR Gram negative bacteremia. All variables that had a value of p <0.25 on bivariate analysis were included in multivariate analysis using logistic regression.
Result: During the study period, there were 131 patients fulfilled the criteria: 42 patients who had MDR Gram-negative pathogen bacteremia (case) and 89 patients who had non-MDR Gram-negative pathogen bacteremia (control group). Based on the bivariate analysis, two variables were statistically significance: history of treatment in ICU/HCU (p=0.003) and history of ventilator (p=0.030). Further multivariate analysis showed that there was one variable statistically significance, which was history of treatment in ICU / HCU (OR: 3.118; CI 95% : 1.443–6.736; p=0,004).
Conclusion: History of treatment in ICU / HCU was risk factor of MDR Gram negative bacteremia among hospitalized patients.
Keywords: bacteremia, Gram negative, MDR, risk factor

P1-GR57

Analysis of the roles of small noncoding RNAs in responses to antibiotics and their applications on erradicating MDR bacteria

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The misuse of antibiotics has resulted in increasing bacterial multidrug resistance (MDR). Small noncoding RNAs (sRNAs), modulators of multiple cellular events, may influence bacterial responses to antibiotics; however, their roles and mechanisms of action remain largely unknown. Here, the susceptibilities of *Escherichiacoli* strains overexpressing each of the 26 known Hfq-dependent sRNAs to major classes of antibiotics were determined. The results suggested that 17 sRNAs modulate antibiotic susceptibility; overexpression of nine of these sRNAs specifically reduced or potentiated antibiotic efficacy. These phenotypes were conserved between species, but the essentialities of the sRNAs were limited. Based on overexpression and knockout studies, the results presented here, firstly, unveil sRNA-mediated modulatory pathways and, secondly, suggest that the sRNAs could be used as biomarkers to identify cephalothin-resistant strains. Furthermore, the sRNAs may potentiate the effect of levofloxacin, allowing the modulation of antibiotic action on MDR strains. In summary, sRNAs have the potential to enable bacteria to adapt smartly to antibiotic challenges via multifaceted approaches.

P1-GR58

Clinical and microbiological characteristics of *Klebsiella pneumonia* bacteremia in a single center

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Background: The aim of present study is to evaluate clinical and microbiological characteristics of *K. pneumonia* bacteremia in a single center.
Methods: The study was conducted at Keimyung University. All episodes of *K. pneumonia* bacteremia (n = 344) during two 2 year periods (2004-5 and 2012-3) were retrospectively compared.
Results: Of a total of 344 patients, 140 (40.6%) were the first period and 204 (59.4%) were the second period. The frequencies of cardiovascular diseases (47.5% vs. 24.3 *P*=0.001), neurologic diseases (19.8% vs. 10.8% *P*=0.035) were significantly higher in the second period than in the first period. The frequencies of cefotaxime (20.1% vs. 7.1% *P*=0.001), cefepime resistance (19.1 vs. 0% *P*=0.001) and ESBL positivity (19.1% vs. 4.3% *P*=0.001) were significantly higher in the second period than in the first period. But the initial empirical antibiotic use of cefepime (17.9% vs. 0% *P*=0.001), carbapenem (19.8% vs. 2.9% *P*=0.001), vancomycin (12.4% vs. 4.3% *P*=0.012) were higher in the second period than in the first period. In the subgroup analysis, the frequencies of cefotaxime (32.4% vs. 10.6% *P*=0.002), cefepime resistance (30.6% vs. 0% *P*=0.001) and ESBL positivity (31.5% vs. 6.1% *P*=0.001) were higher in the second period than in the first period in the healthcare associated *K. pneumonia* bacteremia group. But the initial empirical antibiotic use of cefepime (17.9% vs. 0% *P*=0.001), carbapenem (19.8% vs. 2.9% *P*=0.001) were higher in the second period than in the first period in both groups.
Conclusion: The frequencies of antibiotic resistance in the community associated *K. pneumonia* bacteremia group did not differ between the first period and the second period. But the initial empirical antibiotic use of cefepime (17.9% vs. 0% *P*=0.001), carbapenem (19.8% vs. 2.9% *P*=0.001) were higher in the second period than in the first period in both groups.