

Conclusions: For caring large amount of patients and preventing cluster in hospital during epidemic of enterovirus, we depend on our facility and ability of pediatric department to make up the strategies of enterovirus health-care, which include the flexible administrative policy, the procedure and education of infection control, and team work for serious complications. Therefore, we could feel easy to face the challenge of this communicable disease every year. We not only offer the high quality of healthcare but also perform the effectiveness of infection control.

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RAMR OPERON AND LON PLAY A CENTRAL ROLE IN TIGECYCLINE RESISTANCE IN *KLEBSIELLA PNEUMONIAE*

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Purpose: *Klebsiella pneumoniae* was Gram-negative bacteria caused a lot of diseases, like pneumonia, and urinary tract infection. The rise of multidrug resistance increased the difficult of treatment. Although tigecycline showed activity against a broad spectrum of bacteria, the strains resistant to tigecycline were emerged.

Methods: The whole genomes of both clinical strain and laboratory evolution strains were sequenced to identify the putative mutations related to tigecycline resistance. Fitness cost measurement and transcriptome were also performed. At last, complement experiment was performed to verify the gene's function.

Results: The mutations in seven tigecycline resistant strains were observed in *ramR* (5/7), *lon* (3/7), *ramA* (1/7) and *rpsJ* (1/7). The high fitness cost was observed in laboratory evolution strains but not clinical strain. Of single step evolution mutants, 80% (29/36) of mutants harbored mutation in *ramR*. Five mutations were located in dimerization domain of RamR, and two mutations were observed in DNA-binding domain. Furthermore, single step evolution mutant demonstrated cross-resistance to ciprofloxacin. Transcriptome analysis demonstrated *ramR* operon and *acrA* was high expressed in all tigecycline resistant strains. Genes involved in nitrogen metabolism were induced in laboratory evolution strains when compare with wild type and clinical strain. Complement experiment showed that both wild type *ramR* and *lon* partially restored the tigecycline sensitivity of *K. pneumoniae*.

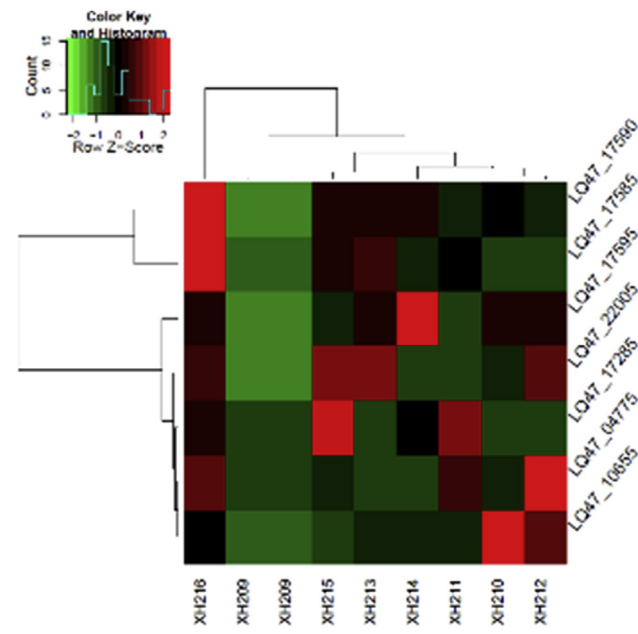


Fig 1 Heatmap of the differentially expressed genes in one clinical strain and six laboratory evolution strains.

Conclusions: These results suggested that *ramR* operon and *lon* play a central role in tigecycline resistance in *K. pneumoniae*.

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ANALYSIS OF TIGECYCLINE'S CLINICAL USE FROM A MEDICAL CENTER IN TAIWAN

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Purpose: The growing numbers of multi-drug resistant organisms (MDRO) usually lack effective antimicrobial agents so tigecycline has been given great expectations as a candidate. The purpose of this study is to assess the efficacy of tigecycline's clinical use and its outcomes in hospitalized patients.

Methods: We retrospectively reviewed the medical records of patients who had received tigecycline at least for 3 days in our hospital from May 1, 2011 to January 31, 2013.

Results: Three hundred and nine patients were analyzed in this study. Almost half patients were shown to have successful clinical response to tigecycline (151/309; 49%), with high clinical success observed in complicated skin and skin structure infections (101/137; 74%). In failure group, treatment failure was mostly seen in hospital-acquired pneumonias and pneumonias complicated with bloodstream infections (83/100; 83%). The eradication rate for totally bacterial isolates mostly collected from sputum was only 30% (33/112). Four patients (1.3%) experienced from gastrointestinal adverse events after the use of tigecycline. The mortality rate was 27% (84/309), which was mainly due to pneumonias (48/101; 48%).

Conclusion: Our study showed good efficacy of tigecycline for the treatment of complicated skin and skin structure infections with relatively lower gastrointestinal adverse events. Regarding the treatment of pneumonia, ineffective response was predictable as most patients with pneumonia were hospital-acquired in our study.

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STUDY OF VARIATION ON DRUG SUSCEPTIBILITY TESTING AND CLASS 1 INTEGRONS OF *ACINETOBACTER BAUMANNII*

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Purpose: Antibiotics-resistant *Acinetobacter baumannii* is a very important cause of healthcare-associated infections, in addition to the highly pathogenic and mortality, it is one of major healthcare-associated infecting pathogens. Integrons are the genetic unit that confer antibiotic resistance to bacteria besides plasmid and transposon.

Methods: In this study, 100 *A. baumannii* clinical blood culture isolates were collected from Show Chwan Memorial Hospital from 2008 to 2010. The drug susceptibility against 14 kinds of antibiotics were tested. The CS-PCR method was used to detect the existence of class 1 integron.

Results: The drug resistance of *A. baumannii* to cephalosporins increased significantly (54% up to 66%), and the resistance to PIP, TZP, SXT, SAM also have an upward trend, but the drug resistance to aminoglycosides decreased (60% down to 48%). And that was found 61.8% of these isolates carried the class 1 integron, and the cassette arrays they carried were only in 4 different sizes: 3.0 kb, 2.5 kb, 1.5 kb and 1.0 kb, among them the isolates carrying 2.5 kb cassette array were at the highest percentage, 87.3%. This study also showed that *A. baumannii* isolates carrying integron were more resistant to various antibiotics tested than non-integron-carrying isolates.

Conclusions: The widespread occurrence of 2.5 kb cassette array in *A. baumannii* isolates from Show Chwan Memorial Hospital was rarely reported in other countries. It is speculating that this phenomenon may be linked to the preference of hospital to certain particular antibiotics, so that the *A. baumannii* strains carrying 2.5-kb cassette array became dominant under antibiotic selection pressure.