susceptibility for four *K. pneumoniae*, their RAPD patterns were different. Although the outbreak showed no sign of cross-transmission, the infection control procedures were still important and needed to be followed.

## PS 1-099

### INVESTIGATE AN OUTBREAK OF *PROVIDENCIA STUARTII* INFECTIONS AT A NURSING HOME

Yi-Chu Lo, Chin-Lu Chang. *Committee of Infection Control, Tainan Municipal Hospital, Tainan, Taiwan*

**Purpose**: At a regional hospital in northern Taiwan, on 19 March 2013, a strain of imipenem-intermediate *Providencia stuartii* (P1) was isolated from pus of a patient came from a nursing home. On 12 May and 18 June 2014, three strains of imipenem-intermediate *P. stuartii* (P2, P3, and P4) were also isolated from urine and blood of two different patients came from the nursing home. P3 and P4 were isolated from urine and blood, respectively, of the same patient. Hence, this study was conducted to investigate an outbreak of *P. stuartii* infections.
**Methods**: Pulsed-field gel electrophoresis (PFGE) was used for bacterial typing. PFGE patterns were interpreted as same (no band difference), similar ($\leqq$3-band differences), or different ($\geqq$4-band differences) strain.
**Results**: PFGE patterns revealed P1 and P3/P4 were the similar strain, those were different from P2. P3 and P4 were the same strain.
**Conclusions**: As a result of this study, PFGE confirmed that this was a true outbreak of imipenem-intermediate *P. stuartii* infections at a nursing home. Although monitoring antibiotic-resistant organisms and intervention of infection control measures are one of important measures to reduce antibiotic-resistant organisms, we suggest those should be performed not only in hospitals but also in long-term care facilities in order to get better effect.

## PS 1-100

### CLINICAL OUTCOMES OF PATIENTS WITH *KLEBSIELLA PNEUMONIAE* OUTBREAK ISOLATES HARBORING A NOVEL KPC-17 VARIANT IN SOUTHERN TAIWAN

Wen-Liang Yu [a], Mei-Feng Lee [b], Yin-Ching Chuang [b,c]. [a]*Department of Intensive Care Medicine, Chi-Mei Medical Center, Tainan, Taiwan;* [b]*Department of Medical research, Chi-Mei Medical Center, Tainan, Taiwan;* [c]*Department of Medicine, Chi Mei Medical Center-Liou Ying, Tainan, Taiwan*

**Purpose**: In 2014, an outbreak of $bla_{KPC-17}$-containing *K. pneumoniae* (KPC-17-KP) occurred in a regional hospital in southern Taiwan. Until July 31, a total of 39 KPC-17-KP isolates were recovered, causing 33.3% mortality rate. We aimed to describe the clinical characteristics and outcome of these episodes involving KPC-17-KP isolation.
**Methods**: We retrospectively reviewed the demographic data (age, sex, and nursing-home resident), source of infection, days of hospital stay before onset of acquiring KPC-17-KP, previous carriage of isolates with extended-spectrum $\beta$-lactamase (ESBL) or AmpC phenotype within 3 months, recent hospitalization with 3 months, specific antibiotic therapy, in-hospital death and days of outcome from acquiring KPC-17-KP.
**Results**: There were 17 women, 22 men, age (mean, 82 years; range, 47$-$102), 23 (60%) chronic nursing-home residents, 23 nosocomial isolates after a mean hospital stay of 12 days (range, 2$-$47), 14 nursing-home acquired isolates and 2 community-acquired isolates. Recent hospitalization or previous carriage of ESBL/AmpC isolates within 3 months occurred in 24 (61.5%) patients. Among 3 blood isolates, 1 each was primary, from pneumonia and from urinary tract infection (UTI), resulting in 2 deaths (66.7%). Among 17 sputum isolates, 8 were from pneumonia (9 colonization), resulting in 7 deaths (41.2%). Among 19 urine isolates, 15 were from UTI (4 colonization), resulting in 4 deaths (21.1%). Effective colistin-based antibiotic therapy was given to only 6 episodes (15.4%) with 3 survivals. 13 patients died in hospital after a mean of 12 hospital days (range, 1$-$24) from onset of acquiring KPC-17-KP.
**Conclusions**: The KPC-17-KP caused 26 (66.7%) significant infections and 13 deaths (33.3%). Mortality was not significantly related to effective colistin-based therapy ($p = 0.38$).

## PS 1-101

### INVESTIGATION OF UPPER RESPIRATORY TRACT INFECTION OUTBREAK IN AN ACUTE PSYCHIATRY WARD OF A MEDICAL CENTER

Yu-Mai Hsu [a], Li-Hsiang Su [a], Jein-Wei Liu [a,b], Yi-Chuan Huang [a,c]. [a]*Committee of Hospital Infection Control, Taiwan;* [b]*Division of Infectious Diseases, Department of Internal Medicine, Taiwan;* [c]*Division of Infectious Diseases, Department of Pediatrics, Chang Gung Memorial Hospital-Kaohsiung Medical Center, Kaohsiung, Taiwan*

**Purpose**: Self care of psychiatric patients was poorer than the general people. Contagious infections (like flu) once happened, it was likely to cause cluster infection. Apart from the patients in the hospital, the staffs may also be sources of infection. Eleven staff members and 12 patients had upper respiratory tract infection symptoms in acute psychiatric wards from February 22 to March 22 in 2014. Person, time and place related investigations were held to clarify the source of infection as soon as possible and avoid the epidemic spread.
**Methods**: 11 staffs and 12 patients started to appear symptoms of fever, cough and sore throat. We suspected flu or *Mycoplasma* infection, so specimens were collected for examination. Infection control measures included: 1. Keep droplet precautions and restrict activity areas of patients. 2. Stop new patient admission. 3. Ask healthcare personnel to wear surgical mask and wash their hands. 4. Enhanced environmental disinfection. 5. Monitor the health status of patients, visitors and staffs.
**Results**: Total 15 specimens were examined. One staff member and one patient were positive for influenza A antigen, and 5 patients had high titer values of *Mycoplasma* IgG, and one patient had low positive titer of *Mycoplasma* IgM. We concluded the outbreak was flu A, but the possibility of *Mycoplasma* infection could not be ruled out.
**Conclusions**: The causes of this cluster infection included staff member did not inform fever immediately, and lack of timely intervention measures. Though we had body temperature monitoring system in our hospital and the ward unit also had standard measures of unusual infections. Neglect to inform early to lead to spread of the infectious disease. Health monitoring of implementation and management measures were needed. Once infection occurred, early detection and notification, identifying the pathogen and effective isolation should be done to prevent cluster infections.

## PS 1-102

### AN OUTBREAK OF *CHRYSEOBACTERIUM INDOLOGENES* BACTEREMIA: PSEUDOBACTEREMIA OF UNRECOGNIZED SOURCES

Chun-Wei Chiu [a,b], Yuan-Pin Hung [a,b,c], Hsiao-Ju Lin [a,b,c], Wen-Chien Ko [b]. [a]*Department of Internal Medicine, Tainan hospital, Ministry of Health and Welfare, Tainan, Taiwan;* [b]*Department of Internal Medicine, National Cheng Kung University Hospital, Tainan, Taiwan;* [c]*Graduate Institute of Clinical Medicine, National Health Research Institutes, Tainan, Taiwan*

**Purpose**: Some of the bacteria from blood culture might be due to contamination but others were true infection. The aim of our study is to investigate the distribution and clinical implication of blood-stream infection.
**Methods**: Bacteria yielded from blood culture in a district hospital between February 2013 and November 2014 was enrolled. If the same pathogen yielded from the blood of the same patient repeatedly, then only the first bacteria from blood culture was enrolled.
**Results**: Total 4319 pathogens from blood culture were enrolled as Figure1. The number of aerobic gram-positive cocci was 2169 (50.2%), with most of them was *Staphylococcus epidermidis* (n = 1395), followed by *Staphylococcus aureus* (n = 388) and *Enterococcus* (n = 226). The number of aerobic gram-negative bacilli was 1705 (39.5%) with 1083 was glucose-fermenting and 621 was glucose-non-fermenting. Most of the glucose-fermenting GNB was *Escherichia coli* (n = 577), *Klebsiella pneumoniae* (n = 250) and *Proteus mirabilis* (n = 54). Most of the glucose-non-fermenting GNB was *Chryseobacterium indologenes* (n = 105), *Acinetobacter baumannii* (n = 95) and *Pseudomonas aeruginosa* (n = 82). The number of fungus from blood culture was 173 with most of them was *Candida albicans* (n = 89), *Candida glabrata* (n = 37) and *Candida tropicalis* (n = 28). Because of unusual number of *Chryseobacterium* from the blood culture result, we did serial of