highly active antiretroviral therapy (HAART) initiation. To evaluate TB risk among HIV infected contacts is needed for countries with moderate TB incidence for future expansion of LTBI treatment in TB control program.

Methods: We conducted a cohort study using contacts of active TB patients from Taiwan TB registry during 2008–2012. All contacts were followed till December 31, 2013 for developing active TB. We performed cross-link with the contacts and both the nationwide HIV surveillance system and national health insurance (NHI) claims database for other medical condition as risk factors of TB. We used Cox proportional hazard model to estimate the hazard ratio (HR) and 95% confidence interval (CI) for the association of TB risk and HIV status among contacts.

Results: A total of 2328 (0.51%) active TB cases among 456,813 contacts were found in our study. The overall incidence of contacts to develop active infection (aHR: 2.89, 95% CI: 1.44–5.81) was 162.76/100,000 person-year after the mean follow-up duration of 3.1 years. The TB incidence among HIV infected contacts was 574.8 (266.9–1091.0)/100,000, which is 3.54 (1.77–7.09) times of the risk among non-HIV infected contacts. After adjusting potential confounders, HIV co-infection (HR: 2.89, 95% CI: 1.44–5.81) was independently associated with active TB. Compared with non-HAART users, contacts receiving HAART had lower risk to develop active TB but not statistically significant (p = 0.512, log-rank test).

Conclusion: Contacts with HIV co-infection whether using HAART or not was needed to be prioritized for contacts investigation, LTBI evaluation and treatment.

CESAREAN SECTION SURGICAL SITE INFECTION CAUSED BY MYCOBACTERIUM MASSILIENSE

Hsiao-Chi Chang 1, Ting-Shu Wu 1,2,*, Ting-Ying Chung 1, Chun-Sui Lin 1, Mao-Cheng Ge 1,3, 1Infection Control Committee, CGMH; 2Division of Infectious Diseases, CGMH; 3Department of Laboratory Medicine, CGMH

Purpose: From August 1, 2012 to October 31, 2012, three patients whose C-section surgical sites infected by Mycobacterium massiliense were reported. We began an environmental surveillance and investigated the infection focus for stopping further diseases clustering.

Materials: Our team of PCI investigated the whole process of preparedness and disinfection of C-section. Environmental surveillance was performed by IPCs. Further molecular epidemiological tool such as PFGE will be applied for the investigation of clonality.

Results: No M. massiliense was cultivated from the environmental specimens during this surveillance. After molecular analysis by PFGE, these 3 clinical isolates were identified as the same clonality (Figure). It means that these strains perhaps came from a common source.

Conclusions: A single clonality of these three isolates represented a probable common infection source. After implementation of measures of PCI, these medical materials became single-used. Until August 31, 2014, there were no more new NTM related C-section surgical site infection.

Figure PFGE of three Mycobacterium massiliense isolates.

FIRST REPORT OF ONE NEGLECTED HYPERVIRULENT (HYPERMUCOVISCOUS) AND PAN-SUSCEPTIBLE KLEBSIELLA PNEUMONIAE ST86 STRAIN CAUSING FATAL INFECTIONS IN CHINA

Yibo Zhang 1, Yongzhang Zhu 1, Cenrong Mi 1, Wenhui Li 1, Qun Wang 1, Dake Shi 1, Yuxing Ni 1, 1Department of Hospital Infection Control, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai, 200025, China; 2Department of Immunology and Microbiology, Institutes of Medical Sciences, Shanghai Jiao Tong University School of Medicine, Shanghai, 200025, China

Purpose: In order to identified a hypervirulent (hypermucoviscous) and pan-susceptible K. pneumoniae ST86 strain of serotype K2, responsible for two lethal bacteremia cases in a university teaching hospital in China.

Methods: We cultured and isolated K. pneumoniae from blood and/or sputum samples from the 2 patients, which were labeled as Kp523 and Kp562, respectively. A combination of Pulsed Field Gel Electrophoresis (PFGE) and Multilocus sequence typing (MLST) methods was used to analyze and compare molecular genetic characteristics of the two isolates. PCR was performed to determine the presence of the specific wzc gene for capsule serovar K1, K2, rpmA and mpa.

Results: MLST typing revealed that the two strains belonged to same ST86. PFGE typing analysis further showed that the two isolates displayed the same PFGE profiles. We found that the two string test positive isolates were also rpmA positive but mpa negative using specific PCR primers targeting rpmA and mpa.

Conclusions: For the first time, we reported a distinct hypervirulent and pan-susceptible K. pneumoniae serovar K2 ST86 strain, responsible for fatal infections in a Chinese university teaching hospital.

Figure Characteristics identification of KPS23 and KPS62.

RESEARCH IN THE VIRULENCE OF CANDIDA

Shuxian Chen 1, Huiling Chen 2, Yaping Ahu 1, 1Dept. of Infection Control, Guangzhou First People’s Hospital, Guangzhou, 510180; 2Dept. of Clinical Laboratory, Guangzhou First People’s Hospital, Guangzhou, 510180

Purpose: Detecting the virulence’s level of lecithinase and hemolysis in Candida, insight the correlative factors about the virulence of Candida.
Methods: During March, 2010 to June, 2013, 98 specimens were collected from patients with Candida infection. We detected the virulence of Candida by lecithinase test and hemolysis test. At the same time, the distribution characteristics of different ages were analyzed among the patients.

Results: For the virulence, there were no difference between Candida albicans and other Candidas (p > 0.05). The virulence of Candida albicans in deep infection were stronger than others in superficial infection(p < 0.01).

Conclusions: In the infection status, different strains of candida have the same virulence’s level of lecithinase and hemolysis. The virulence of Candida albicans relates to the infection site. The lecithinase test and hemolysis test may be regarded as the evaluation index for testing the virulence of Candida.

ASPERGILLUS SPP. IN ICUS: SPECTRUM OF INFECTIOUS WITH ANTIFUNGAL SUSCEPTIBILITY PATTERNS OF CLINICAL AND ENVIRONMENTAL ISOLATES

Yubisha Dabas 1, Immaculata Xess. Department of Microbiology, All India Institute of Medical Sciences, New Delhi, India

Purpose: In this prospective study, we noted spectrum of infections with Aspergillus spp. in ICU along with isolation of any environmental isolates occurring in a Northern India tertiary care hospital during two years (2011-2013) with antifungal susceptibility profiles of all isolates.

Methods: Phenotypic identification was done following standard mycological procedures. Air sampling was done to collect environmental Aspergillus spp. isolates from the ICUs. Antifungal susceptibility patterns to polyene, azole and echinocandin group of drugs were tested by CLSI M38-A2 guidelines and MIC range (g/ml) of the MICs were recorded. 30 Aspergillus fumigatus, 19 Aspergillus flavus and 02 Aspergillus nidulans.

Figure 1: MIC range (μg/ml) of the Aspergillus spp. ICU clinical isolates. (*zone diameter in mm)

There were 08 environmental isolates obtained from the ICUs, 04 Aspergillus fumigatus and 02 Aspergillus flavus and Aspergillus niger each. MICs were lower for environmental isolates except one isolate of Aspergillus flavus to caspofungin and itraconazole. Antifungal susceptibility testing revealed that voriconazole and posaconazole were sensitive to all the isolates suggesting these can be included in the pre-emptive treatment of patients in ICUs.

TOLL-LIKE RECEPTOR POLYMORPHISMS AS RISK FACTOR FOR CLOSTRIDIUM DIFFICILE COLONIZATION AND INFECTION

Yuan-Pin Hung 1,2,3, Hsiao-Ju Lin 1,3,4, Pei-Jane Tsai 1,2,3,4,5, Wen-Chien Ko 1,2,3,4,5,  
1Department of Internal Medicine, Tainan hospital, Ministry of Health and Welfare, Tainan, Taiwan; 2Department of Internal Medicine, National Cheng Kung University Hospital, Tainan, Taiwan; 3Graduate Institute of Clinical Medicine, National Health Research Institutes, Tainan, Taiwan; 4Department of Medical Laboratory Science and Biotechnology, National Cheng Kung University, Medical College, Tainan, Taiwan

Purpose: Patients with TLR4 polymorphisms were more likely to have intestinal infections due to gram-negative organisms. This study is to investigate the impact of toll-like receptor (TLR) polymorphism on Clostridium difficile colonization and infection.

Methods: Adults admitted to medical wards in a district hospital between January 2011 and January 2013 were enrolled, and those with a history of coloectomy, C. difficile fecal colonization or infection or receipt of either metronidazole or oral vancomycin within 3 months, were excluded. Stools collected within 48 hours after admission and every week during hospitalization were cultured for C. difficile.

Results: Among the 445 enrolled patients, 92 (20.7%) developed toxic C. difficile colonization (tCDc) and 21 (4.7) developed C. difficile associated diarrhea (CDAD). The mortality rate was 13.7 %. There was no difference in age, gender, receipt of antibiotics or proton-pump inhibitor or underlying disease (including diabetes mellitus, hypertension, old stroke, chronic kidney disease or having malignancy) among patients with different TLR4 rs1927914 polymorphism (GG, GA or AA type). We found TLR4 rs1927914 polymorphism A-carrier (including GA and AA) was associated with developing CDAD compared to GG type (4.9 and 5.2 vs 2.9 %, P = 0.02) but not correlated with tCDc or mortality. Other TLR4 polymorphism (rs10983755) and three TLR2 SNPs (rs1898830, rs3804099, and rs7656411) were also analyzed but not related to CDAD or tCDc.

Conclusions: The incidence of CDAD is highest in patients with the TLR4 rs1927914 polymorphism GA and AA genotype.

MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME-OF-FLIGHT MASS SPECTROMETRY FOR THE IDENTIFICATION OF BETA-HEMOLYTIC STREPTOCOCCI

Chunmei Zhou 1, Lili Tao 1, Bijie Hu 1, Jian Ma 1, Xiangru Ye 5, Shenglei Huang 1, Yan Ma 1, Yuzhang Shan 1, 2Department of Clinical microbiology laboratory, Zhongshan Hospital, Fudan University; 3Department of Respiratory Medicine, Huadong Hospital, Fudan University; 4Department of Hospital Infection Control and management, Zhongshan Hospital, Fudan University; 5Department of Respiratory Medicine, Yingzhou Hospital, Ningbo University; 6Department of Respiratory Medicine, Zhongshan Hospital, Fudan University

Purpose: To evaluate the application of two mostly utilized commercial platforms of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) for the identification of clinical isolated beta-hemolytic streptococci (BHS).

Methods: Clinical Isolated BHS were identified by BD Phoenix SMIC ID streptococcal panels, VITEK MS system and Bruker MALDI Biotyper system, respectively. In the case of discordant results, 16sRNA sequencing of the strains was performed as reference ID.

Results: A total of 96 isolates of beta-haemolytic streptococci was analyzed. 36 isolates were re-tested a second time to resolve no identification results using the BD Phoenix system. Likewise, 4 isolates had to be re-run on the Bruker system. Identification results were provided for all 96 isolates on the first test run using the VITEK MS system. The BD Phoenix