need to be serotyped to decide on the vaccine.

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SCC*mec* type IX in a community-acquired methicillin-resistant *Staphylococcus aureus* isolate: first report in a patient from Thailand

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is mostly associated with hospital, whereas community-acquired MRSA (CA-MRSA) infections in Thailand have been uncommon. The present study aimed to investigate 14 MRSA strains isolated from outpatients of a university hospital in Thailand.

Methods: Fourteen MRSA isolates were collected between September 2005 and March 2006 from outpatients of a university hospital inThailand. Minimum inhibitory concentrations (MICs) of six antimicrobial agents: vancomycin, cefazolin, oxacillin, cefoxitin, tetracycline, erythromycin and ofloxacin were determined using an agar dilution method. Genotypic studies such as SCC*mec* type, coagulase typ, *agr* type, *spa* type, multilocus sequence type (MLST) were performed using PCR and subsequent nucleotide sequences. Pulsed-field gel electrophoresis (PFGE) of *SmaI*-digested chromosomal DNA was also performed.

Results: All 14 MRSA were multidrug-resistant with high MICs of cefazolin, oxacillin, cefoxitin, tetracycline and erythromycin (32->64 μg/ml), however all isolates were susceptible to vancomycin (MIC 1-2 μg/ml). Of the 14 isolates, 13 carried type III SCC*mec* and belonged to ST239, coagulase type IV, *agr* I and *spa* type-t037 but one isolate was t233. The remaining isolate (strain JCSC6690) carried a new SCC*mec* element, class C2 *mec* gene complex with *ccrA1B1*, type XIc coagulase, *agr* II, *spa* type-t337 and ST9. PFGE of the 14 isolates showed that 12 isolates gave similar bands pattern to a hospital acquired-MRSA (HA-MRSA) from the same hospital. The other isolates with *spa* type t337 and t233 showed a unique DNA profile. The Panton-Valentine Leukocidin gene was not found in these isolates. The strain JCSC6690 was isolated in March of 2006, from a 2-year-old boy underlined with atopic dermatitis, attended the hospital because of suffering from chronic impetigo at left foot. The patient achieved good recovery after receiving cefaclor. He had never been admitted in a hospital during the former year. Nucleotide sequencing of the 57 kb region at the downstream of *orfX* revealed a novel SCC*mec* carrying type I *ccr* gene complex and classC2 *mec* gene complex.

which carried class C2 *mec* gene complex and *ccrA1B1*.

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Differential host gene expression upon exposure to live *Burkholderia cepacia* and its secretory proteins

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Background: *Burkholderia cepacia* causes serious respiratory infections in immunocompromised individuals and patients with cystic fibrosis. The bacterium is known to produce virulence factors such as secretory enzymes which damage host membrane to promote invasion as well as unique pilus which is involved in adhesion and colonisation of the respiratory tract. Understanding this complex cross-talk between the host and pathogen is essential to improve understanding of an infectious disease and to identify host-defense strategies including the underlying regulatory mechanisms. The aim of this study was to investigate the transcriptional changes in the host upon exposure to live *B. cepacia* and its secretory proteins.

Methods: Comparison of host response to live *B. cepacia* (mid-log phase) and its secretory proteins (mid-log and early stationary phases) was performed using the Illumina HumanRef-8 microarray platform. The raw microarray data were analyzed and the web-based softwares GOTerm Finder (http://go.princeton.edu/cgi-bin/GOTermFinder) and GeneTrail (http://genetrail.bioinf.uni-sb.de/) were used to analyse significant pathways. The microarray data were validated using quantitative real-time polymerase chain reaction.

Results: Interaction of the human epithelial cells, A549, with live *B. cepacia* or the secretory proteins was found to differentially regulate genes that are related to metabolism, cell cycle, apoptosis and inflammatory. The host cell cycle and metabolic pathways, particularly glycolysis/glycogenesis and fatty acid metabolism were up-regulated transcriptionally. The host immune response was also found to be manipulated through the suppression of pro-inflammatory cytokines production. Additionally, the microarray analysis indicated that the host cells inhibit the apoptotic pathway during infection. Alteration of these pathways might explain the need for the host cells to survive and proliferate to sustain cell injuries caused by the secretory proteins and/or to allow prolonged survival of *B. cepacia* in the host cells. These pathogens have also been shown to modulate the epithelial bactericidal response in favour of its intracellular survival and persistence in the human host.

Conclusion: The differential gene expression profile of A549 cells towards *B. cepacia* infections has provided preliminary insight into the mechanisms of pathogenesis of *B. cepacia* and its secretory proteins. The microarray results permit a rational design for

future functional experiments to further characterise and elucidate *B. cepacia* infection.

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Study of detection *Vibrio Cholerae* O1 from Karoon river waters and their role in the public health

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Background: The watershed of Dez and Karoon rivers located in middle Zagrous mountain with area about 68481-km, thus watershed is a part of Persian gulf watershed. *Cholera*, an acute intestinal infection caused by the bacterium *Vibrio cholerae*, is a historically feared epidemic diarrheal disease that remains a major public health problem in many parts of Africa, Asia, and Latin America. *Vibrio cholerae* O1 exists as two major serotypes, Inaba and Ogawa, a member of the family Vibrionaceae. *Vibrio cholerae* is transmitted through fresh water contaminated with fecal matter. Foodborne infections have been traced to raw or inadequately cooked shellfish and other seafood. The target of study the segregate *Vibrio cholerae* 01 (*Vibrionaceae*) in the Karun Ahvaz river.

Methods: In four stages (April, May, June and July 2010), a total 100 samples of water from Karoon River Ahvaz were collected. During the study period the recorded river temperature was about 25-28(C and pH ranged from 7 to 8. Swabs were cultured onto thiosulphate citrate bile sucrose and MacConkey, and morphological colonies compatible with *Vibrio* were characterized by oxidase test and agglutinated with antiserum (Difco, Detroit, MI, USA) for serotype determination. Also *V. cholerae* biochemical tests with API 20E (BioMerieux, Marcy-l'Etoile, France).

Results: From 100 samples of water Karoon River in Ahvaz, Iran, 8 (8%) sample were positive for *Vibrio cholerae* strains. The isolated strains from water Karoon River in Ahvaz, Iran, were Vibrio *cholerae* O1 (inaba).

Conclusion: The priorities for cholera control remain public health interventions through improved water and sanitation, improved surveillance and access to health care facilities, and further development of appropriate vaccines.

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Safety of polymyxin-B- based hemoperfusion in kidney and liver transplant recipients

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Background: Infection represents one of the primary barriers to successful organ transplantation and an early diagnosis represent the goal of therapy. Our principal end point was to use a new assay Test EAA which has been developed to rapidly detect endotoxin acivity. Furthermore we aim to prove the validity and safety of removal of endotoxins using Polymyxin-B based hemoperfusion (PMX-DHP).

Methods: The criteria for inclusion in the study were the following findings: infection was suspected when patients had at least 2 of the 4 criteria of systemic inflammatory response syndrome (SIRS). Following these criteria, the Test EAA was performed on 71 patients (29 liver transplant and 42 kidney transplant). Twenty eight patients(39,5%) with EA>0.60 were enrolled in this study and received treatment to remove endotoxins (PMX-DHP). Each treatment was performed for two hours with a blood flow rate of 100mL/min. All the patients were treated with PMX-DHP until an EA<0.4 was found.

Results: No relevant adverse events were observed during the 72 treatments performed.Before performing PMX-DHP treatments, the median EA was 0.81(range 0.62-1.25) and 0.73(range 0.61-0.98) in liver and kidney transplant patients respectively. In liver transplant patients two PMX-DHP treatments were performed on 7 patients [median EA =0.69(0.62-0.76)], three treatments on 4 patients[median EA =0.84(0.77-0.91)] and four treatment on 3 patients [median EA =1.11(0.95-1.25)]. At the end of the endotoxin removal therapy, the median EA level was 0.33[0.22-0.4].The stabilization of hemodynamic and inflammatory frameworks were observed after the PMX-DHP.At 30 days of follow up all patients were alive with a good graft function and low level of endotoxin activity.

Conclusion: Given the progress achieved and considering the particular difficulties in the diagnosis of transplant patients, we think that might be useful to determine the endotoxin activity routinely in these patients. Accordingly, larger multicenter clinical trials will be necessary to accurately assess the benefits of EA essay plus DHP-PMX for transplant patients with endotoxemia and suspect of infection.

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