

PP-004 Detection of resistance to mupirocin in *Staphylococcus aureus* strains isolated from patients in 4 university hospitals in Tehran, Iran, by PCR

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Background: Mupirocin has used to treat staphylococcal skin infections as well as to eliminate nasal carriage of *Staphylococcus aureus*. Mupirocin resistant *S. aureus* strains are seen worldwide but there is no report from Iran. This study was performed to investigate the presence of mupirocin resistant strains in *S. aureus* isolated from patients in Tehran.

Methods: Presence of *mupA* gene, responsible for mupirocin resistance, was determined by PCR method. Disk diffusion and E-test were also used for demonstrating mupirocin resistance. The susceptibility testing of *S. aureus* isolates were carried out by the disk diffusion method. Moreover, PCR method was used for detection of *mecA* gene, which conferring resistance to methicillin and other penicillinase resistant penicillins.

Result: Among 94 isolates of *S. aureus*, six strains were resistant to mupirocin; 5 low-level and 1 high-level resistance. From these 6 strains, *mupA* gene was shown in 5 strains. All mupirocin resistant strains were methicillin resistant by *mecA* gene PCR and disk diffusion test. Disk diffusion test had shown all mupirocin resistant strains were resistant to penicillin G, ampicillin, oxacillin, ciprofloxacin, tetracycline, trimethoprim-sulfamethoxazole, ceftioxin, clindamycin and erythromycin but all strains were shown susceptibility to vancomycin.

Conclusion: This study is the first report about mupirocin resistance in *S. aureus* strains isolated from patients in Tehran and calls further studies for determination the incidence of this resistance. Also, a combination of PCR and phenotypic methods was recommended for a reliable identification of mupirocin resistance in *S. aureus* strains.

PP-005 Research on medical sensitivity of Chinese herbs of *Tujia* minority against ureaplasma urealyticum *in vitro*

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Objective: To investigate the sensitivity of 8 Chinese herbs of *Tujia* minority against Uu.

Methods: Minimal inhibitory concentrations (MIC) and minimal bactericidal concentration (MBC) of 8 Chinese herbs were determined by geometric-progression diluting method and solid cultural method *in vitro*, respectively.

Results: 8 tested Chinese herbs had bacteriostatic and bactericidal activities against Uu at different extent, among which *Rhizoma bletillae* were highly active against Uu. Its MIC and MBC were both 7.8l g/L. However, *Malus hapehensis* has no effect on Uu.

Conclusion: *Rhizoma bletillae* had bacteriostatic effect on Uu *in vitro*, further studies were needed to investigate its effects and the mechanisms on Uu.

PP-006 Analyse of drug-resistance about clinical isolated *Pseudomonas aeruginosa*

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Objective: To find out the distribution and drug-resistance of *Pseudomonas aeruginosa* clinical isolates in our hospital from August 2005 to September 2007, in order to apply direction of reasonable usage of drug for clinician.

Methods: Identification of bacteria was done by ID 32 GN strip of

biomerieux sa 69280 Marcy-l'Etoile of France. Drug susceptibility to 15 antibiotics was detected by ATB-PSE-5 strip.

Results: The isolated rate of *Pseudomonas aeruginosa* in respiratory tract is 88.43%. More 30 percent of the isolates are resistant respectively to Ticarcillin, Ticarcillin- clavulanic acid, Piperacillin, Tobramycin, Ciprofloxacin, Ceftazidime. Drug-resistance to Gentamicin and Cefepime is highest, respectively 53.78% and 44.54%. The resistant rate to Imipenem and Meropenem is 24.37% and 23.53%. The strains are most sensitive to Amikacin and Piperacillin-, respectively 78.15% and 72.27%. The isolates are the most sensitive to polymyxin E. The rate is 96.64%. 19.33 percent of all isolates are multidrug resistant.

Conclusions: Most of the isolates are from respiratory tract. Clinician should strengthen nursing care and monitoring on respiratory tract infection. The situation of multidrug and resistance to Carbapenms is serious. Clinician should pay high attentions and combine reasonably two and more drugs according to sensitive test and practical situations.

Poster Presentation – Bacterial Infections

PP-007 Pathogen distribution and drug resistance analysis of inpatients' infection between 2007 and 2008 in infectious disease hospital

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Objective: To fully understand the distribution of pathogens very often seen in inpatients from infectious disease hospital and analysis of their antibiotic resistance.

Method: To analyze retrospectively distribution of 960 isolates and variance of their drug resistance from inpatients in our hospital between 2007 and 2008.

Results: Total 960 strains were found in different samples. Of the 960 isolates, 371 strains (38.6%) were Gram-positive cocci, 589 (61.4%) were Gram-negative bacilli, 77 (7.92%) were fungi. The positive rate of *Escherichia coli* was the highest followed by *Staphylococcus epidermidis* and *Enterococcus faecium*. 31.8% of all strains were from sputum, 23.7% from blood, 12.6% from ascites. The resistance of different strains to antibiotics used frequently in clinical settings is at different levels.

Conclusion: *Escherichia coli* is still a main cause in our inpatients with pneumonia. Increasing rate of fungi infection becomes a big concern.

PP-008 Evaluation of clinical, laboratory and therapeutic findings of brucellosis among children hospitalized at Ardabil's hospitals

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Objectives & background: Brucellosis is the common disease between human and animal and that is transmitted through contaminated animals. This study has been conducted to determine the clinical manifestation, laboratory findings and therapeutic approach of children afflicted by brucellosis, hospitalized at 2 hospitals (Aliasghar and Imam Khomaini) of Ardabil within 2000-2005.

Methods: This study is a retrospective one, based on existing data of 51 medical units, belonging to patients who were hospitalized within 2000-2005 at these two centers diagnosed as brucellosis patients.

Results: From all 51 patients 76.5% were male. Familial history of brucellosis was positive among 38% of patients. Precedence of non-pasteurized dairy consumption was seen among 62% of cases. 69% of patients were belonging to high risk families. Clinical man-

ifestations of disease were fever (84.2%), arthralgia (81.2%), perspiration (60.2%), lack of appetite (54%), Hepatomegaly (31%), splenomegaly (21%), and lymphadenopathy (18%). Laboratory findings were anemia (52.3%), leucopenia (41.2%), thrombocytopenia (4.5%), and leukocytosis (1.96%). Treatment in the majority of patients (76.2%) was Cotrimoxazole besides Rifampin or Gentamycin. The brucellosis was the cause of FUO in the 17.6% of cases.

Conclusion: According to the findings, it seems that among children with fever and Arthralgia and especially with precedence of non-pasteurized dairy consumption and being male, this is essential to evaluate brucellosis possibilities. On the other hand, it is advised to perform programs to inform members of high risk families about this disease.

PP-009 **Molecular epidemiology of community-acquired, methicillin-resistant *Staphylococcus aureus* infections in children in China**

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Background: Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has emerged worldwide since 1990s.

Methods: Ninety-nine MRSA isolates were analyzed by multilocus sequence typing (MLST), SCCmec typing and spa typing. Panton-Valentine Leukocin (PVL) gene was detected. Susceptibility tests were performed for twelve antimicrobial agents.

Result: Eleven sequence types (STs) were identified. The predominant SCCmec types were type IV (77.1%) and type V (22.9%). SCCmec type IVA, IVC, IVg were found. All strains were differentiated into twelve spa types, 57.6% (57/99) of MRSA isolates were found to carry the PVL gene. The prevalent strains were ST59-MRSA-IVA and ST59-MRSA-V. Four ST910 and ST338 isolates were found countrywide, ST1349 were found from healthy children. Multidrug resistance was observed.

Conclusion: ST59, ST910-MRSA-IV and ST910-MRSA-V were spread all of China, and ST338 was also found in south of China. Isolates from healthy Children had different genetic background.

PP-010 **Determination of prevalence antibiotic resistance of isolated bacteria from tracheal aspirated in intubated patients admitted to intensive care unit at Toohid hospital, Sanandaj in Iran**

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Background: Low respiratory tract infection is the first agent mortality in nosocomial infection, and among ICU patients are 5-10 time higher than other ward.

The aim of this study was determination of prevalence and antibiotic resistance of bacteria isolates from tracheal aspirated in intubated patients admitted in ICU ward

Material & methods: This is prospective descriptive study included 185 specimens of secretion respiratory tract admitted to ICU during a period of 13 month 2006/4/1 to 2007/5/1.

In order to isolation bacterial the specimens were cultured in enrichment and differential media. The data analyzed by means of SPPSS- win software.

Results: 112 (60.3%) of 185 specimens had culture positive. Prevalent microbial agent in this group were: Enterobacter 19.6%, *Pseudomonas* spp, 19.6%, *Serratia* 18.8%, *klebsiella* 15.2%, *E. coli* 10.7% and *staphylococcus* 4.5%. Isolated bacteria resistance to often antibiotics and highest resistant to amoxiciline. Prevalence of *Acinetobacter* with age over 40 year and sex (female) ($p < 0.05$) and also prevalence of enterobacter and *Serratia* with history of previous antibiotic use ($p = 0.2$, $p < 0.05$) has showed a signification statistically correlations.

Conclusion: This study shows that gram negative bacteria have

high prevalence in patients admitted to ICU. The increased of these species in most cases due to administration of inadequate and irrational antimicrobial therapy. To overcome this problem it needs to develop new antimicrobial and increasing compliance.

PP-011 **High level macrolide resistant *Streptococcus pyogenes* Isolated from Chinese children and the relationship with Tn6002**

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Background: The macrolide resistance rate in Chinese had been reported. This research was to investigate the high level macrolide resistant *Streptococcus pyogenes* in Chinese children. A total of 191 streptococcus pyogenes were contained.

Methods: Susceptibility to 11 antibiotics were detected, together with the Macrolide resistance phenotype of the strains. Macrolide resistance genes (*ermB*, *ermTR*, *mefA*), tetracycline resistance gene (*tetM*, *tetO*), *int*, *xis* of Tn916 family and also two special fragments of Tn6002 were detected by PCR and sequencing.

Result: Among the 191 isolates, 87.93% were resistant to telithromycin, 92.63% were resistant to tetracycline, none of the isolates were resistant to penicillin G, ceftazidime, levofloxacin and trimethoprim-sulfamethoxazole. And all of the isolates belong to the cMLS phenotype. 95.81% (183/191) of the 191 strains had the *ermB* gene, 4.19% (8/191) of the isolates contained the *ermTR* gene, *mefA* was not detected. Among the *ermB* positive strains, 92.35% (169/183) of them carried the *tetM* gene, 93.99% (172/183) was positive for the genes of *int* or *xis*. *ErmB*, *tetM*, *int*, *xis* positive profile account for 86.91% (166/191) of the 191 strains and all of them carried the special fragment of Tn600.

Conclusion: This study indicated that there may be a high prevalence of transposon Tn6002 carrying *ermB* gene among high level macrolide resistant *Streptococcus pyogenes* from Chinese children.

PP-012 **Novel blaCTX-M-79 gene from community isolates in association with ISEcp1 in Shenyang, China**

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Objectives: This study was conducted to analysis the ISEcp1 element in association with *blaCTX-M* genes in a community ESBL producing *E coli* isolates.

Methods: 19 *Escherichia coli* producing CTX-M-type β -lactamase were collected from five communities in elderly people in Shenyang, China. PCR amplification and direct sequencing was used to detect the insertion sequence ISEcp1 element in genetic environment *blaCTX-M* genes.

Results: ISEcp1 element was associated with several *blaCTX-M* types, such as CTX-M-14, CTX-M-24, CTX-M-22, and CTX-M-79. Sequence analysis revealed that all these ISEcp1-like DNA sequences contained the putative promoter region involved in the transcription of *bla* CTX-M genes. ISEcp1 insertion sequences have been observed 42-127 bp upstream of the ORFs encoding the CTX-M enzymes in all 19 strains. CTX-M-79 β -lactamase encoding gene was observed with different insertion site of ISEcp1 and variable sequences between the ISEcp1 and *blaCTX-M-79* gene. For one strain (T298) ISEcp1 element was disrupted by IS10.

Conclusions: This work confirmed the ISEcp1 elements were closely related to *blaCTX-M* genes in community isolates in Shenyang, China.