ies are required to elucidate the epidemiology of CA-MRSA and to improve strategies to control MRSA in both community and hospital settings.

doi:10.1016/j.ijid.2008.05.726

44.037

Activity of Fosfomycin on Clinical Isolates of MSSA and MRSA from Austria During 1994 to 2006


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The aim of the study was an evaluation of the activity of fosfomycin (F) against strains of methicillin-susceptible S. aureus (MSSA) and of methicillin-resistant S. aureus (MRSA) isolated from clinical material during 1994 to 2006 in Austria.

Material and Methods: 748 MSSA strains consecutively isolated from blood cultures in our laboratory during 1994 to 2004 and 655 MRSA strains isolated from various clinical materials all over Austria during 1994 to 2006 and collected in our laboratory were tested to F by an agar dilution method as recommended by CLSI. The media were supplemented with 25 mg/L Glucose 6 Phosphate. The breakpoints used for interpretation of F results were < 16 mg/L for susceptible, 32–64 mg/L for intermediate and > 128 mg/L for resistance. We determined the mecA and femA gene in all MRSA strains using a multiplex PCR. For subtyping we performed coagulase gene PCR with restriction digestion of PCR products with Alul, and we further analyzed the PFGE patterns.

Results: The % of strains susceptible to F maintained always above 90% without significant changes along the years for the MSSA isolated from blood culture in our laboratory. The % MRSA susceptible to F varied, from the least 51.2% in 1996 to the greatest 82.4% in 2005. The distribution of different ST (sequence type) changed along the years: 1998 to 2002 we found ST228: 52%; ST247: 21%, ST8:12% and ST36: 6% whereas in 2005-2006 we found a more diverse spectrum: ST228: 30%; ST8: 29%, ST22:15%, ST5:12%, ST30: 3%. The resistance to F of MRSA seemed to be associated more with ST228.

Conclusions: We conclude that F is most active against MSSA and exhibits also good activity against MRSA. Hence, F can be a valuable combination partner for the therapy of severe staphylococcal infections.

doi:10.1016/j.ijid.2008.05.727

44.038

Antibacterial and Synergistic Effects of Extracts of Chinese Traditional Herbs Against Staphylococcus Aureus

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Background: Resistance to conventional antibiotics has increased the need for novel agents with antibacterial activity. Herbs used in traditional Chinese medicine were tested for antibacterial properties both alone and in combination with antibiotics.

Method: Powdered herbs were diluted in Mueller-Hinton (MH) agar for determination of the MIC of the herb against strains of S. aureus. Strains included penicillin resistant, multi-drug resistant methicillin-sensitive, methicillin-resistant strains including all SCCmec cassette types, and vancomycin intermediate resistant (VISA) strains. In addition, herb-containing agar was used for disc diffusion sensitivity testing of a range of antibiotics. The zone size on the herb-containing agar was compared to that obtained on unsupplemented MH.

Results: Rhizoma coptidis at a concentration of 1% consistently inhibited the growth of all strains. Some strains of MRSA and VISA were inhibited by concentrations as low as 0.2%. Radix scutellariae inhibited growth of all strains at 0.8%. Results for Herba andrographitis and Cortex phellodendri varied greatly between strains. Combinations of Radix, Rhizoma or Cortex at concentrations of 0.1%, which was not itself inhibitory, with beta-lactam antibiotics did lead to increased zone sizes for penicillin, oxacillin, and cefoxin in penicillin-resistant strains, reversing resistance to penicillin to sensitivity in 3/6 strains tested. Methicillin resistance however was not reversed and there were only limited increases in penicillin and cefoxitin zones sizes in MRSA. Combination of the herbs with linezolid led to substantial increases in zone size (from 30 to 40 mm) in VISA strains.

Conclusion: At concentrations tested, the herbs appear to interfere with beta-lactamase-associated resistance and to enhance linezolid susceptibility of VISA. VISA strains were inhibited by very low concentrations of Radix and Rhizoma. These findings suggest that use of these herbs in combination with conventional antibiotics may reverse penicillin resistance and enhance effects of other antibiotics especially with respect to VISA.

doi:10.1016/j.ijid.2008.05.728

44.039


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Background: Staphylococcus aureus is a major pathogen within hospital and in the community and causes a wide range of disease. MRSA infection has recently become a serious problem in anti-microbial chemotherapy. The aim of the study was to detect and analyze the antibiotic diversity and isolation of methicillin resistance gene (mecA) of S.
Evaluation of Tigecycline and Other Antimicrobials in Latin America Against Multi-drug Resistant (MDR) Staphylococcus aureus

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Objectives: The emergence of MDR S. aureus in Latin America has highlighted the need for surveillance and the continued documentation of the efficacy of existing and new antimicrobials. The Tigecycline Evaluation Surveillance Trial (T.E.S.T.) evaluated the activity of tigecycline and comparators to MDR S. aureus (including MR+MS strains) isolated in Latin America.

Methods: 10 hospital sites in 6 countries, between 2004 and 2007, collected 367 clinically significant S. aureus. MICs were determined at each site using broth microdilution panels and results interpreted as specified by CLSI at each site.

Results: MIC90 of tigecycline and comparators to MDR groups 0–5 are shown in the table below.

Conclusions: Tigecycline in comparison to 10 relevant comparators exhibited the lowest MIC90 to S. aureus isolated in Latin America irrespective of MDR phenotype and multiple drug class resistance.

doi:10.1016/j.ijid.2008.05.729

44.040
Antibiotic Susceptibility Patterns and Detection of Coa and MecA Genes in the Iranian Isolates of Staphylococcus aureus

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Background: Nosocomial infections caused by Staphylococcus aureus especially methicillin-resistant Staphylococcus aureus (MRSA) belong to the most important multiresistant pathogens worldwide. Therefore, genotypic surveillance of these strains in patients with staphylococcal infections is crucial in control of Nosocomial Infections. The aim of this study was determination of antibiotic susceptibility patterns and detection of coa and mecA genes of the Iranian isolates of Staphylococcus aureus.

Methods: In this survey, 65 isolates of Staphylococcus aureus were collected from Tehran University hospitals. Antibiotic susceptibility patterns of the all isolates were determined to the 12 antibiotics (methicillin, oxacillin, vancomycin, chloramphenicol, rifampin, tobramycin, gentamicin, ceftriaxone, ciprofloxacin, tetracycline, cotrimoxazole and clindamycin) by the standard disk-diffusion method. According to the genome sequence of the standard strains of S. aureus, col and 8325/4, two pairs of primers were designed for coa and mecA genes.

Results: Thirty three isolates (50.8%) were resistant to methicillin and oxacillin. All the isolates were susceptible to vancomycin, and chloramphenicol. Sixty isolates (92.3%) were sensitive to rifampin. The studied isolates showed different susceptibility patterns to the other antibiotics. The PCR results showed all the isolates (100%) were positive for coa gene. Seven patterns (C1–C7) of coa gene were detected with C1 being the most prevalent; 38 (58.46%), Ten (15.38%), 6(9.23%), 3 (4.61%), 3 (4.61%), 3 (4.61%), and 2 (3.1%) isolates displayed patterns C2, C3, C4, C5, C6 and C7 respectively. The mecA gene was detected in all the methicillin resistant isolates.

Conclusion: The results of the present study showed high rate of methicillin resistance among Iranian isolates of S. aureus. The examined isolates showed high variation of the coa gene according to the PCR results. Therefore, continuous surveillance on resistance patterns and characterization of S. aureus is highly recommended to control the community and hospital acquired infections caused by this bacterium.

doi:10.1016/j.ijid.2008.05.731