P2698 Molecular and phenotypic characteristics of 543 consecutive Staphylococcus aureus clinical isolates from one university-affiliated hospital in central Taiwan

Wei-Yao Wang*1, Shin-Ming Tsao2

1 Feng-Yuan Hospital Ministry Of Health And Welfare, Taichung, Taiwan, 2 Chung Shan Medical University Hospital, Taichung, Taiwan

Background: Staphylococcus aureus, especially methicillin-resistant S. aureus (MRSA), frequently causes severe healthcare- and community-associated infections worldwide. Varied associations between molecular types and phenotypes have been reported. The goals were to demonstrate and to correlate the molecular types and phenotypes among consecutive S. aureus isolates from one university-affiliated hospital in central Taiwan.

Materials/methods: Consecutive S. aureus clinical isolates were collected and identified initially by BD Phoenix system from April, 2016 to December 2017. MRSA were confirmed by meca gene existence and SCCmec types were determined by multiplex PCR. The phenotypes were manifested by minimal inhibitory concentration (MIC) against oxacillin (OX), cefoxitin (FOX), and vancomycin (VA) through agar dilution. Correlation between MRSA molecular types and median MICs were also analyzed by Fisher’s exact test.

Results: A total of 546 consecutive S. aureus isolates determined by Phoenix system were included, among them 3 were excluded by gram stain and standard biochemistry tests. There were 128 (23.7%) S. aureus isolated from sterile sties (mostly from blood), and 415 were isolated from non-sterile sites [249 (45.8%) from pus and 112 (20.6%) from sputum, respectively]. The median MICs for OX, FOX, and VA were > 8 (0.25 - > 8), 16 (0.5 - > 16), and 1 (0.25 – 4) μg/ml, respectively. The sensitivity/specificity for Phoenix system, OX agar dilution, and FOX agar dilution to identify meca+ MRSA were 89.5%/93.7%, 96.7%/92.4%, and 96.0%/98.7%, respectively. Among 543 S. aureus isolates, 464 (85.4%) meca+ MRSA were identified, which SCCmecII (21, 4.5%), SCCmecIII (118, 25.4%), SCCmecIV (205, 44.2%), SCCmecV (49, 10.6%), SCCmecV1 (70, 15.1%), and untypable (1, 0.2%) were determined. Nine (1.9%) isolates with OX-susceptible phenotypes (OX MIC ≤ 2 mg/L) was identified among 464 meca+ MRSA, and all of them belonged to molecularly community-associated MRSA (CA-MRSA) (p <0.01).

Conclusions: Agar dilution for OX and FOX had excellent sensitivity and specificity to identify meca+MRSA. Oxacillin-susceptible phenotype was associated with CA-MRSA (SCCmecIV, V, and V1).