

**P2698 Molecular and phenotypic characteristics of 543 consecutive *Staphylococcus aureus* clinical isolates from one university-affiliated hospital in central Taiwan**Wei-Yao Wang\*<sup>1</sup>, Shin-Ming Tsao<sup>2</sup><sup>1</sup> Feng-Yuan Hospital Ministry Of Health And Welfare, Taichung, Taiwan, <sup>2</sup> 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 sites (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%), *SCCmecV<sub>T</sub>* (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 *V<sub>T</sub>*).

