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MRSA - one health worldwide

Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* bloodstream isolates in Changhua, Taiwan, 2007-2013

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) has continuously been an important medical pathogen. The molecular epidemiology of MRSA offers essential information for infection control and management of diseases caused by this pathogen. The purpose of this study was to investigate the molecular characters of clinical bloodstream isolates and the epidemiological change from 2007 to 2013 of two regional hospitals in central Taiwan by a variety of molecular typing techniques.

Material/methods: A total of 409 consecutive non-duplicate *S. aureus* bloodstream isolates (203 isolates of hospital A and 206 of hospital B) were collected over a 7-year period from two regional hospitals in Changhua, Taiwan. All MRSA isolates were characterized by molecular typing targeting the staphylococcal chromosomal cassette (SCCmec) and protein A (*spa*) genes and antibiogram analysis. Detection of the *mecA* gene, Panton-Valentine leukocidin and *sasX* gene were performed. Multilocus sequence typing (ST) was carried out on 100 representative strains.

Results: The distribution of SCCmec types in this study was II (77, 18.8%), III (158, 38.6%), IV (84, 20.5%), V (24, 5.9%) and VT (45, 11%), respectively, and 33 different *spa* types were identified amongst these 409 clinical isolates. The most common 4 *spa* types in order were t037-III (142, 34.7%), t002- II (75, 18.3%), t437- IV or VT (73, 17.8%), and t1081- V (27, 6.6%). SCCmec VT and SCCmec III types respectively contained PVL and *sasX* genes with high frequency (82.2% and 96.2%, respectively). The most common sequence types for each SCCmec category were ST5-II (18%), ST239-III (32%) and ST59-VT (28%). In particular, a well-known livestock associated MRSA strain in Asia, ST9-UT-t2922 strain, was isolated from an elder man with septic arthritis and bacteremia. The annual MRSA isolation rate ranged from 54.3 to 75.7% of hospital A and 51 to 69% of hospital B during the study period. There was a significant decrease in trend for detecting MRSA in hospital B ($p = 0.031$) but not in hospital A ($p=0.34$) from 2010. In addition, the proportion of hospital associated and community associated MRSA (HA-MRSA vs CA-MRSA) was significantly different between these 2 hospitals (67.5% vs 37.5% for hospital A and 50.0% vs 41.7% for hospital B, $p<0.001$). Moreover, CA-MRSA has become the predominant MRSA strains in hospital B since 2011 ($p=0.031$) but HA-MRSA strains continuously remained stable in hospital A ($p=0.06$).

Conclusions: MRSA genotypes, ST239-III-*sasX* positive and ST59-VT-PVL positive, were the two major MRSA strains in central Taiwan. CA-MRSA (ST59) emerged as the predominant MRSA strain type in a certain hospital. In addition, livestock-associated MRSA (ST9) invasive infection was identified in this study. Our study described the epidemiological changes of MRSA in Taiwan and pointed out the potential threats of certain MRSA genotypes.