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sequential isolation from an elderly patient with pneumonia, during long-term linezolid treatment. Methods: A retrospective analysis was conducted to calculate the cumulative incidence of linezolid administered to an elderly patient with pneumonia during prolonged therapy with linezolid. Three sequential isolates were identified, its minimum inhibitory concentration (MIC), homology and drug resistant genes (crf, 235 RNA) were investigated. Results: One linezolid-resistant strain of methicillin-resistant Staphylococcus aureus (MRSA) was isolated from sputum of the patient at Xijing Hospital. The MIC of linezolid had increased from 1.5 µg/ml of initial strain 083 in March 2012 to subsequent 4.0 µg/ml of strain 158 in November 2012 and 16.0 µg/ml of strain 231 in March 2013 respectively. The increasing MIC values to linezolid were directly correlated with the cumulative amount of linezolid 118.8 g administered over 99 days. Strain 158 had heterogeneous resistance to linezolid. Molecular typing showed that three MRSA strains belonged to MLST ST-239 (spa t-030) with 98.8% homology. Cfr mutation was not detected but 235 RNA mutation G2603T was confirmed in strains 158 and 231.

Conclusions: This is the first case of linezolid-resistant MRSA isolated in China. The long-term use of linezolid for the treatment of MRSA infection was associated with a 235 RNA G2603T mutation, which mediates heterogeneous resistance to linezolid. And the strain with heterogeneous resistance might progress to a high-level linezolid-resistant strain when re-exposed to linezolid.

**CORRELATION OF MOLECULAR TYPES WITH ANTIMICROBIAL SUSCEPTIBILITY PROFILES AMONG 670 MECA-POSITIVE MRSA ISOLATES FROM STERILE SITES (TIST STUDY, 2006-2010)**

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**Background:** Methicillin-resistant Staphylococcus aureus (MRSA) is the most frequent organism that causes severe healthcare- and community-associated infections. Association of molecular types and antimicrobial susceptibility test (AST) profiles has been reported. The goal is to correlate various molecular types with AST profiles of MRSA isolates from Taiwan.

**Materials and Methods:** MRSA from sterile sites were collected during 5 years from 22 hospitals (Tigecycline In-vitro Surveillance in Taiwan – TIST 2006–2010) and AST including seventeen antibiotic regimens and inducible macrolide-lincosamide-streptogramin B (MLSb) phenotype were determined by Vitek-II automated system. Molecular types including SCCmec, spa, and dru were determined by PCR and nucleotide sequencing. Multidrug resistance (MDR) was defined an isolate with resistance to more than or equal to three non-beta-lactam antibiotics. Correlation with molecular types with antibiotic resistance was determined by Fisher’s exact test.

**Results:** Totally 670 meca+ MRSA were collected, among which most were from blood (627, 93.6%). The susceptibility rates determined by Vitek-II were as followed: linezolid and teicoplanin (100%), vancomycin (99.9%), tigecycline (99.7%), daptomycin (95.1%), fusidic acid (85.5%), rifampicin (68.7%), trimethoprim (53.7%), moxifloxacin (36%), tetracycline (34.2%), and less than 10% for cefoxitin, cefazolin, penicillin, oxacillin, erythromycin, clindamycin, and ampicillin/sulbactam. MRSA with MDR (542, 80.9%) was associated with molecularly HA-MRSA (e.g., SCCmecIIbIII; spa t0026t037; agr group II; dru4, 12, and 14). (p from < 0.001 to < 0.01). MLSbI (57, 8.5%) correlated with molecular types of SCCmecIIbIII, spa t3525, and agr group III (p < 0.01). The compound annual growth rate of susceptibility from 2006 to 2010 ranged from -2% of fusidic acid to 13% of clindamycin and 17% of erythromycin, respectively.

Conclusions: MRSA from Taiwan had varied AST profiles and some with increasing susceptibility within 5 years. Strains with particular molecular phenotypes had corresponding AST profiles that were distinct from those of endemic MRSA clones reported.