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MRSA - one health worldwide

Molecular typing and virulence profiling of *Staphylococcus aureus* isolates from a non-tertiary hospital in South Korea

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Background: *Staphylococcus aureus* (*S. aureus*) is a major human pathogen associated with both nosocomial and community acquired infections. In South Korea, the spread of methicillin-resistant *S. aureus* (MRSA) is a problem in healthcare setting, but the genetic characteristics of *S. aureus* prevalent in non-tertiary hospitals and community have not been known yet. In this study, we investigated the characteristics of *S. aureus* isolated from non-tertiary hospitals.

Material/methods: *S. aureus* isolates recovered from clinical specimens in non-tertiary hospitals were collected from five laboratory centers during 2013-2014 as a part of National Antimicrobial Resistance Surveillance Project. Antimicrobial susceptibility test for all isolates was performed, and molecular types were characterized by MLST, SCC*mec*, *agr*, and *spa* typing. The virulence genes including Pantan-Valentine Leukocidin (PVL) gene, toxin shock syndrome toxin 1 (TSST) gene, exfoliative toxins (ETs) and staphylococcal enterotoxins (SEs; SEA to SEE, SEG to SEJ) were identified by conventional PCR or multiplex DNA amplification.

Results: Among a total of 447 *S. aureus* isolates, 272 MRSA (60.9%) and 175 MSSA (39.1%) were identified. The 43 sequence types (STs) were determined by MLST (primarily ST72, ST5, ST239, ST188 and ST1) and 84 *spa* types were confirmed. The most frequent STs of MRSA isolates were ST5 (*n*=113), ST72 (*n*=83), and ST239 (*n*=27), while those of MSSA isolates were ST72 (*n*=39), ST188 (*n*=20) and ST1 (*n*=19). The 130 isolates (47.8%) of all MRSA isolates were SCC*mec* type II, 106 (39.0%) were SCC*mec* type IV, and 33 (12.1%) were SCC*mec* type III. The most prevalent combinations of enterotoxin genes in MRSA isolates were *seg-sei* (41.2%) and *sec-seg-sei* (34.2%), and the most of MRSA isolates containing *sec-seg-sei* harbored *tsst* gene (91.4%). Among all *S. aureus* isolates, 19 (4.3%) and 9 (2.0%) isolates were positive to PVL and ET genes, respectively.

Conclusions: This study suggests that ST5-SCC*mec* II-t2460 (16.2%), ST5-SCC*mec* II-t002 (12.5%), and ST72-SCC*mec* IV-t324 (11.0%) were predominant MRSA clones in non-tertiary hospitals in South Korea.