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Genotypic Diversity of *Staphylococcus aureus* from Asian Countries Including Korea

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The ability to distinguish accurately between different strains within a bacterial species is a fundamental requirement for epidemiological surveillance and microevolutionary studies. Molecular technologies have been extensively exploited in typing tools for the bacterial epidemiology. For many bacterial pathogens, pulsed-field gel electrophoresis (PFGE) is currently regarded as the molecular typing 'gold standard'. However, it has some defect in terms of reproducibility, speed, and costs of analysis. However, multilocus sequence typing (MLST) using nucleotide sequences of several housekeeping genes was developed in 1998 as a general approach to provide accurate, portable data, and has since been applied to many pathogenic species. In particular, MLST data are revealing evidence concerning the emergence and spread of antibiotic resistant clones. MLST are coming to be more frequently used for *Staphylococcus aureus*. In addition to MLST based on several housekeeping genes, a single-locus sequence typing method for *S. aureus* using the sequences of polymorphic region X of the *S. aureus* protein A (*spa*) gene was developed. *spa* typing was shown to be nearly as discriminatory as PFGE.

In this presentation, I present genotypic diversity of *S. aureus* (mainly, methicillin-resistant *S. aureus*, MRSA) isolates from Asian countries including Korea based on MLST, *spa* typing, and other genotyping methods.

S. aureus is a frequent and important human pathogen both in the community and in hospitals. In *S. aureus*, methicillin resistance has emerged by the introduction of SCC*mec* into phylogenetically distinct successful methicillin-susceptible *S. aureus* (MSSA) lineages, resulting in a relatively small number of pandemic MRSA clones spread worldwide. That is, population genetic studies based on MLST have shown that major MRSA clones have emerged from five clonal complexes (CCs), i.e., CC5, CC8, CC22, CC30, and CC45, while PFGE has identified five major pandemic MRSA clones, i.e., Iberian, Brazilian, Hungarian, New York/Japan, and pediatric clones. The Iberian, Brazilian, and Hungarian clones belong to CC8, and the New York/Japan and pediatric clones belong to CC5. Our data revealed two major genotypes of MRSA strains in Asian countries, with unique geographic

distributions. By MLST analysis, MRSA strains from Korea and Japan belonged to CC5 while most MRSA strains from other Asian countries belonged to CC239. SCC*mec* typing showed that most isolates from Korea and Japan were SCC*mec* type II whereas SCC*mec* type III (or IIIA) was the most common type in strains from other Asian countries.

Although MRSA strains from Korea and Japan share the same sequence type (ST) in MLST and SCC*mec* type, genetic differentiation between two countries was observed by *spa* type and SCC*mec* type. Several *spa* types might be differentiated from a prevalent prototype (TJMBMDMGMK) that is shared by the two countries, revealing a unique geographic distribution. SCC*mec* type II lacking pUB110 was found more frequently in Korea than in Japan. These findings suggested that MRSA strains from Korea and Japan might have originated from a common ancestor, but then clearly differentiated according to locality.

Genetic analysis of MRSA strains isolated from eight tertiary care hospitals in Korea revealed their genotypic diversity. In Korean hospitals, the most predominant MRSA genotype was ST5-MRSA-II, as in a previous study. Strains of ST5-MRSA-II showed several different *spa* types, which suggested the genetic evolution of this genotype for a long period. The second prevalent genotype, ST239-MRSA-III (or IIIA), showed a single *spa* type, which suggested a recent introduction of this genotype into Korea.

Molecular characterization of MRSA isolates from neonatal patients transferred from primary obstetric clinics to a tertiary care hospital showed that their genotypic characteristics are similar to typical community-associated MRSA (CA-MRSA) rather than hospital-acquired MRSA (HA-MRSA) strains common in Korea. This suggests that CA-MRSA can spread in primary care clinics and be imported into tertiary care settings. In addition, molecular characterization of *S. aureus* isolates from nasal swabs of children in pediatrics also indicated that MRSA clones distinct from hospital-associated MRSA have disseminated in community.

References

1. Ko KS, Lee JY, Suh JY, Oh WS, Peck KR, Lee NY, Song JH. Distribution of major genotypes among methicillin-resistant *Staphylococcus aureus* clones in Asian countries. *Journal of Clinical Microbiology* 43(1):421-426, 2005.
2. Ko KS, Peck KR, Oh WS, Lee NY, Hiramatsu K, Song JH. Genetic differentiation of methicillin- resistant *Staphylococcus aureus* strains from Korea and Japan. *Microbial Drug Resistance* 11(3):279- 286, 2005.
3. Ko KS, Kim YS, Song JH, Yeom JS, Lee H, et al. Genotypic diversity of methicillin-resistant *Staphylococcus aureus* isolates in Korean hospitals. *Antimicrobial Agents and Chemotherapy* 49(8):3583-3595, 2005.
4. Ko KS, Park S, Peck KR, Shin EJ, Oh WS, Lee NY, Song JH. Molecular characterization of methicillin-resistant *Staphylococcus aureus* isolated from neonates transferred from primary obstetric clinics in Korea. *Infection Control and Hospital Epidemiology* (In press).