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英文題目：Genotyping of 670 methicillin-resistant *Staphylococcus aureus* isolates from invasive infections using *spa* typing and their correlation with antibiotic susceptibility

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Background: Invasive infections caused by methicillin-resistant *Staphylococcus aureus* (MRSA) lead to significant morbidity and mortality. Genotyping using the gene encoding staphylococcal protein A (*spa*) has been universally used for MRSA. The goal of this study was to delineate the molecular typing results and to correlate these with antibiotic susceptibility.

Methods: Non-duplicate *mecA*+MRSA isolates from patients with invasive infections were collected from a 5-year nationwide antimicrobial surveillance program (TIST). The allelic profile of the *spa* gene was identified using PCR and nucleotide sequencing, and the *spa* type was determined using the Ridom SpaServer. Antimicrobial susceptibility was performed with agar or microbroth dilutions for various antibiotics and Etest was used for both daptomycin and vancomycin. The correlation of *spa* types with antibiotic susceptibility was analyzed.

Results: In total, 670 *mecA*+MRSA were collected, and 58 *spa* types were determined among 639 (95.4%) isolates. Six major types, including *spa* t002 (103, 15.3%) and t037 (253, 37.8%), were classified as healthcare-associated MRSA (HA-MRSA, 53.1%); while t437 (151, 22.5%), t441 (13, 1.9%), t1081 (19, 2.8%), and t3525 (14, 2.1%) were classified as community-associated MRSA (CA-MRSA, 29.4%). The declining trend in the vancomycin MIC occurred in parallel with an increasing frequency of CA-MRSA. The *spa* clone complex (*spa*-CC) analysis showed wide genetic heterogeneity, and antibiotic susceptibility patterns were correlated with particular *spa* types.

Conclusion: Genotyping MRSA with *spa* can differentiate MRSA isolates for epidemiological purpose. Correlation of antibiotic susceptibility to given *spa* types will help physicians select appropriate antibiotics for treatment of invasive MRSA infections.