554. The Changing Epidemiology of Methicillin-Resistant Staphylococcus aureus Causing Bacteremia in Hiroshima, Japan During 2008–2017
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Background. Recently, the Japanese intrinsic community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) clone (CA-MRSA/J) has been identified as a predominant cause of community-acquired MRSA infections in Japan. The CR3-IVa and ST6-IV MRSA strains were predominant in the initial period of CA-MRSA/J spread in Japan. In 2017, ST764-IIa MRSA has emerged as the most common MRSA strain in Japan.

Methods. Whole genome sequencing of MRSA isolates causing bacteremia at Hiroshima University Hospital between January 2008 and December 2017. MRSA isolates were subjected to multilocus sequence typing, SCCmec typing and were analyzed for virulence factors. Clinical data of patients with MRSA bacteremia were analyzed.

Results. A total of 193 MRSA strains causing bacteremia were identified during the study period. Among these, most belonged to ST764-IIa (30%, 59 of 193) and ST5-IIa (26.9%; 52 of 193). The proportion of ST5-IIa MRSA decreased from 39.6% (42 of 106) in 2008–2012 to 11.5% (10 of 87) in 2013–2017, and that of ST764-IIa MRSA increased from 23.6% (25 of 106) to 39.1% (34 of 87) in the same time period. The proportion of CA-MRSA (MRSA carrying SCCmec type IV or V) increased from 28.3% (30 of 106) in 2008–2012 to 42.5% (37 of 87) in 2013–2017. In CA-MRSA strain 764-IIa, the CC8-IV MRSA isolates were predominant (76.1%; 51 of 67). Those belonging to CC8-IV MRSA isolates were ST380-IVa (18 of 51), ST7-IVa (CA-MRSA/J); 15 of 51), ST7-IVb (15 of 51), ST8-IVa (2 of 51), and ST4803-IVa (1 of 51). The rate of hospital-onset infections of ST380-IVc, ST7-IVa and ST7-IVb were 83.3%, 46.7%, and 60%, respectively.

Conclusion. The changing epidemiology of MRSA causing bacteremia in Japan..

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