29th ECCMID Amsterdam, Netherlands 13 – 16 April 2019

The congress of ESCMID

P2746 Molecular characterisation of methicillin-resistant *Staphylococcus aureus* outbreak isolates collected from neonatal and burns patient wards at public hospitals in Gauteng, South Africa

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) causes infections ranging from skin and soft tissue infections to systemic infections such as endocarditis. The global burden of MRSA infections is largely attributed to *S. aureus* antibiotic resistance, which is due to the acquisition of the methicillin A (*mec*A) gene that encodes for a modified penicillin-binding protein (PBP2a) with a low binding affinity for β-lactam antibiotics. The *mec*A gene is carried on a staphylococcal cassette chromosome methicillin (SCC*mec*) element. Several typing methods are employed to characterise MRSA strains as either healthcare-associated MRSA (HA-MRSA) or community-associated MRSA (CA-MRSA) by determining the SCC*mec* types. The aim of this study was to use SCC*mec* typing to characterise clinical MRSA isolates collected (2015 to 2016) from burn and neonatal wards during outbreaks at three public hospitals in Gauteng Province, South Africa.

Materials/methods: Eighty-four isolates from blood, catheter, pus and tissue specimens were phenotypically identified as MRSA by the Vitek® 2 automated system. Total genomic DNA extraction using a commercial kit was carried out followed by molecular identification using multiplex PCR (M-PCR) assays targeting the *Staphylococcus*-specific 16S rRNA gene, the *S. aureus*-specific *nuc*, *mec*A and *pvl* genes as well as M-PCR assays for SCC*mec* typing.

Results: The M-PCR assays confirmed all the isolates as MRSA and that none was positive for the *pvl* gene. The SCC*mec* typing results showed that: 37% (31/84) of the isolates carried SCC*mec* type III; 19% (16/84) carried type IV; 13% (11/84) carried type I; 13% (11/84) carried type II; 5% (4/84) carried type V; 2% (2/84) carried combinations of two SCC*mec* elements (I/II and II/III), while 11% (9/84) were nontypeable.

Conclusions: The dominant SCC*mec* type was type III, which is associated with HA-MRSA. These HA-MRSA strains typically possess large SCC*mec* elements that can carry multiple antibiotic resistance genes making treatment of infections more difficult. Diverse SCC*mec* types were detected indicating multiple introductions of MRSA into the clinical settings. Therefore, improved infection control as well as continuous monitoring and surveillance of MRSA strains circulating in these hospital wards is required to prevent outbreaks and the emergence of a dominant clone.