eP165
ePoster Viewing
Molecular typing of staphylococci

MOLECULAR CHARACTERISATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS SURVEILLANCE ISOLATES IN SOUTH AFRICA

A. Singh-Moodley[1], O. Perovic[1]

[1]Center for Opportunistic Tropical and Hospital Infections, National Institute for Communicable Diseases, Johannesburg, South Africa

Objectives

Methicillin resistant *Staphylococcus aureus* (MRSA) infections are a significant cause of morbidity and mortality and is increasing in some public hospitals in South Africa. It accounts for more than 50% of bacteraemic staphylococcal infections. In this study we aimed to molecularly characterise MRSA isolates using staphylococcal cassette chromosome *mec* (SCC*mec*)- and *spa*- typing to provide information on strain interrelationship.

Methods

Methicillin susceptible *Staphylococcus aureus* (MSSA) and MRSA isolates were submitted to the laboratory on Dorset transport media. Each isolate was plated onto a blood agar plate followed by organism identification and antimicrobial susceptibility testing (AST) using automated systems (VITEK II for identification and MicroScan® MIC dried Gram Positive panel for AST). All MRSA isolates were screened for methicillin resistance using real time PCR (LightCyler 480) and then typed using conventional typing methods.

Results

In this study, a total number of 1432 confirmed MRSA isolates from all provinces in South Africa were typed to identify the current prevalent *mec* element types. A subset of this was further molecularly characterised using *spa*-typing. The most prevalent SCC*mec* type identified was SCC*mec* type III (n=666) followed by types IV (n=473), II (n=87) and VI (n=7). No types I and V were observed but unknown typing patterns were identified (n=177). Twenty-two isolates were negative for SCC*mec* typing although classified as MRSA and requires further investigation. *Spa*-typing of 10% of the isolates per site revealed 24 different *spa*-types, 4 of which were novel and have not as yet been classified. The five most common *spa*-types were t037 (n=83), t1257 (n=29), t045 (n=10), t064 (n=8) and t012 (n=5) which accounted for 85% of the isolates tested. The *spa*-types clustered into 4 *spa* clonal complexes (*spa*-CC) using the Based Upon Repeat Pattern (BURP) algorithm at a cost setting of ≤4 and excluding *spa*-types with 5 or fewer repeats. *Spa*-CC-021 and -1257 were the largest of the clonal complexes. *Spa*-CC-021 contained isolates that displayed SCC*mec* types II, III, IV and unknown typing patterns. *Spa*-CC-1257 contained isolates displaying predominantly the SCC*mec* type IV element. In addition, some unknown SCC*mec* type patterns were present. One isolate in this clonal complex was negative for SCC*mec* typing but positive for real time PCR and requires further investigation. These clonal complexes were widespread in South Africa. *Spa*-CC-021 was identified in Gauteng, Western Cape and the North West Province and *spa*-CC-1257 was identified in these provinces as well as in KwaZulu Natal.

Conclusion

By molecular characterisation we have gained insight in pathogen distribution and relatedness of MRSA isolates from South African sentinel sites. SCC*mec* type III was most common and the most common *spa*-type was t037.