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Genome sequencing, assembly, annotation and analysis of methicillin-resistance of *Staphylococcus aureus* strain SO-1977 reveals genes responsible for antibiotic resistance**Sofia Bashir Mohamed Ali**

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Background: *Staphylococcus aureus* is a ubiquitous bacterial pathogen and a leading cause of morbidity and mortality worldwide. The epidemiology of infections is influenced by rapid and widespread emergence of multidrug-resistant methicillin-resistant *S. aureus* (MRSA). *Staphylococcus aureus* (MRSA) is a major cause of nosocomial infection in Sudan. The relatively small genome size and rapid evolution of antibiotic resistance genes in the species have been drawing an increasing attention in public health. To extend our understanding of the species and use the genome data for comparative genomic studies, we sequenced the whole genome of Methicillin-resistant of *Staphylococcus aureus* strain SO-1977 isolated from Sudan.

Methods: Genomic DNA was sequenced using the Illumina MiSeq. The complete genome was annotated and the presence of antimicrobial resistance genes was identified.

Result: The draft genome of MRSA strain SO-1977 consisted of 2,827,644 bp with a G+C content of 32.8 %, 2,629 predicted coding sequences (CDSs) and 55 RNAs. The final assembly contained 151 contigs of N50 contig length of 62,783 bp and the largest contig assembled measured was 146,886 bp. Comparative studies of the MRSA strain SO-1977 and MRSA 252 through RAST server showed a total of 20 were annotated to antibiotic resistance genes. Interestingly, one gene related to methicillin resistance and four-genes related to Tetracycline resistance were found only in SO-1977 strain.

Conclusions: This study is the first to report on the whole genome sequence of a Sudanese MRSA isolate. Antibiotic resistance genes found in the genome indicate the presence of antibiotic resistance mechanism prior to the usage of antibiotics. The finding of this study would help to understand the evolution of resistance mechanism and dissemination of the resistance genes of MRSA

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