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Data in Brief

Draft genome sequence of *Staphylococcus aureus* KT/312045, an ST1-MSSA PVL positive isolated from pus sample in East Coast Malaysia

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ABSTRACT

Most of the efforts in elucidating the molecular relatedness and epidemiology of *Staphylococcus aureus* in Malaysia have been largely focused on methicillin-resistant *S. aureus* (MRSA). Therefore, here we report the draft genome sequence of the methicillin-susceptible *Staphylococcus aureus* (MSSA) with sequence type 1 (ST1), spa type t127 with Panton-Valentine Leukocidin (*pvl*) pathogenic determinant isolated from pus sample designated as KT/314250 strain. The size of the draft genome is 2.86 Mbp with 32.7% of G + C content consisting 2673 coding sequences. The draft genome sequence has been deposited in DDBJ/EMBL/GenBank under the accession number AOCP00000000.

Specifications

Organism/cell line/tissue	Methicillin-susceptible *Staphylococcus aureus*
Strain	*KT/314250*
Sequencer or array type	Illumina GA IIx
Data format	Assembled
Experimental factors	Bacterial strain
Experimental features	Assembled and annotated draft genome of a strain of methicillin susceptible *Staphylococcus aureus* PVL^+ from east coast Malaysia
Consent	Not applicable
Sample source location	*Pus*

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=AOCP00000000

2. Experimental design, materials and methods

MRSA evolved over the times from Methicillin susceptible *S. aureus via* acquisition of mobile genetic elements called staphylococcal cassette chromosome *mec* (SCC*mec*) [1,2]. Thus, this makes MSSA to be a potential reservoir for the MRSA strains. *S. aureus* strains producing PVL have been associated with a variety of illness ranging from skin and soft tissue infections to necrotizing pneumonia as well as septicaemia that are invariably fatal [3]. The genome sequencing of KT/314,250 strain was performed using the Illumina genome analyzer IIx 100-bp paired-end reads. The paired-end reads were trimmed and assembled *de novo* using CLC genomics workbench 5.1 (CLC Bio, Denmark). Multi Locus Sequence Typing (MLST) was performed by using Local BLAST identification and manually aligned based on primers used to amplified seven gene fragments (*arcC*, *aroE*, *glpF*, *gmk*, *pta*, *tpi* and *yqiL*) [4]. Meanwhile the spa typing was assigned using DNAGear freely available Software [5]. Thus, all genotypic analysis revealed this strain as ST1, *spa* type t127, *agr* III and *dru* type dt10ao.

The draft genome were annotated by using free accessible bioinformatics tools Blast2GO 2.5.0 [6] and subsequently validated using Rapid Annotation Subsystem Technology (RAST) [7] and Bacterial Annotation System (BASys) [8]. Initial sequence analysis revealed a total of 69 contigs from the *de novo* assembly with an accumulate length of 2,846,051 bp with G + C content of 32.7%. A total of 2673 coding sequences (CDSs) and 48 RNAs regions were annotated. Of the CDS,

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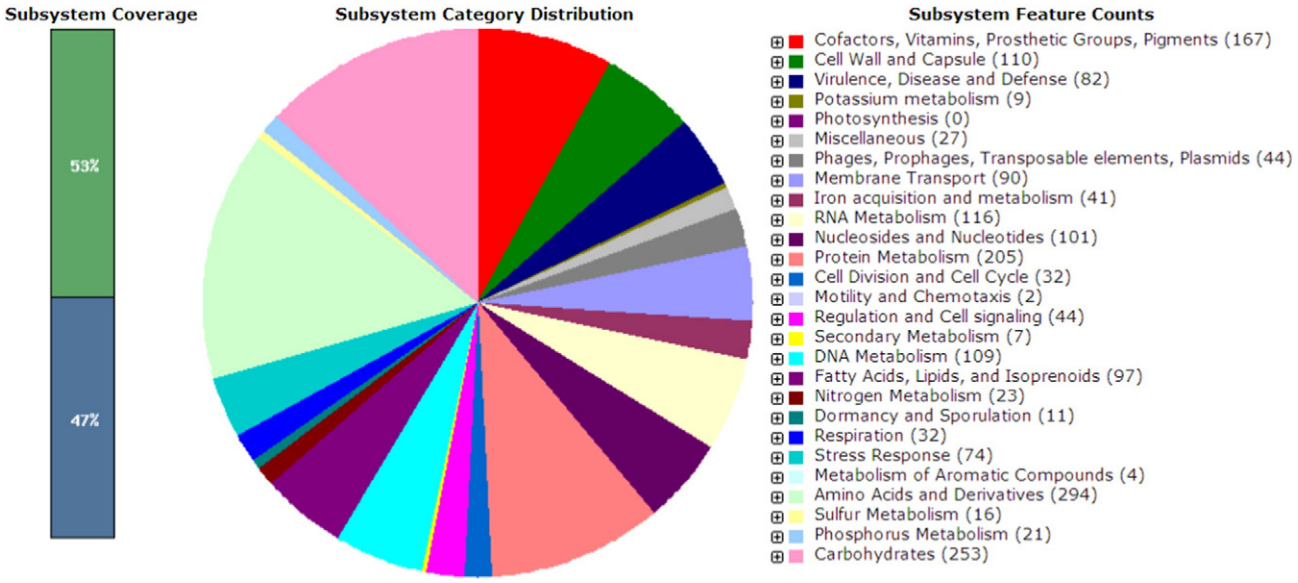

Fig. 1. Subsystem distribution of methicillin-susceptible *S. aureus* KT/314,250 (based on RAST annotation server).

4.12% were associated with cell wall and capsule; 3.07% were associated with virulence, disease and defence mechanism and 2.77% were related with stress response which is contributed in host adaptation and survival (Fig. 1).

Nucleotide sequence accession number

The Draft genome sequence of Methicillin-susceptible *Staphylococcus aureus* (MSSA) KT/314,250 strain has been deposited under the accession number AOCP00000000. The version described in this paper was the first version, AOCP00000000.

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