Deciphering a rare methicillin resistant Staphylococcus aureus strain: Genome sequencing and molecular characterization of CC15-MRSA

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Introduction

Clonal complex 15 Staphylococcus aureus:
- Methicillin-susceptible strains from this lineage (CC15-MSSA) are ubiquitous
- Methicillin resistant strains from this lineage (CC15-MRSA) have only been sporadically described in literature

Recently, we reported the first identification of CC15-MRSA from the Middle East
- Isolates were from patients with nosocomial infections and from retail meat products
- Whole genome sequences has previously been reported for CC15-MSSA,
- No whole genome sequencing data are yet published for CC15-MRSA.

Methods

Isolates:
- Four isolates identified in Riyadh, Saudi Arabia were studied
  - Nosocomial infection (n=2)
  - Retail meat product (n=2)

S. aureus identification & confirmation of methicillin resistance:
- Standard laboratory techniques according to CLSI guidelines

Whole genome sequencing:
- Genomic DNA was extracted
- Sequencing was carried out using the Illumina HiSeq2500 genome analyzer
- Reads were assembled & resulting contigs were mapped on a similar GenBank entry, AHVD0000000.1, derived from a ST15-MSSA
- Due to presence of repeats, the SCC element could not be scaffolded into a single contiguous sequence

Results

All the CC15-MRSA isolates had a new MLST profile 13-13-1-1-81-11-13, which is a single locus variant of ST15
- Presence of pta=81 instead of pta=12 in canonical ST15; pta-81 differs from pta-12 by only 1 SNP
- pta=81 was observed in all four CC-15 MRSA (Figure)

Four copies of trplS256 (size 1200 nt) and five copies of trplS431 (size 700 nt)

Two identical copies of a trplS256-based insertion element carrying aacA-aphD identified
- one copy inserted between SCC and fusC; one copy disrupting the chromosomal outer surface protein gene sasC

SCC element was spread over three contigs with each contig terminating in trplS431
- One contig comprised a recombinase gene “ccrA” (an undescribed recombinase gene homologue accompanying ccrC), ccrC-P1, fusC and a helicase. Another contig included mvaS, dnu, mecA and the third contig included yobV
- This constellation is consistent with a novel SCCmecV /SCCfus composite element

CC15-MRSA has a deviant variant of hsdM/hsdS at the major pathogenicity island vSat2 compared to the reference CC15-MSSA genome

One nosocomial isolate harbored a 30-kb plasmid packed with additional antibiotic resistance genes (cadD, cadX, bial, blalR, blaz, lnuA, aadD); 3 copies per cell

Conclusions

We provide the first molecular characterization of a MRSA strain from a common lineage that until recently gave rise only to very few MRSA. It might be speculated that changes in the hsdM/hsdS system facilitated uptake of foreign mobile genetic elements, i.e., of SCCmec / SCCfus. This strain apparently emerged among humans and livestock in Saudi Arabia and warrants further surveillance, especially with regard to further spread in the Middle East and to the emergence of further CC15 MRSA strains.

Objectives

To describe the genetic characteristic of an emerging CC-15 MRSA strain from Saudi Arabia using whole genome sequencing