

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

Abiola Senok^{1,2}, Ali Somily³, Peter Slickers^{4,5}, Muhabat Raji², Ghada Garaween², Atef Shibl², Stefan Monecke^{4,5,6}, Ralf Ehricht^{4,5}

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¹College of Medicine, Mohammed Bin Rashid University of Medicine and Health Sciences, Dubai, United Arab Emirates

²Department of Microbiology and Immunology, College of Medicine, Alfaisal University, Riyadh, Saudi Arabia

³Department of Pathology and Laboratory Medicine, College of Medicine, King Khalid University Hospital and King Saud University, Riyadh, Saudi Arabia

⁴Alere Technologies GmbH, Jena, Germany

⁵InfectoGnostics Research Campus, Jena, Germany

⁶Institute for Medical Microbiology and Hygiene Technische Universität Dresden, Dresden, Germany



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 in nosocomial infection & retail meat products from the Middle East
- Whole genome sequences has previously been reported for CC15-MSSA
- Whole genome sequencing data are yet to be published for CC15-MRSA.

Objectives

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

Methods

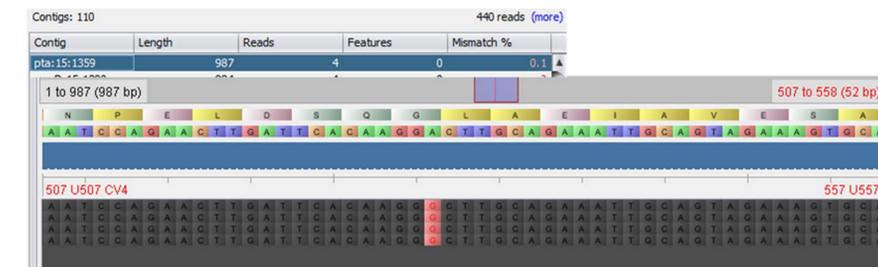
- **Isolates:**
 - Four isolates identified in Riyadh, Saudi Arabia were studied
 - Nosocomial infection (n=2)
 - Retail meat product (n=2)
- ***S. aureus* identification & confirmation of methicillin resistance:**
 - Standard laboratory techniques according to CLSI guidelines
- **Whole genome sequencing :**
 - 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, AHVD00000000.1, derived from a ST15-MSSA
 - Due to presence of repeats, the SCC element could not be scaffolded into a single contiguous sequence

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* & emergence of this strain among humans & livestock in Saudi Arabia
- Close surveillance is needed especially with regard to spread in the Middle East and emergence of further CC15 MRSA strains

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 *tnpIS256* (size 1200 nt) and five copies of *tnpIS431* (size 700 nt)
- Two identical copies of a *tnpIS256*-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 *tnpIS431*
 - One contig comprised a recombinase gene "*ccrAA*" (an undescribed recombinase gene homologue accompanying *ccrC*), *ccrC-PM1*, *fusC* and a helicase. Another contig included *mvaS*, *dru*, *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 *vSaa* compared to the reference CC15-MSSA genome
- One nosocomial isolate harbored a 30-kb plasmid packed with additional antibiotic resistance genes (*cadD*, *cadX*, *blaI*, *blaR*, *blaZ*, *InuA*, *aadD*); 3 copies per cell