

Microbiology 2018: A Genomic Infection Control Study for *Staphylococcus aureus* In Two Ghanaian Hospitals

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Whole genome sequencing analysis (WGS) has the highest resolution for bacterial isolate typing and the potential to detect transmission channels. The study's goal was to utilise WGS to clarify putative transmission events involving two suspected outbreaks of *Staphylococcus aureus* in a Ghanaian hospital, as well as to define genomic features of the *S. aureus* isolates in the outbreaks.

The science of microbial genomics is advancing at a rapid rate, thanks to the introduction of next generation sequencing tools.

Whole genome sequencing analysis (WGS) outperforms bacterial typing approaches because it provides better resolution of bacterial isolates and is especially useful for highly clonal bacteria like *S. Aureus*. WGS had previously been used on *S* in prior investigations. Aureous and utilised to explain MRSA's global and local spread, examine outbreaks, forecast antibiotic resistance, and classify bacterial strains. In general, WGS applications to investigate *S*.

Methods: The study was conducted at Korle-Bu Teaching Hospital and Lekma Hospital, where the purported epidemics occurred in 2012 and 2015, respectively. The *S*- There were three sources of aureus isolates acquired from the two hospitals: transportation, infectious disease, and climate. The *S* genome has been sequenced in its entirety. The aureus isolates are performed, and the sequence reads are mapped to the USA300 FPR3757 *S. Aureus* strain reference genome. A maximum likelihood phylogenetic tree was constructed. Typing of multilocus sequences The SRST2 for fast reading mapping was used in conjunction with antimicrobial resistance studies and virulence genes.

Results: In January 2012, an epidemic of three *S* was reported at KBTH's Department of Child Welfare. Cases aureus is an abbreviation for Cases aureus. *S. Aureus* was extracted from the blood of a 4-month-old infant girl referred to the Emergency Department in case one. She had spent 5 days in the emergency room before being transferred to another ward (marked P2), where she died. The second instance was discovered four days after the first and was isolated from the cerebrospinal fluid of a 5-day-old baby boy who was taken to the emergency room. The youngster was then transferred to ward P2. Two days after the second case *S. Aureus* was found in the sperm of a 4-month-old baby girl. This infant, like the first two, was adm

Following the baby's death, the KBTH Infection Prevention and Control Unit requested an investigation into the matter.

It has been determined that it is the newborns with whom *S. Aureus* shared the same breathing apparatus. Babies shared the same cot and were linked to one oxygen cylinder via tubes (which provided set lines). Clinical professionals confirmed that they are turning to this technique due to insufficient respiratory apparatus.

As a result of this news, KBTH has taken steps to sanitise the deceased baby's belongings (cot and bedding). Blood samples for culture were gathered from adjacent babies who shared tubes with the deceased infant,

but no bacteria grew in the specimens. In the unit, a Nasal Carriage Test for *S. Aureus* was performed, as well as environmental screening of babies, mothers, and health-care staff. *S* carriage Nasal. Aureus and MRSA were 49.7% (88/147) and 4.8% (7/147), respectively.

Environmental specimens taken from hospital ward equipment and surfaces revealed *S. aureus* and MRSA prevalences of 27.5 percent (39/142) and 11.3 percent (16/142), respectively.

KBTH's bacteriology laboratory kept track of *S. Aureus* isolates collected from patients during this time. all hospital patients; five *S* clinical isolates on average. This lab receives reports on aureus on a daily basis. The *S. aureus* isolates belonged to several types of sequences (STs), with ST15 and ST152 being the most common. All isolates carried the *blaZ* gene, and there was also a low prevalence of the *tetK* and *dfrG* genes. All of the isolates tested negative for *mecA*.

Conclusion: The ST15 clone's distribution pattern at the Korle-Bu Teaching Hospital emergency ward demonstrates a fundamental problem with the hospital's cleaning of environmental surfaces. The high prevalence of *pvl* genes across *S. aureus* isolates is likely to be mediated by many phage populations rather than a single highly transmissible species of phage.