TSST-1 Carriage in *Staphylococcus aureus* Isolates

Clara Hipp, Dr. Mandy Brosnahan, Dr. Taylor Mach

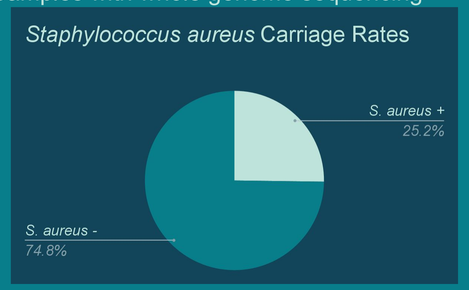
Science Department, Concordia University, St. Paul

Abstract

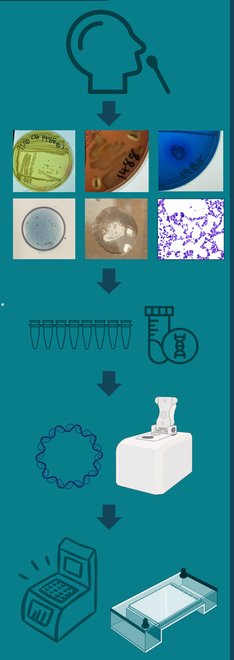
Staphylococcus aureus is an opportunistic bacteria that is carried commensally by approximately 30% of the population. Superantigens like TSST-1 are toxins produced by *S. aureus* and are important contributors to its pathogenicity. In order to examine the superantigenic profile of nasally carried commensal isolates, DNA from multiple *S. aureus* positive samples were isolated and then amplified using polymerase chain reaction (PCR). The amplified DNA was visualized through DNA gel electrophoresis to see if each sample contained the TSST-1 superantigen. Results showed that few strains contained TSST-1.

Study Overview & Methods

- 1605 Swabs Collected
- 1432 Swabs Processed through culture tests
- 361 Positive samples
- 25.2% Carriage Rate
- 142 Samples with whole genome sequencing



1. Collected nasal swab samples from willing participants on CSP campus.
2. Ran various culture tests on samples to identify which strains are *Staphylococcus aureus.*
3. Biobasic genomic prep kits were used to extract and purify DNA from each *S. aureus* strain.
4. Samples put into Nanodrop to identify the purity and concentration of each sample.
5. Amplify DNA by running PCR set for TSST-1 and visualize results using agarose gel electrophoresis.
6. Confirm results by repeating step 5.



TSST-1 Superantigen is present at low levels in *Staphylococcus aureus*

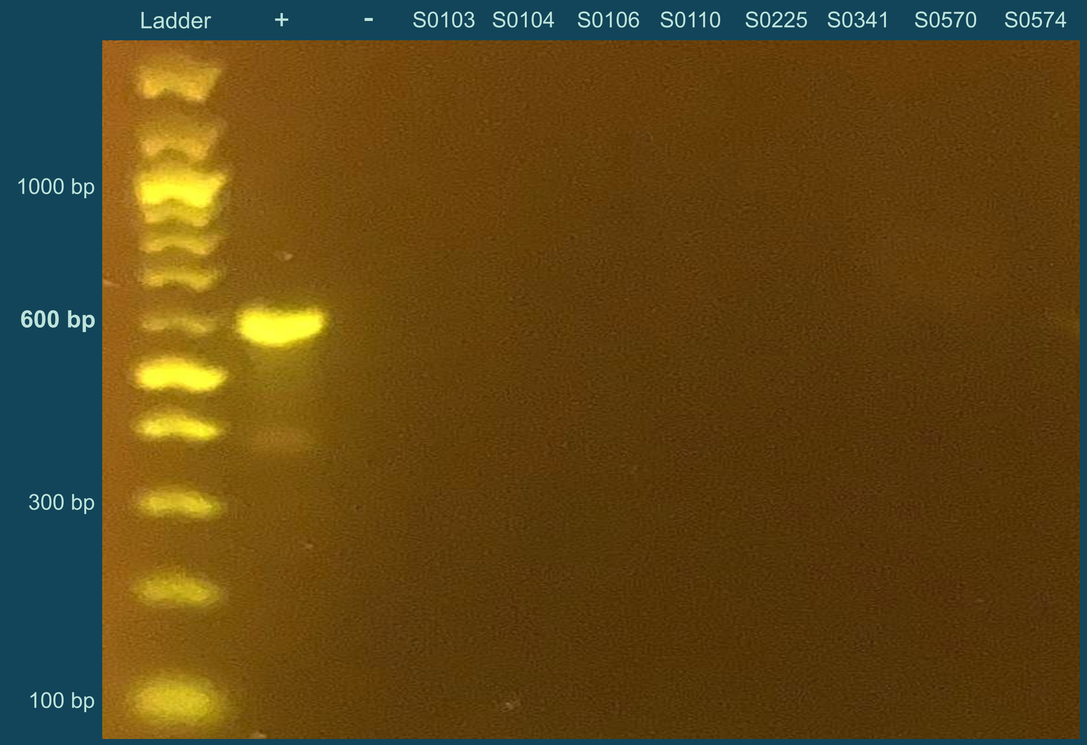
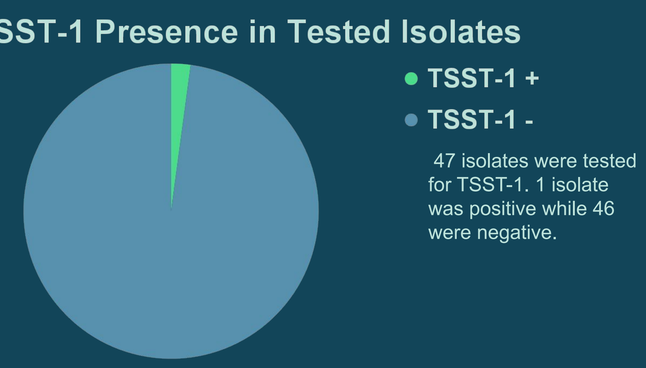


Figure 1. Agarose gel electrophoresis of *S. aureus* isolates (1.5% agarose) after PCR for TSST-1. The expected band length for TSST-1 is **655 bp**. The DNA ladder shows bands every 100 base pairs. The positive control (+) contains an isolate that was confirmed to contain TSST-1 through whole genome sequencing, PCR, and gel electrophoresis prior to testing other isolates. It will show a band at about 655 bp. The negative control (-) contains H_2O instead of a DNA sample and is expected to show no band.



TSST-1

- Toxic shock syndrome toxin-1 (TSST-1) is a superantigen that is a major contributor to the pathogenicity of *Staphylococcus aureus*. It is also the main cause of both menstrual toxic shock syndrome and non-menstrual toxic shock syndrome (1).
- Superantigens have the ability to bind and stimulate T-cell hyperactivation leading to toxic shock syndrome and potentially death
- 20% of natural isolates produce TSST-1(1).

It has been found that the *tst* gene is carried on a SaPI (Superantigen pathogenicity island) which is found in most isolates of CC30, a known pathogenic strain of *S. aureus* (2). It is also known that TSST-1 is most closely related to SEIX and that the *selx* gene is not found in CC30 (3). This implies that almost all *S. aureus* strains can produce either TSST-1 or SEIX and that there is likely an important role that this sub-group of toxins plays in the pathogenesis of *S. aureus* (3). After looking at the samples that we have collected at CSP we can see that SEIX is commonly found in *S. aureus* strains with a carriage rate of 78.2% while 9.9% of strains carry TSST-1 and only 1.4% of strains carry both TSST-1 and SEIX.

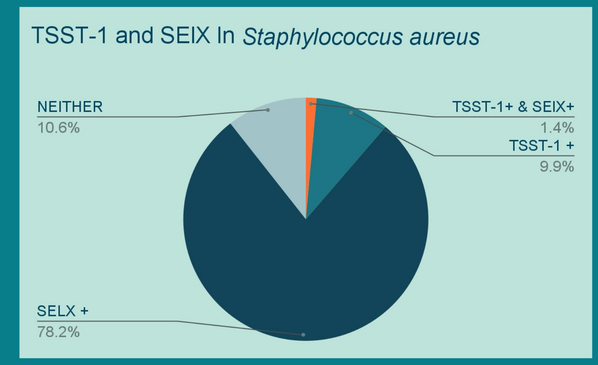


Chart based on whole genome sequencing data of 142 *S. aureus* strains.

Structurally, both toxins are similar but SEIX lacks a ubiquitous N-terminal SAg/SSL OB-fold domain but despite this difference both toxins appear to have the ability to bind TcRVβ (4). The lack of OB-fold could mean that SEIX is unable to bind to MHC Class II molecules and could explain the change in function between the two toxins (4).

References and Acknowledgements

1. J.A. Lindsay, A. Ruzin, H.F. Ross, N. Kurepina, R.P. Novick. The gene for toxic shock toxin is carried by a family of mobile pathogenicity islands in *Staphylococcus aureus*. Molecular Microbiology. ***29***,527-543(1998).
2. J.A. Lindsay, C.E. Moore, N.P. Day, S. J. Peacock, A.A. Witney, R. A. Stabler, S. E. Husain, P.D. Butcher, J. Hinds. Microarrays Reveal that Each of the Ten Dominant Lineages of *Staphylococcus aureus* Has a Unique Combination of Surface-Associated and Regulatory Gene. *ASM.* ***188***. (2006).
3. G.J. Wilson, K.S. Seo, R.A. Cartwright, T. Connelley, O.N. Chuang-Smith et al. A Novel Core Genome-Encoded Superantigen Contributes to Lethality of Community-Associated MRSA Necrotizing Pneumonia.*PLoS Pathog.****7***,10.(2011).
4. R.J. Langley, Y.T. Ting, F. Clow, P.G.Young, F.J. Radcliff et al. Staphylococcal enterotoxin-like X (SEIX) is a unique superantigen with function features of two major families of staphylococcal virulence factors.*Plos Pathog.****13***, 9 (2017).

Special thanks to Dr. Patrick Schlievert (University of Iowa) for helpful conversations. This research was partially funded by several CSP Faculty Development Grants. This work has IRB approval from CSP (studies 2016_42 & 2018_37).
A partnership with the Minnesota Department of Health Infectious Disease Laboratory allowed for whole genome sequencing of an initial subset of *S. aureus* strains from the campus study.