

Toxins produced from *Staphylococcus aureus* Strains at CSP

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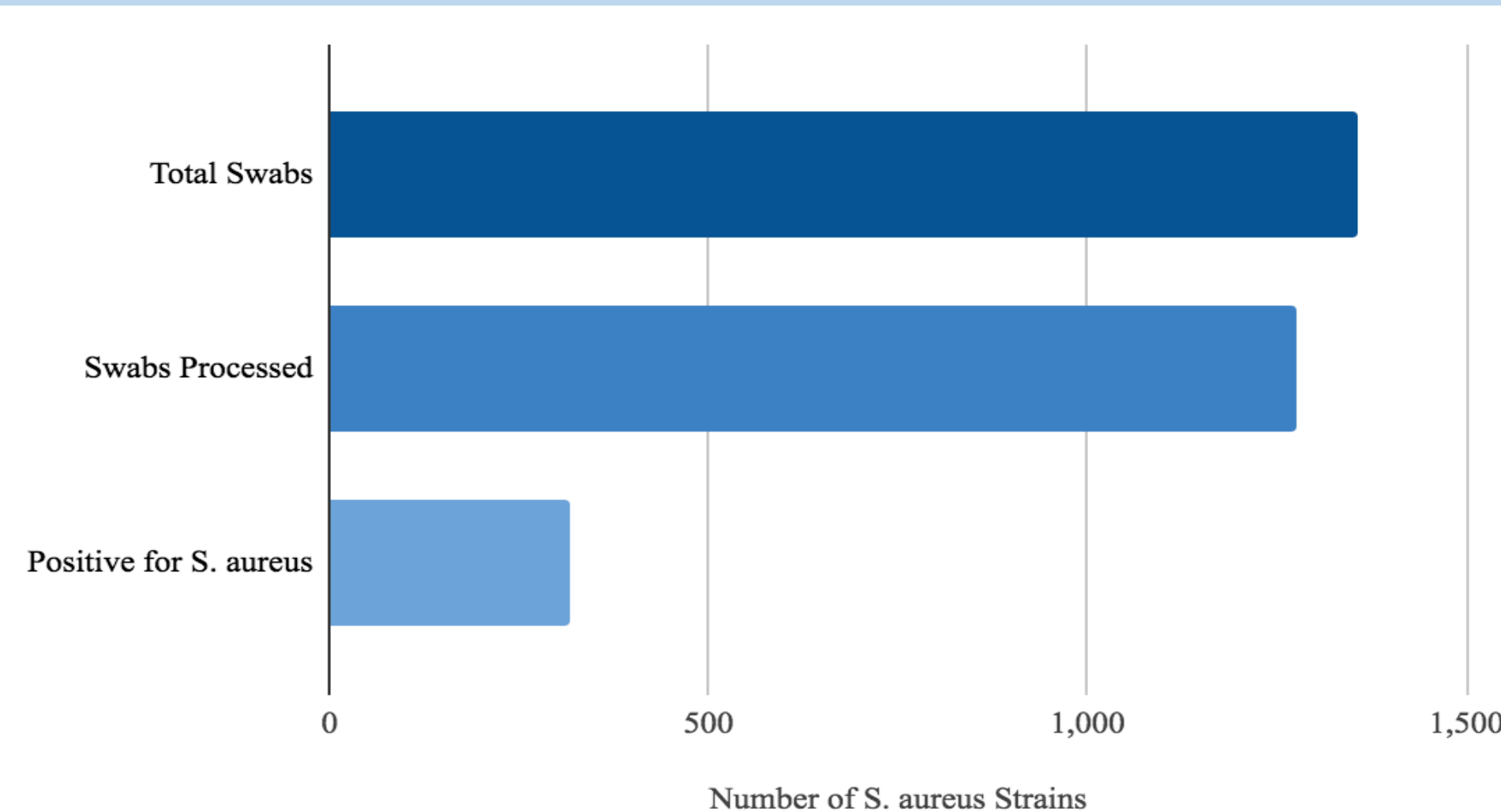
ABSTRACT

Nasal swabs were obtained from participants at the Minnesota State Fair as well as events on the Concordia University campus. The purpose of this study is to isolate and test for the presence of *Staphylococcus aureus* via various testing methods. Positive strains then underwent secondary testing to identify characteristic elements such as superantigens (SAGs) which can lead to diseases like Toxic Shock Syndrome (TSS). Identified from data is a known gene cluster made of enterotoxins SEG, SEI, SEM, and SEN that contribute to the symptoms of TSS.

BACKGROUND

- *Staphylococcus aureus* is a commensal bacteria that is of growing concern as it is known to lead to various human diseases such as TSS, endocarditis, sepsis, food poisoning and necrotizing pneumonia.
- *S. aureus* is also found to be carried in the noses of 30% of the population, but can also be found on the skin and mucosal surfaces.
- This is concerning because *S. aureus* in many cases may not display its presence through identifiable symptoms, in addition it is difficult to treat due to its ability to be antibiotic resistant.

STAPH STUDY NUMBERS



- Swabs Obtained: 1,355
- Swabs Processed: 1,277
- Positive *S. aureus* Strains: 318
- Carriage Rate: 25%



Enterotoxin Gene Clusters are Observed by Nasal Swabs Taken from CSP Students with TSST-1

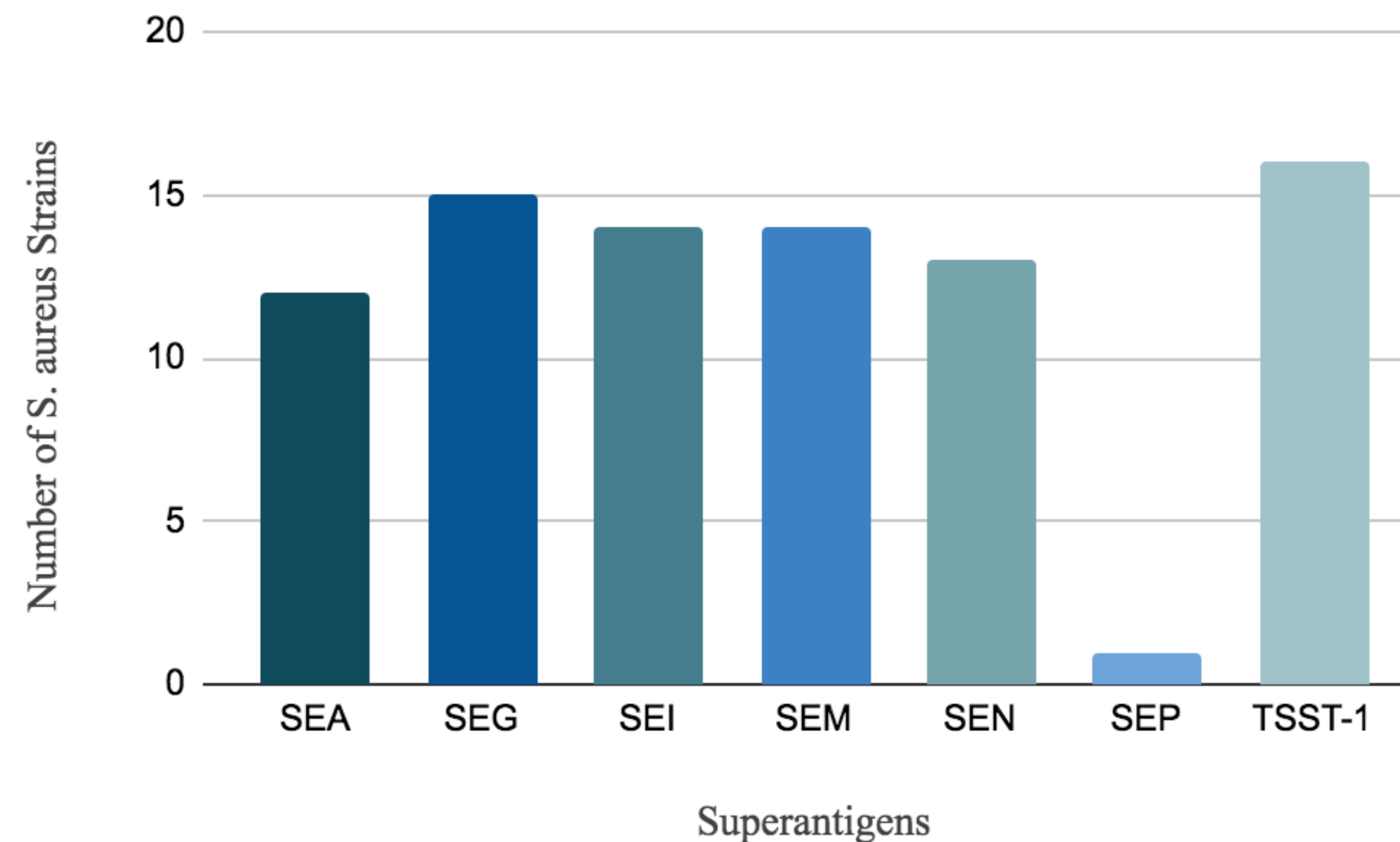


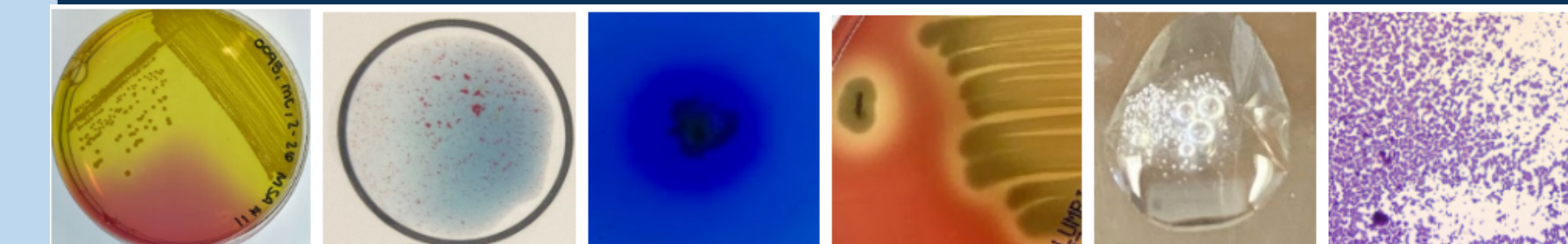
Figure 1: *S. aureus* strains that are also positive for toxic shock syndrome (TSS) have similar gene clusters. SEA, SEG, SEI, SEM, SEN superantigens have been found to be common amongst various strains of *S. aureus*. This is due to the ability of bacteria to organize functional genes in close proximity to each other and are known as gene clusters. This data shows that within TSST positive strains, these genes can be clustered and may express similarities in their functionality. This data also shows the presence of SEA and in one strain SEP. SEA is known to contribute to significant illnesses such as food poisoning and TSST-1. While SEIP is known to contribute to emesis and promotes inflammatory responses via amplified cytokine release when bound to T cells.

What are we looking for?

Strain Isolation and Culture Testing



- **MSA:** Growth and color change caused by halophiles.
- **Coagulase:** Presence of enzyme that converts fibrinogen to fibrin that clots blood.
- **DNase:** Presence of pink halo caused by DNase enzyme that breaks down DNA on the plate.
- **CNA:** Presence of beta hemolysis, indicating ruptured red blood cells.
- **Catalyze:** Bubbles form in the presence of catalyze enzyme
- **Gram Stain:** Gram negative is indicated by a red strain while gram positive is indicated by a purple stain.



Why are Gene Clusters Significant?

- Superantigens are molecules produced by bacteria that act as mitogens and bind to T-cells evoking inflammation, shock and food poisoning.
- SEG, SEI, SEM, SEN, and SEO are common genes found on pathogenicity islands, which are responsible for carrying genes that contribute to virulence factors.
- In collection, these superantigens make up a common gene cluster because of their ability to share a similar function.
- These genes can be passed onto another bacterium through horizontal gene transfer, thus various strains have the ability to adopt new traits or become genetically similar.

References and Acknowledgments

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_3).
 J. Dicks, J.D. Turnbull, J. Russell, K Parkhill, S. Alexander, Genome Sequencing of a Historic *Staphylococcus aureus* Collection Reveal New Enterotoxin Genes and Sheds Light on Evolution and Genomic Organization of This Key Virulence Gene Family. *Journal of Bact.* **203**, (2021).
 J.M King, K. Kulhankova, C.S. Stach, B.G.Vu, W. Salgado-Pabon, Phenotypes, and Virulence among *Staphylococcus aureus* USA100, USA200, USA,300, USA400 and USA600 Clonal Lineages. *mSphere*. **1**, 1-16, (2016).