Environmental Surveillance and Characterization of Staphylococcus aureus at Beaches and Rivers on Hawai‘i Island

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Introduction

Staphylococcus aureus is a ubiquitous colonizer and pathogen in both humans, domestic, and wild animals around the world.

- In Hawai‘i, Native Hawaiians and Pacific Islanders, and children are particularly susceptible to community-acquired methicillin-resistant Staphylococcus aureus (MRSA) infections.
- Previous studies have found a correlation between swimmer density and staphylococcal isolated from seawater in Hawai‘i and beachgoers with a history of seawater exposure were four times more likely to develop staphylococcal skin infections compared to beachgoers without exposure to seawater in the previous 10 days.
- Limited studies in Hawai‘i have molecularly characterized MSSA and MRSA for the carriage of antibiotic resistant and virulence genes from recreational marine, river, and sand reservoirs in Hawai‘i.
- The aim of this study was to isolate S. aureus from shoreline beach water, river water, sand, and wastewater stations on Hawai‘i Island, Hawai‘i (U.S.A) and to characterize the S. aureus isolates using whole-genome sequencing. However, the pandemic hit as the project started closing tourism to the State of Hawai‘i, reducing the beach activities of the local population. Therefore, the levels of staphylococci and presence of MSSA/MRSA measured in this study can be considered close to background levels in the environment with limited visitors during the sampling period.

Study Locations

- 361 water samples were collected between 6AM–12PM from 36 stations between July–Dec. 2020

Methods

- Isolation and quantification of staphylococci, MSSA/MRSA:
  - Water samples were processed using broth-enrichment in Quanti-Tray 2000®.
  - An aliquot of broth from up to 20 wells were plated onto mannitol salt agar and Oxacillin-resistance Selective Agar Base (ORSAB) with supplement, followed by screening for β-hemolysis.
  - Biochemical confirmation was performed using latex agglutination test kits.

Whole Genome Sequencing Assembly and Analysis

- Thirty-six (9 MRSA, 27 MSSA) S. aureus isolates were characterized using whole genome sequencing.
- Assembled contigs were uploaded to the Center for Genomic Epidemiology to assign the Staphylococcus multi-locus sequence type (ST), identify the SCCmec elements in the MRSA isolates, and determine the carriage of antibiotic resistance and virulence genes.
- Phylogenetic trees and a matrix of single-nucleotide polymorphism (SNP) differences were constructed.

Results

- 98% (354/361) of samples were positive for Staphylococcus spp.
- 26 (7.2%) samples were positive for MSSA/MRSA.
- 5 (1.6%) water samples were positive for MRSA.
- 3 (8.6%) of sand samples were positive for MRSA.
- No MSSA/MRSA was detected in wastewater.
- The 9 MRSA were ST8 (CC8) SCCmec IVa and carried 6–9 AMR genes, 16–19 virulence genes, and were closely related (0–16 SNPs).
- The 27 MSSA identified included 11 ST, eight CCs, and carried 0–5 AMR genes, and 5–19 virulence genes.

Conclusion

- The MRSA in this study are genetically closely related to the USA300 MRSA previously characterized in the Hawaiian Islands in 2011.
- MRSA was commonly detected at shoreline beach stations with visibly high counts of swimmers and beachgoers.
- This may be considered a background study due to limited human activity along the beaches.
- Future studies should examine the risk of swimming in S. aureus contaminated waters and the development of skin infections.

References:


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