Beth Israel Lahey Health
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# Identification of subclinical healthcare-associated clusters of *Staphylococcus epidermidis* in an orthopedic patient population.

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## Introduction

Prosthetic joint infections (PJIs) cause increased morbidity and mortality for patients. *Staphylococcus epidermidis (S. epidermidis)* can readily form biofilm on implanted medical devices, making this typically commensal species a common cause of PJIs[1,2]. In comparison with *Staphylococcus aureus* or Gram-negative causes of PJI, monomicrobial infections caused by *S. epidermidis* tend to manifest farther out from the original procedure and may demonstrate more subtle clinical manifestations of infection such as indolent pain, swelling, and less pronounced elevations in synovial cell count and systemic inflammatory markers[1].

It is currently thought that the majority of *S. epidermidis* infections originate from a patient's own flora and are seeded into the prosthetic joint at the time of surgery (perhaps aided by resistance or virulence determinants) or at a later time through direct inoculation or hematogenous spread[3].

## Objective

This study investigates genetic, epidemiologic, and environmental factors contributing to positive *S. epidermidis* joint cultures and PJI.

## Methods

We identified 60 *S. epidermidis* isolates from hip or knee cultures obtained between 2017-2020 in patients with one or more prior intraarticular procedures at our hospital. Whole genome sequencing and single nucleotide polymorphism (SNP) based clonality analysis was performed using the epiXactPRO® service at Day Zero Diagnostics, including species identification, in silico multi-locus sequence typing (MLST), phylogenomic analysis, along with genotypic assessment of the prevalence of specific antibiotic resistance and virulence genes. Additional epidemiologic review was performed to compare cluster and non-cluster cases.

## Results

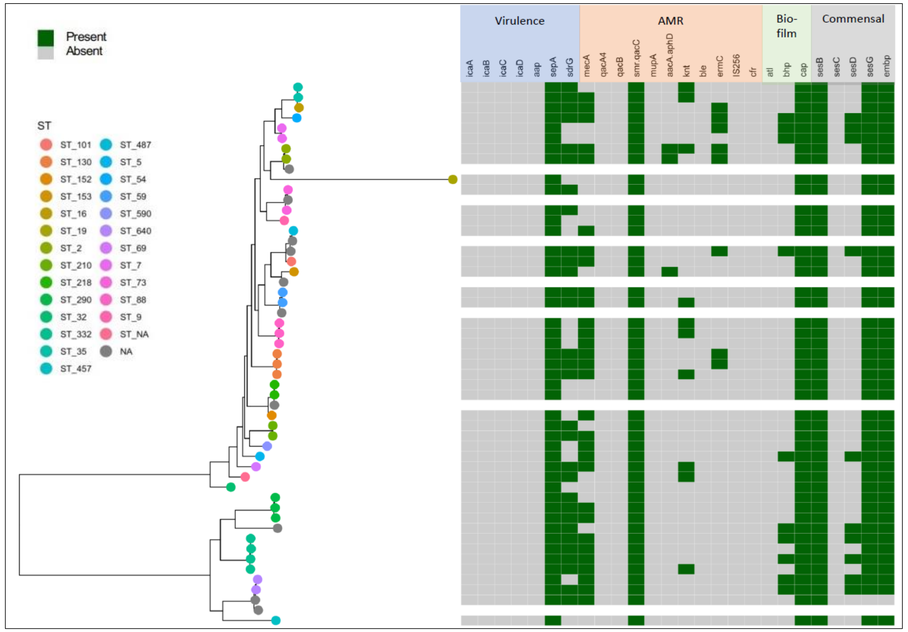
**Table 1.** Univariate table of select patient demographics, healthcare history, and infection information.

| Variable | Total | Non-Clonal Isolate | Clonal Isolate | |
|---|---|---|---|---|
| | No. (%) | No. (%) | No. (%) | P-Value |
| Total | 45 | 31 (68.9) | 14 (31.1) | . |
| Age: < 65 | 25 (55.5) | 15 (48.4) | 10 (71.4) | 0.150 |
| Age: ≥ 65 | 20 (44.5) | 16 (51.6) | 4 (28.6) | |
| Male | 35 (77.8) | 24 (77.4) | 11 (78.6) | 0.931 |
| Female | 10 (22.2) | 7 (22.6) | 3 (21.4) | |
| Hip | 17 (37.8) | 10 (32.3) | 7 (50.0) | 0.256 |
| Knee | 28 (62.2) | 21 (67.7) | 7 (50.0) | |
| Primary | 16 (39.0) | 12 (41.4) | 4 (33.3) | 0.631 |
| Revision | 25 (61.0) | 17 (58.6) | 8 (66.7) | |
| Native Joint | 4 (8.9) | 2 (6.4) | 2 (14.3) | 0.393 |
| Arthroplasty | 41 (91.1) | 29 (93.6) | 12 (85.7) | |
| Met MSIS* criteria for PJI | | | | |
| No | 18 (43.9) | 12 (41.4) | 6 (50.0) | 0.613 |
| Yes | 23 (56.1) | 17 (58.6) | 6 (50.0) | |
| Days between prior intervention and positive culture | | | | |
| < 30 (ref) | 16 (35.6) | 12 (38.7) | 4 (28.6) | . |
| 30 -119 | 15 (33.3) | 11 (35.5) | 4 (28.6) | 0.916 |
| ≥ 120 | 14 (31.1) | 8 (25.8) | 6 (42.9) | 0.305 |
| Prior surgery at an outside hospital | | | | |
| No | 20 (44.5) | 14 (45.2) | 6 (42.9) | 0.886 |
| Yes | 25 (55.5) | 17 (54.8) | 8 (57.1) | |
| Number of surgeries at this hospital prior to positive culture | | | | |
| 0 | 4 (8.9) | 2 (6.4) | 2 (14.3) | 0.418 |
| 1 (ref) | 24 (53.3) | 17 (54.8) | 7 (50.0) | . |
| ≥ 2 | 17 (37.8) | 12 (38.7) | 5 (35.7) | 0.986 |
| Number of aspirations at this hospital prior to positive culture | | | | |
| 0 | 25 (55.6) | 17 (54.8) | 8 (57.1) | 0.942 |
| 1 (ref) | 9 (20.0) | 6 (19.4) | 3 (21.4) | . |
| ≥ 2 | 11 (24.4) | 8 (25.8) | 3 (21.4) | 0.769 |
| *mecA* present** | | | | |
| No | 15 (34.9) | 11 (36.7) | 4 (30.8) | 0.709 |
| Yes | 28 (65.1) | 19 (63.3) | 9 (69.2) | |
| Resistance to Oxacillin | | | | |
| No | 18 (40.0) | 12 (38.7) | 6 (42.9) | 0.793 |
| Yes | 27 (60.0) | 19 (61.3) | 8 (57.1) | |

* MSIS: Musculoskeletal Infection Society.
** *mecC* was not present in any of the isolates.

## Results

**Figure 1.** Phylogenetic tree of *S. epidermidis* population and heatmap showing the presence/absence of specific genomic features.




## Results

**Figure 2.** SNP distance values for all pairs of samples of matching multi-locus sequence types. Only samples belonging to MLSTs with more than one sample are shown.

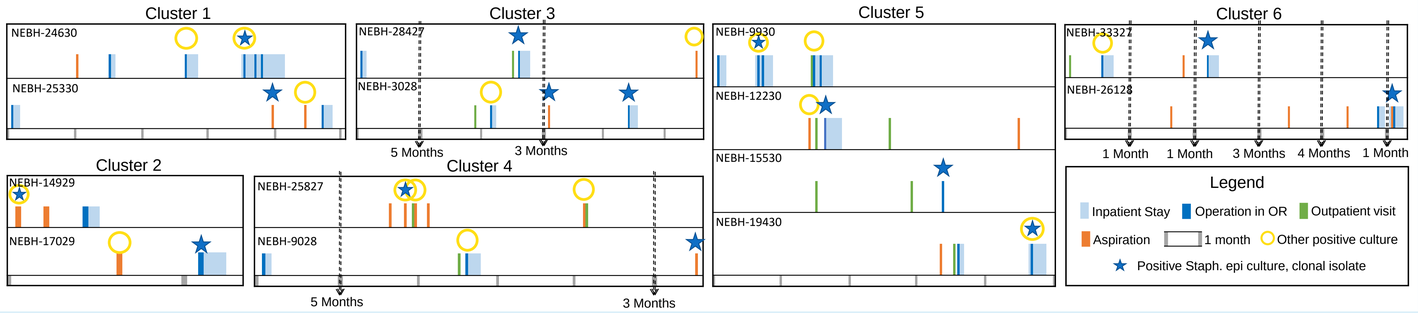
| | | | No match | ST_130 | | | ST_210 | ST_218 | ST_332 | | | ST_88 | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| isolate | MLST | Cluster | NEBH-14929 | NEBH-17029 | NEBH-17829 | NEBH-1928 | NEBH-24630 | NEBH-25330 | NEBH-28427 | NEBH-3028 | NEBH-26128 | NEBH-33327 | NEBH-9930 | NEBH-12230 | NEBH-15530 | NEBH-19430 | NEBH-9028 | NEBH-26630 | NEBH-25827 |
| NEBH-14929 | No match | C1 | | 0 | | | | | | | | | | | | | | | |
| NEBH-17029 | | C1 | | | | | | | | | | | | | | | | | |
| NEBH-17829 | | | | | | 4416 | 4513 | 4519 | | | | | | | | | | | |
| NEBH-1928 | ST_130 | | | | | | 360 | 366 | | | | | | | | | | | |
| NEBH-24630 | | C2 | | | | | | 0 | | | | | | | | | | | |
| NEBH-25330 | | C2 | | | | | | | | | | | | | | | | | |
| NEBH-28427 | ST_210 | C3 | | | | | | | | 0 | | | | | | | | | |
| NEBH-3028 | | C3 | | | | | | | | | | | | | | | | | |
| NEBH-26128 | ST_218 | C4 | | | | | | | | | | 2 | | | | | | | |
| NEBH-33327 | | C4 | | | | | | | | | | | | | | | | | |
| NEBH-9930 | | C5 | | | | | | | | | | | | 0 | 0 | 0 | | | |
| NEBH-12230 | ST_332 | C5 | | | | | | | | | | | | | 0 | 0 | | | |
| NEBH-15530 | | C5 | | | | | | | | | | | | | | 0 | | | |
| NEBH-19430 | | C5 | | | | | | | | | | | | | | | | | |
| NEBH-9028 | | C6 | | | | | | | | | | | | | | | | 382 | 7 |
| NEBH-26630 | ST_88 | | | | | | | | | | | | | | | | | | 379 |
| NEBH-25827 | | C6 | | | | | | | | | | | | | | | | | |

## Conclusion

The majority of *S. epidermidis* isolated from clinical joint samples are diverse in origin, but we identified a subset of 31% that belonged to subclinical healthcare-associated clusters. Clusters appeared to resolve spontaneously over time, suggesting benefit to routine infection control practices. Of the specific resistance and virulence genes tested, ubiquitous presence of the *smr/qacC* gene is of particular concern.

## Results

**Figure 3.** Overview of healthcare visits for patients with clonal *S. epidermidis* isolates. Each row represents one patient. The bottom row of each cluster's figure shows the time scale by month. Arrows indicate months that are not shown in the figure. Positive cultures are shown only for the specified joint where the clonal isolate was taken from. Yellow circle indicates other positive culture from the same join that was not a clonal *S. epidermidis* isolate.




## References

1. Lowy, Franklin D. "Staphylococcus Epidermidis Infections." *Annals of Internal Medicine*, vol. 99, no. 6, 1983, p. 834.

2. Post, Virginia, et al. "Comparative Genomics Study of Staphylococcus Epidermidis Isolates from Orthopedic-Device-Related Infections Correlated with Patient Outcome." *Journal of Clinical Microbiology*, vol. 55, no. 10, 2017, pp. 3089–3103.

3. Sánchez, A., et al. "Pathogenesis of Staphylococcus Epidermidis in Prosthetic Joint Infections: Can Identification of Virulence Genes Differentiate between Infecting and Commensal Strains?" *Journal of Hospital Infection*, vol. 105, no. 3, 2020, pp. 561–568.