Beth Israel Lahey Health
New England Baptist Hospital

Poster 1230

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

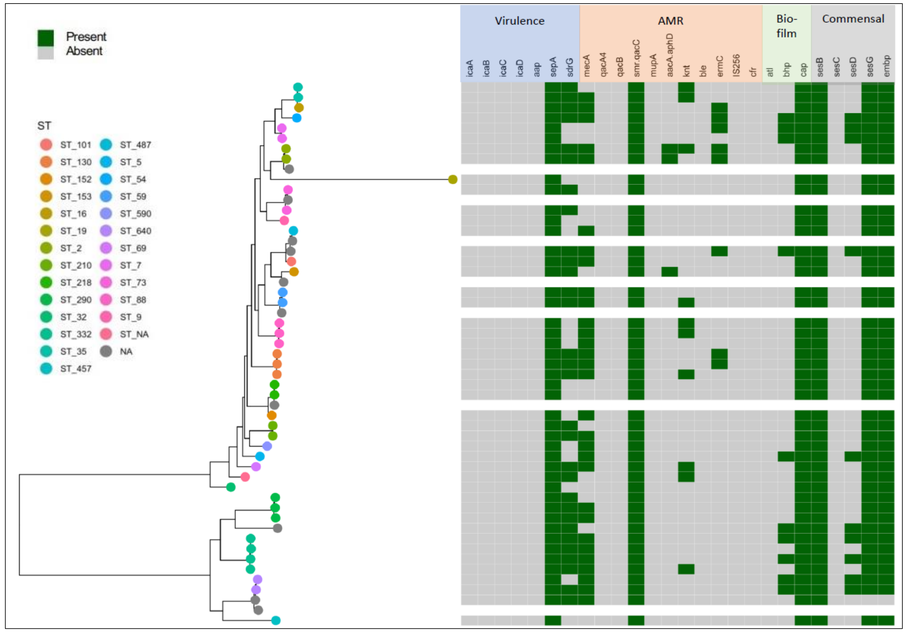
Table 1. Univariate table of select patient demographics, healthcare history, and infection information.

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.

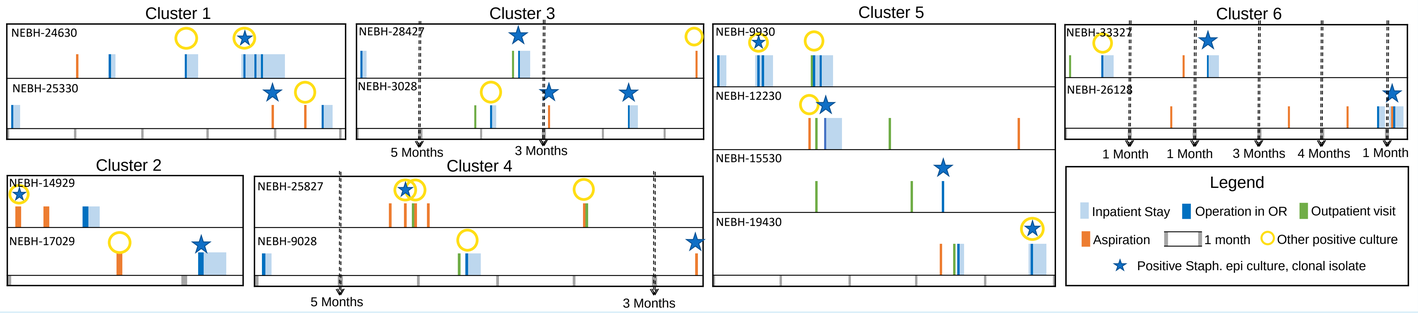
			No match	ST_130			ST_210	ST_218	ST_332			ST_88		
isolate	MLST	Cluster	NEBH-14929	NEBH-17029	NEBH-17829	NEBH-1928	NEBH-24630	NEBH-25330	NEBH-28427	NEBH-3028	NEBH-26128	NEBH-33327	NEBH-9930	NEBH-12230	NEBH-15530	NEBH-19430	NEBH-9028	NEBH-26630	NEBH-25827
NEBH-14929	No match	C1		0															
NEBH-17029		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

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