A National Analysis of Organism Variation by Race and Sex Among Patients Undergoing Revision Arthroplasty for Periprosthetic Joint Infection

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INTRODUCTION: Periprosthetic joint infection (PJI) is a highly morbid complication after total joint arthroplasty (TJA). While demographic factors have been associated with differential outcomes following primary TJA, demographic-specific microbial profiles among patients undergoing revision arthroplasty for PJI remains underexplored. Here we sought to characterize the microbial patterns of infecting organisms among PJI patients by race and sex.

METHODS: The Premier Healthcare Database was retrospectively queried from 2016-2023 for patients aged ≥18 years who underwent antibiotic spacer placement for a hip or knee PJI. Microbiology data was extracted from synovial and tissue cultures obtained during the hospital admission. The microbiological profiles were compared with respect to patient race via analysis of variance testing. A race-sex subanalysis was then conducted via chi-squared testing. A p-value <0.05 was considered significant.

RESULTS: In total, 9,014 patients undergoing antibiotic spacer placement for PJI with microbiology data were identified. Data was most commonly obtained from urban (89.7%) teaching (63.5%) hospitals. Significant differences in microbial isolates across racial designations was observed (p=0.001). White males were significantly more likely to develop PJI with methicillin-sensitive Staphylococcus aureus (MSSA) than Black patients (20.3% vs. 14.5%, p<0.001). Conversely, Black males demonstrated significantly higher rates of PJI with methicillin-resistant Staphylococcus aureus (MRSA) compared to White patients (15.1% vs. 10.4%, p=0.003). Black patients were also more likely to develop PJI caused by gram-negative enteric organisms than white patients (10.2% vs. 7.7%, p=0.01).

DISCUSSION AND CONCLUSION: MRSA and gram-negative infections were more common among Black patients with PJIs compared to White patients. These data are critical in addressing potential sources of health outcome inequality in patients undergoing PJI-related care and may be used to better guide patient-specific treatment regimens.

Table 1. Causative Organisms in Periprosthetic Joint Infection by Race

Race/Ethnicity	Asian	%	Black	%	Other	%	White	%	Hispanic	%	P-value
MSSA	26	26.26%	120	14.55%	68	18.63%	1,477	18.04%	47	16.91%	
MRSA	13	13.13%	120	14.55%	53	14.52%	853	10.42%	26	9.35%	
e-negative stap	4	4.04%	41	4.97%	16	4.38%	483	5.90%	11	3.96%	
Enterococcus sp.	1	1.01%	24	2.91%	7	1.92%	271	3.31%	7	2.52%	
Staphylococcus sp. other	4	4.04%	21	2.55%	16	4.38%	432	5.28%	19	6.83%	
Streptococcus sp. other	4	4.04%	64	7.76%	25	6.85%	665	8.12%	20	7.19%	
Fungal sp.	1	1.01%	28	3.39%	12	3.29%	300	3.66%	9	3.24%	
Gram-negative enterics	8	8.08%	84	10.18%	33	9.04%	627	7.66%	25	8.99%	P=0.001
C. acnes	1	1.01%	6	0.73%	1	0.27%	112	1.37%	3	1.08%	
Pseudomonas sp.	6	6.06%	23	2.79%	8	2.19%	216	2.64%	11	3.96%	
VRE	0	0.00%	1	0.12%	0	0.00%	15	0.18%	1	0.36%	
Polymicrobial	22	22.22%	193	23.39%	86	23.56%	1,899	23.19%	65	23.38%	
Clostridium sp	0	0.00%	6	0.73%	2	0.55%	14	0.17%	0	0.00%	
Corynebacterium sp.	2	2.02%	11	1.33%	3	0.82%	107	1.31%	8	2.88%	
Other	7	7.07%	83	10.06%	35	9.59%	718	8.77%	26	9.35%	

Table 2. Subanalysis of Causative Organisms in Periprosthetic Joint Infection by White versus Black race and Sex

	White Male		White Female		Black Male		Black Female	
	N	%	N	%	N	%	N	%
MSSA	894	20.32%	583	15.39%	64	15.80%	56	13.33%
MRSA	421	9.57%	432	11.40%	61	15.06%	59	14.05%
Coagulase-negative staphylococci	270	6.14%	213	5.62%	19	4.69%	22	5.24%
Staphylococcus sp. other	288	6.55%	144	3.80%	8	1.98%	13	3.10%
Streptococcus sp. other	384	8.73%	281	7.42%	29	7.16%	35	8.33%
Fungal sp.	150	3.41%	150	3.96%	19	4.69%	9	2.14%
Gram-negative enterics	302	6.86%	325	8.58%	42	10.37%	42	10.00%
Enterococcus sp.	148	3.36%	123	3.25%	14	3.46%	10	2.38%
C. acnes	73	1.66%	39	1.03%	1	0.25%	5	1.19%
Pseudomonas sp.	105	2.39%	111	2.93%	12	2.96%	11	2.62%
VRE	3	0.07%	12	0.32%	0	0.00%	1	0.24%
Polymicrobial	1,002	22.77%	897	23.67%	91	22.47%	102	24.29%
Clostridium sp	6	0.14%	8	0.21%	3	0.74%	3	0.71%
Corynebacterium sp.	35	0.80%	72	1.90%	6	1.48%	5	1.19%
Other	319	7.25%	399	10.53%	36	8.89%	47	11.19%