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Case Report

Coagulase Negative Staphylococcal Isolates from Prosthetic Knee Infections Show Diverse Speciation and a High Rate of Antibiotic Resistance

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ABSTRACT

The incidence of infection associated with primary total knee arthroplasty (TKA) is up to 2.5% with \$1.62 billion estimated in system costs. Adverse outcomes depend on bacterial species with methicillin resistant strains carrying the highest burden. Prior research has focused on *Staphylococcus aureus*. Our study identifies the species and resistance patterns of coagulase negative *Staphylococcus* species that infect knee prostheses. TKA infections positive for coagulase negative *Staphylococcal* species subsequently treated by four joint surgeons from 2015-2019 were included. Matrix-assisted laser desorption ionization (MALDI) time of flight mass spectrometry was used and scores greater than 2.00 were considered to identify unique species. There were 68 TKA infections treated during the study period and 29 (42%) cultured a coagulase negative *Staphylococcal* species. Of these, 16 (55%) were *S. epidermidis*, 6 (21%) were *S. lugdunensis*, 5 (17%) were *S. capitus*, 1(3%) was *S. warneri* and 1 (3%) was *S. haemolyticus*. Further, 14 (48%) were positive for the mecA gene conferring resistance to methicillin. All species were identified by MALDI with an average score of 2.12 ± 0.13. Coagulase negative *Staphylococcal* species from TKA infections showed a range of species which could suggest multiple etiologies for sustaining an infection . While the mecA gene was present more commonly than reported averages, it was present in strains with resistance to many antibiotics not just beta lactams.

Keywords: Prosthetic joint infection, Antibiotic resistance

Introduction

Prosthetic joint infection (PJI) is a devastatingly complication after total knee arthroplasty (TKA). The incidence of PJI after primary TKA is estimated up to 2.5% with an overall cost to the health system estimated at \$566 million in 2009 rising to \$1.62 billion by 2020 [1,2]. The specific subtypes implicated in PJI are extensively discussed in a review by Tande and Patel with *Staphylococcus* species accounting for 62% of all infections across an aggregated 2,435 joints [3]. Methicillinresistant *Staphylococcus aureus* (MRSA) rates vary widely having been quoted from 23% to 61% [4-7]. The diversity and resistance patterns of infectious agents together with predisposing medical comorbidities create an adverse environment for patient outcomes from shorter infection-free periods, more revision surgeries, longer hospital stays, and higher costs [8-11].

However, the rate of adverse outcomes depends on bacterial subtype. A recent study of 149 infections of hip prostheses demonstrated *Pseudomonas*, *Proteus*, and MRSA infections were each correlated with lower infection-free rates, additional surgeries, and longer hospital stays compared to PJI with other organisms [12]. These findings have been corroborated by other studies investigating multi-drug resistant (MDR) PJI with failure rates from 10% to 33% [5,13]. The rate of PJI with MDR strains are less prevalent than susceptible strains in nearly all studies with no consensus on whether the rates are rising [14,15]. To better quantify these differences, a more detailed molecular understanding is necessary.

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Matrix-assisted laser desorption ionization time of flight (MALDI-TOF) mass spectrometry provides increased specificity in organism detection through analysis of unique molecular signatures [16]. This has improved diagnostic sensitivity and led to new tools for species determinations even in approximately 60% of infections with normal erythrocyte sedimentation rate and C-reactive protein [17]. It has emerged as a cost effective, highly accurate alternative to polymerase chain reaction based strain identification and demonstrated accuracy above 93% to 99% in analysis of coagulase negative *Staphylococcal* species [18-23]. To our knowledge, there is no study of MALDI-TOF mass spectrometry molecular signatures for PJI in resistant bacterial strains. This study was designed to elucidate whether there were molecular commonalities between coagulase negative *Staphylococcal* species strains in the service of understanding the pathogenesis of PJI.

Methods

Following institutional review board approval, a retrospective chart review was undertaken for all primary periprosthetic knee infections treated by four knee arthroplasty surgeons (DFA, JIH, SBG, WJM) at a single institution from 2015-2019. All infections met Musculoskeletal Infection Society criteria initially with either a draining sinus tract or combination of minor criteria as delineated in Parvizi, et al. [24]. They also required confirmatory culture and sensitivity data from revision surgery (either synovial fluid or tissue) with ≥ 2 samples positive for the same organism to avoid the issue of contamination. Patients were included with coagulase negative *Staphylococcal* species grown in traditional fashion. Patients with chronic infections or culture negative infections were excluded.

MALDI-TOF mass spectrometry was performed on overnight grown bacterial cultures. Individual colonies were picked with the sterile toothpick from nonselective sheep blood agar plates and thinly smeared directly on polished steel target. Smeared target spots were overlaid with 1 μ l of a MALDI-TOF mass spectrometry matrix (portioned solution of α -cyano-4-hydroxycinnamic acid, Bruker Daltonics, Bremen, Germany with 50% acetonitrile, 47.5% mass spectrometry grade water and 2.5% trifluoroacetic acid, Sigma-Aldrich, Germany) and allowed to dry at room temperature. Mass spectra, ranging from 2,000 to 20,000 Da, were acquired using Microflex LT Biotyper (Bruker Daltonics, Bremen, Germany) in a linear positive mode at laser frequency of 30 Hz. The rest of detection parameters were set by the manufacturer. Instrument calibration was performed before spectra acquisition using freshly made bacterial test standard (BTS; Bruker Daltonics, Bremen, Germany). Data was analyzed using the Bruker Biotyper 3.4 software and MBT Compass Library – RUO 7311 (Bruker Daltonics, Bremen, Germany). Species level identification was determined by using an in-house validated score criteria, where scores from 1.800 to 3.000 indicate species level identification, sores from 1.700 to 1.799 indicate genus level identification, scores -1.699 indicate no reliable identification. Resistance was determined by diffusion disc method and the mecA testing was performed by nucleic acid amplificationin the traditional fashion on the same isolates.

Categorical variables are expressed as number and percent while continuous variables are expressed as mean and standard deviation. Statistics were computed in STATA (StataCorp College Station, TX). Regressions were performed with statistical significance determined at p<0.05. When relevant, 95% confidence intervals (CI) are reported. For binary variables, chi-square proportion testing or logistic regressions were used reporting odds ratios (OR) while for count variables, Poisson regression was used reporting incidence rate ratios (IRR).

Results

There were 68 TKA infections treated during the study period and 29 (42%) cultured coagulase negative *Staphylococcal* species. Of these, 16 (55%) were *S. epidermidis*, 6 (21%) were *S. lugdunensis*, 5 (17%) were *S. capitus*, 1 (3%) was *S. warneri* and 1 (3%) was *S. haemolyticus*. Further, 14 (48%) were positive for the mecA gene conferring resistance to methicillin and all of these were *S. epidermidis* (Table 1). All species were identified by MALDI-TOF mass spectrometry speciation with a mean score of 2.12 ± 0.13 .

The patients had a mean age of 67.0 \pm 7.9 years at the time of revision operation; 17 (59%) were male and 12 (41%) were female. Their mean body mass index was 34.0 \pm 7.3 kg/m². The mean time from primary arthroplasty to infection identification was

Table 1: Antibiotic resistance data by species subtype following disc diffusion resistance testing. Per laboratory protocol, not all isolates were tested

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against an antibiotics.					
Antibiotic	S. epidermidis	S. lugdunensis	S. warneri	S. capitus	S. haemolyticus
Penicillin	16 (100%)	3 (100%)	1 (100%)	4 (100%)	1 (100%)
Moxifloxacin	10 (77%)				
Erythromycin	11 (69%)	3 (50%)	1 (100%)	1 (20%)	0 (0%)
Levofloxacin	12 (80%)		0 (0%)		
Oxacillin	15 (94%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Clindamycin	8 (50%)	3 (50%)	0 (0%)	1 (20%)	0 (0%)
Trimethoprim-Sulfamethoxazole	10 (63%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Gentamicin	7 (44%)	1 (17%)	0 (0%)	0 (0%)	0 (0%)
Tetracycline	2 (13%)				
Rifampin	1 (7%)		0 (0%)		
Daptomycin	0 (05%)				
Linezolid	0 (0%)				
Vancomycin	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)



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Table 2: Chi-squared testing of mecA positivity predicting resistance to other antibiotics. Penicillin, moxifloxacin, daptomycin, vancomycin, and linezolid were excluded because in our culture data they did not vary among CNS species.

Antibiotic	Chi-squared Statistic	p-value
Oxacillin	25.3	<0.001*
Trimethoprim- Sulfamethoxazole	10.6	0.001*
Gentamicin	3.2	0.075
Erythromycin	0.9	0.340
Clindamycin	0.8	0.362
Levofloxacin	0.8	0.383
Tetracycline	0.2	0.685
Rifampin	0.2	0.696

approximately 3.6 \pm 4.7 years (range 0.1 – 18.8) and only 2 cases (7%) were documented within 90 days of the index procedure. Charlson comorbidity index (CCI) was calculated for each patient (mean 3.4 \pm 2.0, range 1-9).

MecA positivity correlated but did not significantly predict resistance to other antibiotic agents except trimethoprimsulfamethoxazole and oxacillin (Table 2). Regarding demographic predictors, mecA positivity also showed a trend toward more complicated patients (increased CCI) but was not significant (OR 1.23, CI 0.82-1.83, p=0.314). Current or past smoking history was significantly correlated with less mecA positivity (OR 0.20, CI 0.05-0.94, p=0.041). Time to infection did not correlate with mecA positivity (OR 1.15, CI 0.95-1.39 p=0.161), however it did correlate significantly with *S. epidermidis* in so far as later presenting infections were more likely to be infection with *S. epidermidis* than any other isolate (IRR 2.68, CI 1.70-4.21, p<0.001).

Discussion

PJI continues to be a morbid complication of TKA. Of the infections we analyzed further, coagulase negative Staphylococcal speciesdefined an important subgroup. Coagulase negative Staphylococcal species comprises a ubiquitous set of pathogens that demonstrate a range of clinical presentations from acute to chronic. In this series of TKA-PJI, all species were uniquely identified with MALDI species level specificity. S. epidermidis comprised most of the specific cultures. This is consistent with demonstrated epidemiologic incidence of indolent presentations [25]. S. epidermidis produces adhesive proteins specific for fibrinogen that mediate attachment to areas of scar formation facilitating localization to surgical wound beds. Further, it is known to produce polysaccharide intercellular adhesin when under hypoxic, osmotic, or antibiotic stress that in conjunction with implant hydrophobicity stimulates the production of biofilm [26]. A full review of biofilm and other pathogenic behavior of coagulase negative Staphylococcal speciesis beyond the scope of this article, but is well summarized elsewhere [27].

Unlike *S. epidermidis* which can be considered a contaminant (though not in the setting of clinically meaningful PJI), *S. lugdunensis* and *S. warneri* are always considered pathogenic. [28]. *S. lugdunesis* is classically penicillin-sensitive but in our cohort all strains were penicillin-resistant [28]. Recently, it was shown that *S. lugdunensis* PJI leads to increased clinical symptoms than either *S. epidermidis* or *S. aureus* [28]. This speaks to varying acuity of chronic infection

exacerbations as well as the pathogenicity of *S. lugdunensis* in particular. *S. warneri* is isolated more rarely and is known to engage in biofilm production [29].

The results for mecA gene positivity in 48% of the cohort is consistent with if not slightly higher than other studies. MecA positivity was also correlated with resistance to many antibiotics not just cell wall synthesis inhibitors. In our cohort, 88% of *S. epidermidis* infections were resistant to gentamicin (of those resistant all were positive for mecA). Aminoglycoside resistance correlates with a "not cured" clinical outcome for coagulase negative *Staphylococcal* species-PJI – from testing at 2 year follow up, patients with "not cured" clinical status had ongoing treatment for PJI of any type medical or surgical [30]. To this end, it is interesting that all mecA positive strains were *S. epidermidis* and that smoking was both protective against mecA positive infection and associated with an earlier time to infection. It is well known that smoking increases the risk of PJI, but our data suggests smoking increases susceptibility to less virulent organisms at an earlier time point.

The varying species of coagulase negative *Staphylococcal* species in our isolates suggest multiple organism strains have the capability to generate clinical infection predicated on biofilm formation and MDR status. However, many infections are considered to be polymicrobial [31]. Questions therefore remain concerning the specific molecular factors that permit PJI, how the infectious agent(s) change over time, and what specific treatments should be employed to target those mechanisms [32]. This will be particularly relevant as new data regarding mechanisms like quorum sensing emerge with targeted quorum inhibitors and bacteriophage therapy [33].

In addition to the limited number of patients included, this study was limited by MALDI-TOF requiring species that result in a positive culture. This study also relied on traditional methods for determining antibiotic resistance and mecA gene positivity.

Conclusion

MALDI-TOF identified a range of coagulase negative *Staphylococcal* species that had wide and varied antibiotic resistance pattern. Interestingly, a history of smoking was protective against mecA positivity.

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Author Contribution Statement

ARB harvested data, ran analysis, and drafted the manuscript. NB contributed to study design and bacterial analysis. IB ran the MALDI experiment. SBG, JIH, and WJM provided patient cases SBG, JIH, WJM, RM, and DFA reviewed the manuscript. DFA was the senior design author RM and DFA coordinated the project's completion.

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