

Microbiome Assessment in Patients Undergoing Removal of Hardware

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INTRODUCTION:

Next-generation DNA sequencing (NGS) technology is increasingly being used to identify bacterial cultures and assess their impact on patients undergoing orthopaedic procedures. While NGS has previously been applied in orthopaedics, its use in foot and ankle research remains limited. The purpose of this study is to utilize NGS to determine whether a distinct microbiome is present on hardware in patients undergoing removal of hardware in the foot and ankle.

METHODS:

Thirty-four patients undergoing elective foot and ankle hardware removal surgery were prospectively recruited between 2020 and 2023 by one of two fellowship-trained foot and ankle surgeons. Patients with a preoperative diagnosis of infection were excluded. Removed hardware was collected intraoperatively and submitted to a CLIA-certified molecular diagnostics laboratory for analysis. Data collected included preoperative demographics, comorbidities, surgical indication, postoperative complications, readmissions, and reoperations. Preoperative patient-reported outcome measures were also obtained using the Foot and Ankle Outcomes Score (FAOS), assessing all subscales. The primary indications for surgery were painful orthopedic hardware (64.6%) arthritis (20.4%), nonunion (5.8%), hindfoot varus (2.9%), bunion (2.9%), and crossover toe deformity (2.9%). Concomitant procedures varied and commonly included calcaneal osteotomies, subtalar arthrodesis, tenolysis, bone grafting, and capsulotomies. The cohort was predominantly female (67.6%), with a mean age of 53.2 years (range: 18–78). The mean follow-up duration in the current cohort was 474.26 days (range: 18-1562).

RESULTS:

Of the 34 samples sent for NGS, 5 (14.7%) were positive, indicating the presence of nine bacterial species, while the remaining 29 samples (85.3%) were negative for any bacterial growth. Among the identified organisms, the most common genera were *Staphylococcus* (4 isolates, 44.4%) and *Corynebacterium* (2 isolates, 22.2%). *Cutibacterium acnes* was detected in only one sample. There was no significant association between bacterial presence and hardware removal due to pain ($p = 0.617$). Overall complication (8.8%) and reoperation (8.8%) rates were low. Overall infection rates were also low (3/34, 8.8%), and there was no significant association found between the presence of bacteria and occurrence of superficial (2/34, 5.9%) and/or deep infections (1/34, 2.9%). Patient demographics and postoperative complications were not significantly associated with the presence of bacteria on NGS. The presence of bacteria on NGS was also not associated with worse preoperative scores across all subscales of FAOS.

DISCUSSION AND CONCLUSION:

NGS identified bacterial DNA in 14.7% of foot and ankle hardware removal cases, with *Staphylococcus* being the most commonly detected genus. This rate of positive NGS culture is similar to prior literature on normal ankle microbiome flora, suggesting that deep hardware is colonized with bacteria at a similar rate to the normal flora of the ankle joint. Additionally, we found no statistically significant association between bacterial presence and postoperative superficial or deep infection rates. These results suggest that positive NGS samples in patients without a clear infection may not be pathologic.