vertebral osteomyelitis due to Candida is still rare and can be difficult to diagnosis and treat. We evaluated the incidence of vertebral osteomyelitis due to Candida species at our facility to try to identify risk factors and determine outcomes.

Methods. We used our electronic record databases to search for patients with a diagnosis of osteomyelitis, and a positive fungal culture. From 2006 to 2018 our hospital treated 14 cases of native vertebral osteomyelitis and 2 cases of proven Candida vertebral osteomyelitis.

Results. Candida albicans was the most frequently isolated organism, being cultured in 10/14 (71.4%) patients, followed by C. tropicalis (2/14), C. krusei (1/14), and C. parapsilosis (1/14). The two most common risk factors for infection were injection drug use (50%) and prior antibiotic use (50%). Almost all patients were treated (90%) for cefepime followed by fluconazole. Ten patients (71.4%) required surgery. Short-term outcomes were favorable with no deaths.

Conclusion. The incidence of vertebral osteomyelitis due to Candida may be increasing. In our state, injection drug use seems to be a factor in the increase of infection. We have seen a rise in injection drug use as prescription narcotics are becoming more difficult to obtain. Physicians must have a high index of suspicion for fungal disease when treating osteomyelitis in patients with these risk factors. Short-term outcomes seem favorable, but further studies are needed to evaluate long-term outcomes and to determine optimal management.

Disclosures. All authors: No reported disclosures.

301. The Use of Multiplex Touchdown PCR to Genotype Catibacterium (Propionibacterium) acnes Isolated from Periprosthetic Shoulder Infections

Penny H. BSC, Stuart A. MC, Isbel S. PhD, Bay L. MD, Nada M. MD, 1; University of Ottawa, Ottawa, ON, Canada, 2Pathology, Ottawa Hospital, Ottawa, ON, Canada, 3Pathology, University of Ottawa, Ottawa, ON, Canada, 4The Ottawa Hospital, University of Ottawa, Ottawa, ON, Canada, Infectious Diseases, Ottawa, ON, Canada

Session: 54. Bone and Joint Infections
Thursday, October 4, 2018: 12:30 PM

Background. As biographic surveys of the human skin microbiome have shown that C. acnes is a major component of the residual microflora, the organism is frequently isolated from synovial tissue and joint aspirates obtained from patients with suspected periprosthetic shoulder infections. We hypothesized that multilocus sequence typing (MLST) applying a prior validated rapid high-throughput multiplex PCR protocol would provide useful Clusters associated with periprosthetic infections compared with commensal strains.

Methods. C. acnes collected between 2015 and 2017 were correlated with the presence or absence of infection in a detailed retrospective chart review. To determine the C. acnes genotype each patient was cultured and the joint aspirate samples were examined. Intravenous (IV) perfusion is the standard route of administration. The Subcutaneous (SC) route may present an interesting alternative in case of outpatient care or when IV perfusion is not possible. The aim of this study was to demonstrate that the SC route of administration provides effective serum concentrations in the treatment of BJI without route-specific side effects.

Results. Of the 94 patients collected, 14 (14.9%) were from patients with PJI, 10 (10.6%) from patients with SJNFBSA, 48 (51.1%) were from patients with NFBSA, while 12 (12.8%) were from patients with SJNFBSA, 48 (51.1%) were from patients with NFBSA, while 12 (12.8%) were from patients with NFBSA. No genetic difference was present in the lineage of strains not causing infection. The assignment of a diagnosis of prosthetic joint infection (PJI) conformed to the definition recommended by the IDSA Clinical Practice Guidelines of PJI.

Conclusion. Our results mirror those from a previous investigation using a less robust four gene MLST PCR based scheme that showed a lack of a phylogenetic association with shoulder PJI. Our test identified a unique phylogen group composition of the circulating C. acnes sequence types in our community.

Disclosures. All authors: No reported disclosures.

302. Role of inflammatory Markers in Diagnosing Diabetic Foot Infection: A Meta-Analysis

Aneela Majeed, MD, 1; Adeela Mushag, MD, 2; Ahmad Itikhar, MD, 2; Umar Zaidi, MD, 3; Fnu Sagar, MD, 4; Mohammad Usman, MD, 5; Muhammad Fraz, MD and Mayer Al-Mahdawi, MD, 1; Department of Orthopaedics, Division of Infectious Diseases, 2Arizona College of Medicine, Tucson, Arizona, 3University of Arizona, Tucson, Arizona, 4Infection Prevention and Control-Bismarck, Mayor College of Medicine, Houston, Texas

Session: 54. Bone and Joint Infections
Thursday, October 4, 2018: 12:30 PM

Background. Diabetic foot ulcers (DFUs) cause significant morbidity and put great economic burden on patient and healthcare facilities. Infection is the main driving force behind admissions related to DFU. Culture of soft tissue or bone is available in diagnosing infection but it is time consuming. Inflammatory markers including erythrocyte sedimentation rate (ESR), C-reactive protein (CRP), and procalcitonin (PCT) are rapid, simple, and inexpensive laboratory tests that can aid in early diagnosis of diabetic foot infection (DFI) and monitor response to treatment. We did a meta-analysis to compare diagnostic performance of inflammatory markers for detecting DFI.

Methods. We searched PubMed, Embase, and Cochrane databases from their inception to December 2017. This meta-analysis was performed according to PRISMA guidelines. We included studies based on following inclusion criteria: (1) at least one of the four biomarkers (ESR, CRP, PCT) were isolated from biological markers including inflammatory markers as targets for detecting DFI.

Results. We searched PubMed, Embase, and Cochrane databases from their inception to December 2017. This meta-analysis was performed according to PRISMA guidelines. We included studies based on following inclusion criteria: (1) at least one of the four biomarkers (ESR, CRP, PCT) were isolated from biological markers including inflammatory markers as targets for detecting DFI, (2) sensitivity or specificity were measured as outcomes; and (3) sufficient data were available to construct 2 x 2 contingency table. We used bivariate random effect regression model to pool the sensitivity and specificity of the targeted biomarkers.

Conclusion. Our results mirror those from a previous investigation using a less robust four gene MLST PCR based scheme that showed a lack of a phylogenetic association with shoulder PJI. Our test identified a unique phylogen group composition of the circulating C. acnes sequence types in our community.

Disclosures. All authors: No reported disclosures.