Septic Arthritis of a Native Knee Joint Due to Corynebacterium striatum

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Journal Title: Journal of Clinical Microbiology
Volume: Volume 52, Number 5
Publisher: American Society for Microbiology | 2014-05-01, Pages 1786-1788
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.1128/JCM.02641-13
Permanent URL: https://pid.emory.edu/ark:/25593/s5hxd

Final published version: http://dx.doi.org/10.1128/JCM.02641-13

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Accessed December 3, 2019 8:10 PM EST
CASE REPORT

An 84-year-old male with a past medical history of poorly controlled diabetes, coronary artery disease, hypertension, deep vein thrombosis, and anticoagulant use presented with right knee pain and fever. A week prior to admission, he had fallen while trying to climb onto a bus.

Four days prior to admission, a right knee arthrocentesis at his primary care doctor’s office, by report, revealed grossly bloody fluid. This was followed by worsening right knee pain upon weight bearing and increasing right knee swelling followed by malaise and subjective fever with chills.

On presentation to the emergency department (ED), he was febrile to 38.5°C. The patient’s right lower extremity was edematous, and examination of the right knee revealed minimal erythema, tenderness to palpation, effusion, and a decreased range of motion secondary to pain. In the ED, his knee was aspirated under sterile conditions and yielded 35 ml of straw-colored cloudy fluid. Analysis of the fluid revealed a few calcium pyrophosphate crystals and a white blood cell count elevated to 52,500/µl with 80% neutrophils. A Gram stain of the specimen was negative for organisms. He was empirically started on vancomycin and cefepime and admitted for arthroscopic lavage of the septic knee. He underwent knee lavage in the operating room (OR) 24 h after admission. Two specimens taken from the arthrocentesis procedure in the ED and two from the arthroscopic knee washout in the OR recovered pure cultures of catalase-positive, cream-colored organisms. Gram stain of all four isolates revealed pleomorphic, palisading Gram-positive rods.

The isolates were initially identified as Corynebacterium striatum with >99% probability using the RapID CB Plus phenotypic system (Remel, Lenexa, KS) (1). Subsequently, the isolates were analyzed by matrix-assisted laser desorption–ionization time of flight mass spectrometry using the recently U.S. Food and Drug Administration (FDA)-cleared Vitek MS v2.0 system (bioMérieux, Durham, NC) (2) and were identified as C. striatum with a confidence level of 99.9%. Finally, for one of the isolates, fragments of the 16S rRNA gene (3) and the rpoB gene (4) were amplified using the PCR and the PCR products sequenced. However, although they are highly accurate for bacterial identification, neither of these sequence-based methodologies is cleared by the FDA for bacterial identification and both remain restricted to research use only.

The resultant 16S rRNA gene sequence data were analyzed using SmartGene IDNS (Integrated Database Network System) software (SmartGene GmbH, Lausanne, Switzerland) (5), and the results revealed that the best match was C. xerosis type strain ATCC 6940, with 99.6% similarity (470 bp/472 bp), while the next-best match was C. xerosis, with 98.9% similarity (467 bp/472 bp). According to the standards adopted by the Clinical Laboratories Standards Institute (CLSI), the 16S rRNA gene sequence analysis satisfied genus-level but not species-level identification.

We report a case of septic arthritis of a native knee joint due to Corynebacterium striatum, a rare and unusual cause of septic arthritis of native joints. The isolate was identified by a combination of phenotypic, mass spectrometric, and nucleic acid-based assays and exhibited high-level resistance to most antimicrobials.

Corynebacterium striatum

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Received 23 September 2013 Returned for modification 13 November 2013 Accepted 11 February 2014 Published ahead of print 26 February 2014

Editor: A. M. Caliendo

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the offending *C. striatum* isolate gained access to the patient’s circulation either during the episode of pneumonia or through open venous stasis ulcers.

There are significant similarities between our case and the aforementioned case, namely, the blunt trauma of the knee prior to presentation and the underlying immunosuppression associated with the patients. However, rather than interpreting ours as a second case of spontaneous infection of a joint due to *C. striatum*, we believe that iatrogenic inoculation of the joint with skin-associated *C. striatum* during the first knee aspiration likely resulted in the infection described in our case.

The identification of *Corynebacterium* species to the species level is often difficult or unreliable if phenotypic testing is the sole identification method utilized (8, 9). Therefore, to confirm the phenotypic identification of *C. striatum*, we utilized mass-spectrometric and nucleic acid-based methodologies, with both methodologies convincingly identifying the isolates as *C. striatum*. Mass spectrometric identification of microbes, including *Corynebacterium* species, is revolutionizing the fields of clinical microbiology and infectious diseases and has the ability to rapidly identify *Corynebacterium* species to a level comparable to that achievable with the more labor-, time-, and cost-intensive sequence-based methods (16).

Antimicrobial susceptibility testing of *Corynebacterium* species should be performed if the isolate is considered clinically relevant, as antimicrobial susceptibility is not predictable on the basis of genus- and species-level identification (8). This is partially due to the fact that, historically, many laboratories were unable to reliably identify coryneform bacteria to the species level. Further, *Corynebacterium* species, especially *C. striatum*, demonstrating multidrug resistance have been recovered from clinical specimens, with isolates displaying resistance to several classes of antimicrobials, including beta-lactams, fluoroquinolones, macrolides, lincosamides, and tetracyclines. Typically, these multidrug-resistant isolates are susceptible only to vancomycin, daptomycin, and linezolid (8, 14). The isolates obtained from our patient were multidrug resistant; of all the antimicrobials assayed, vancomycin was the only antimicrobial that tested as susceptible.

This case further highlights the role of *C. striatum* in native joint infections. Additionally, it emphasizes the importance of identifying *Corynebacterium* species isolates recovered in multiple cultures to the species level and performing antimicrobial susceptibility testing due to the increased frequency of multidrug resistance in this genus.

**ACKNOWLEDGMENTS**

A.B. has received consultancy fees from Cubist Pharmaceuticals and Forest Pharmaceuticals. C.-A.D.B. has received research funding from bioMérieux and consultancy fees from Thermo Fisher Scientific. C.C.G. has received research funding and consultancy fees from bioMérieux. The other authors declare that we have no conflicts of interest.

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