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A case of prosthetic joint septic arthritis caused by *Gordonia jacobaea*

Dear editor,

A 74-year-old woman was admitted to the hospital for septic arthritis suspicion with fever (39 °C) and severe knee pain for 1 day. Her medical history included rheumatoid arthritis and Crohn's disease with previous ileocecal resection. She had been taking long-term prednisolone, adalimumab and methotrexate. She had right knee replacement in 2017, and central venous catheter (CVC) placement three months ago for vitaminic supplementation. On examination, she presented an inflammatory right knee. The knee radiography showed joint effusion without unsealing of the prothesis. Knee joint fluid and blood from CVC and peripheral venipuncture cultures were taken at the admission prior to antibiotherapy. Cytologic analysis of the joint fluid showed 1,300,000 leukocytes/mm^3 with 88% neutrophils; neither microorganism nor crystals were seen on Gram stain or at polarized microscopy. Investigations revealed hyperleukocytosis (9.27 × 10^9/liter), the C-reactive protein was 40.5 mg/L. The blood cultures drawn from the CVC and venipuncture were flagged as positive by the VIRTUO® microbial detection system (bioMérieux) within 14.2 and 29.2 h, respectively, in aerobic condition only. Branched Gram-positive rods suggesting *Corynebacterium*, *Actinomyces* or *Nocardia* species were observed on Gram-stain. Although these results were first interpreted as contamination, they prompted the initiation of intravenous ceftriaxone and linezolid administration on day 3 of admission. The CVC was suspected to be the source of the bloodstream infection and was removed. Small numbers of opaque, rough, orange, dry and non-haemolytic colonies were obtained from the blood cultures and culture of the CVC after 72 h of incubation (blood agar plate, 5% CO_2). The knee joint fluid culture was negative on agar plates after 14 days of incubation, but positive results were obtained using the VIRTUO® microbial detection system. Gram-stain and subculture results from the joint fluid were consistent with those obtained from blood and CVC. Despite the use of formic acid, colonies were unreliably identified by matrix-assisted laser desorption ionization-time of flight mass spectrometry (Bruker). Sequencing of the 16S rRNA gene[1] showed the presence of *Gordonia* spp DNA both in blood and knee joint fluid cultures. Identification at the species level was performed through newly designed *gyrB* and *secA1* PCRs (supplementary method).[2,3] Phylogenetic constructions of *gyrB* gene sequences clustered the isolate close to *Gordonia jacobaea* and *G. sputi* (96% identity), while phylogenetic trees based on *16S rDNA* and *secA* genes showed that the isolate was closely related to *G. jacobaea* (98.8% and 99.7% identity, respectively) (Fig. 1). The *G. jacobaea* isolate was susceptible to all tested antibiotics, except to daptomycin (eTab.1). On day 10 of admission, antimicrobial treatment was adapted to ceftriaxone, levofloxacin and cotrimoxazole. After knee prosthesis lavage and CVC removal, a three-month antibiotic tritherapy led to a favourable evolution.

In conclusion, we described here the first case of prosthesis joint septic arthritis caused by *G. jacobaea*. *Gordonia* spp. are emerging as potential nosocomial human pathogens, which may be mistaken for contaminating bacteria. Accurate identification is challenging and requires molecular approaches. The *secA* gene sequencing appears to be a useful tool for phylogeny analysis of *Gordonia* spp.

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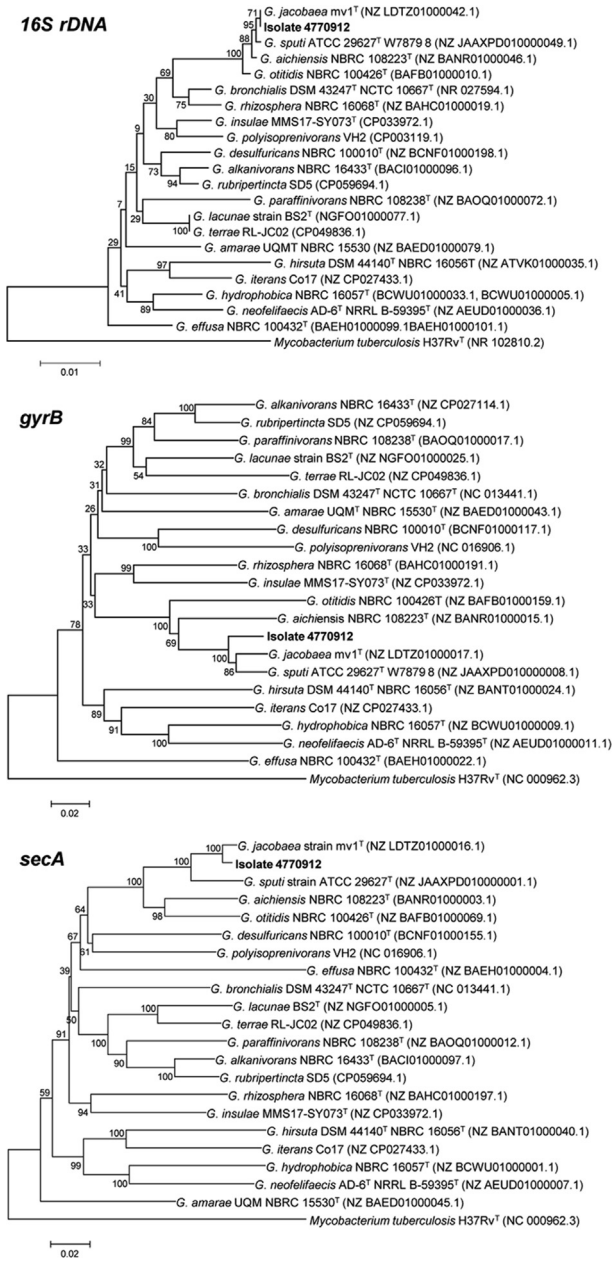

Figure 1. The phylogenetic analyses were generated with the Neighbor-Joining method. The phylogeny presented is based on the nucleotide sequence alignment of the 16S rRNA (~1444 nt), *gyrB* (~1229 nt) and *secA* (~1827 nt) genes of 21 Gordonia strains and the *G. jacobaea* isolate (accession numbers. MW564897, MW573972 and MW573971, respectively). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is not rooted and drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method and are represented in the units of the number of base substitutions per site. Evolutionary analyses were conducted using MEGA6. All sequences are labeled by species, strain name, collection number and GenBank accession number in brackets. ^{T}, type strain.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jmii.2021.08.001.

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