Cardiac Device-Related Endocarditis Caused by Paenibacillus glucanolyticus

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We report the first case of *Paenibacillus glucanolyticus* infection in a 65-year-old patient with type 2 diabetes who developed a cardiac device-related endocarditis. The identification of the isolate was performed using phenotypic methods, including mass spectrometry-based methods, and 16S rRNA gene sequencing.
including 19 Bacillus species (465 spectra) and 11 Paenibacillus species (132 spectra). The Vitek MS RUO database encompassed 8 genera and 49 species of AGPSFR, including 21 Bacillus species (427 spectra) and 13 Paenibacillus species (139 spectra). Species identification was confirmed by PCR amplification and sequencing of the 16S rRNA gene using the same primers as described previously (1). A consensus sequence of 589 bp was trimmed and submitted to the Ribosomal Database Project and GenBank for comparative analysis using the Basic Local Alignment Search Tool. The sequence of the 16S rRNA gene showed 99.66% homology with P. glucanolyticus NBRC 15330T (GenBank accession no. AB680838) and 99.32% homology with P. glucanolyticus DSM 5162T (GenBank accession no. NR_040883). The next highest homology (97.79%) was found for the 16S rRNA gene sequence of Paenibacillus lautus JCM 9073T (GenBank accession no. NR_040882). P. glucanolyticus was also detected in the vegetation by broad-range bacterial 16S rRNA gene PCR followed by sequencing. Antibiotic susceptibility was tested using Etest strips (bioMérieux). Non-species-related breakpoints established by the Antibiogram Committee of the French Society for Microbiology (http://www.sfm-microbiologie.org) were used for interpretation. The isolate was intermediate to penicillin G and amoxicillin (MIC, 2 and 3 μg/ml, respectively), and susceptible to ceftriaxone (MIC, 0.5 μg/ml). β-Lactamase production was detected by the nitrocefin test (Cefinase disc; bioMérieux) (2). The isolate was found to be intermediate to ciprofloxacin (MIC, 0.94 μg/ml) and susceptible to erythromycin, trimethoprim-sulfamethoxazole, gentamicin, tobramycin, vancomycin, rifampin, and linezolid (MICs, 0.19, 0.002/0.018, 0.64, 1, 0.5, 0.002, and 0.125 μg/ml, respectively).

Except for a postoperative course complicated by a noninfectious pericardial effusion that required surgical drainage 13 days after epicardial pacemaker implantation, the outcome was favorable and the patient was discharged after 30 days of hospitalization. Ceftriaxone was continued for another 2 weeks. No recurrence of infection was noted during the short-term follow-up.

Over the past few years, cardiac device-related infections, including endocarditis, have emerged as the consequence of an increased use of electrophysiological devices, especially in elderly and frail patients (3). Pacemaker-related endocarditis is due mainly to the migration of microorganisms from the implantation site to the distal intravascular part. Several factors, although under debate, have been associated with an increased risk of cardiac device infections, including device-related procedures, chronic renal failure, corticosteroid use, and diabetes (4–6). These infections may progress slowly and occur late after pacemaker implantation or last device manipulation (4). In our patient, diabetes mellitus could have been a contributing factor and the contamination might have occurred during the replacement of the generator 2
years earlier, leading to the development of a late-onset infection. The diagnosis of lead-related endocarditis may be difficult, since patients with pacemaker infections may present without fever and blood cultures may be negative (6). These two features were observed in our case.

Device-related endocarditis is caused mainly by *Staphylococcus* spp., but other microorganisms that can be found on the skin and in the environment may be involved (6). So far, there have been only three reports of device-related endocarditis caused by Gram-positive endospore-forming rods (7–9). In all of these cases, a *Bacillus* sp. was involved. In our case, cardiac device-related infection was due to *P. glucanolyticus*, which has never so far been reported as a cause of human infection. *Paenibacillus* spp. are facultatively anaerobic or strictly aerobic, mostly motile endospore-forming Gram-variable rods that may be isolated from various environmental sources as well as from diseased insects and foods (10). Several *Paenibacillus* species have been reported as the cause of human infections, including bacteremia, endocarditis, meningitis, brain abscess, endocarditis, pneumonia, mediastinitis, prosthetic aortic valve infection, and chronic prostatitis (11–23). *Paenibacillus glucanolyticus*, formerly included in the genus *Bacillus* (24), is a facultatively anaerobic, long and thin rod-shaped bacterium that may be isolated from various soils (25). This organism appears mostly Gram negative and may produce oval spores that swell the sporangia (10). The Gram-negative appearance may be misleading for proper identification of these organisms, especially when spores have not become apparent. It is noteworthy that when we tested the *P. glucanolyticus* strain using a Vitek 2 Gram-negative identification card (GN card) and an API ID 32GN strip, results similar to those obtained with the apparently Gram-negative isolate found in October 2012 were observed. This suggests that the isolate obtained in October might have been misidentified. However, this remains a hypothesis, since the initial strain was no longer available for further characterization. *P. glucanolyticus* produces colonies that are flat, smooth, and white opaque and may show spreading growth. It is noticeable that the presence of motile colonies that rapidly migrate over agar media is a feature shared only by some taxa previously included in the genera *Bacillus* and related endospore-forming species, on the combined use of API 20E and API 50CH kits (10). However, the precise identification of these bacteria to the species and even genus level may be difficult, considering the absence of clear-cut discriminating phenotypic characteristics and the fact that many proposals of new species have been made on the basis of the characterization of single isolates. Thus, molecular methods, including 16S rRNA gene sequence analysis, are often needed for the final identification of these organisms.

It has been shown that MALDI-TOF MS, which is increasingly used in clinical microbiology laboratories for the rapid identification of microorganisms, performed as well as extended phenotypic methods and specific molecular methods to identify aerobic Gram-positive rods, including *Bacillus* spp. and *Paenibacillus* spp. (26, 27). In our case, the *P. glucanolyticus* isolate, which could not be identified by using the Vitek 2 GP card since the *Paenibacillus* genus is not included in the database, was correctly identified using either the API 50CH and API 20E strips, MALDI-TOF MS, or 16S rRNA gene sequence analysis.

The two major commercial MALDI-TOF MS systems are the Bruker Biotyper and the bioMérieux Vitek MS systems (28). The databases of both systems contain mass spectra of *P. glucanolyticus*. SuperSpectra, which are consensus spectra that are typical at a defined taxonomic level, are used in the Vitek MS RUO system during the fully automated first-line identification step. Our isolate could not be identified beyond the genus level using this approach since no SuperSpectrum specific for *P. glucanolyticus* was, at the time, included in the RUO database. With the Vitek MS IDV system, the isolate was also only identified to the genus level using the Advanced Spectra Classifier approach, which represents an extension of the SuperSpectrum approach (28). Our isolate could be identified beyond the genus level with the Bruker Biotyper system and the Vitek MS RUO system when the compare mode was used. The latter approach represents a second-line identification method based, as is the case for the Biotyper system, on the direct comparison of the isolate spectrum to all reference spectra of the database. This result highlights the fact that results obtained with MALDI-TOF MS systems depend not only on the database contents but also on the algorithms used for interpretation of crude data.

This is, to the best of our knowledge, the first report showing that *P. glucanolyticus* may be a pathogen in humans and that a member of the genus *Paenibacillus* may be involved in device-related endocarditis. This case also highlights the fact that the routine use of mass spectrometry is a rapid and accurate method that may be used for the identification of Gram-positive aerobic rods, such as *Paenibacillus*, for which the Gram staining reaction may be misleading.

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