

Endocarditis Caused by *Cardiobacterium valvarum*

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A fastidious, gram-negative bacterium was isolated from the blood of a 51-year-old man who had acute infectious endocarditis (IE). Characterization of the organism through phenotypic and genotypic analyses revealed the causative role of *Cardiobacterium valvarum*. This is the third reported case of IE caused by *C. valvarum*.

CASE REPORT

In March 2005, a 51-year-old man was admitted to the Timone Hospital in Marseilles, France, with clinical signs of insidious endocarditis. He had gradually developed anorexia, weight loss, and asthenia over the course of the previous 2 months. The patient had no significant medical history but had presented with a dental abscess 1 month before the onset of illness. On admission, he had a temperature of 38°C and a blood pressure of 120/70 mm Hg. His medical records showed that the patient had an aortic insufficiency complicating a congenital bicuspid aortic valve. The leukocyte count was 11.65×10^9 /liter, the hemoglobin level was 97 g/liter, the platelet count was 302×10^9 /liter, and the erythrocyte sedimentation rate was 136 mm in the first hour. Multiplane transesophageal echocardiography showed on the aortic valve vegetations in which the largest mass measured 14 mm and an abscess. Three blood samples for culture were drawn before therapy. The first blood culture was performed with a set of BACTEC Plus Aerobic/F and BACTEC Lytic/10 Anaerobic/F bottles (BD Diagnostic Systems, Sparks, Md.). Then, every 2 h, second and third blood samples for culture were drawn and cultured in BACTEC Plus Aerobic/F bottles. Subsequently, the patient was empirically treated intravenously with amoxicillin at 2 g every 4 h and gentamicin at 3 mg/kg of body weight once a day. The bottles containing blood were incubated, with continuous automated monitoring for bacterial growth in the medium. All aerobic bottles grew a gram-negative bacterium within 5 days. All subcultures were plated on blood agar and chocolate agar (BioMerieux, Marcy l'Etoile, France) and incubated aerobically at 37°C with 5% CO₂. Nonhemolytic colonies appeared within 2 days of culture on blood agar but reached a size of 2 mm after 4 days. By using the miniaturized API 32E (BioMerieux) and BBL CRYSTAL N/H and E/NF (BBL, Becton Dickinson Microbiology Systems, Franklin Lakes, N.J.) systems, the bacterium was identified as a *Cardiobacterium* sp. It was positive for

cytochrome oxidase, potassium-5-ketogluconate, 4-nitrophenyl- α -D-glucopyranoside, L-aspartic acid-4-nitronylide, *p*-nitrophenyl-phosphate, L-serine, L-phenylalanine, glycine, L-arginine, and indole production and negative by other tests, including catalase production. By using partial 16S rRNA gene amplification and sequencing with the 536f and rp2 primers, as described previously (4), the bacterium was identified as *Cardiobacterium valvarum* on the basis of a 99.6% similarity of its nucleotide sequence with that of the *C. valvarum* sequence in the GenBank database (GenBank accession number AF506987). Our patient had a normal cerebral magnetic resonance imaging scan and demonstrated no neurologic symptoms. On day 6 following admission, cardiac surgery was performed because of heart failure. The aortic valve was replaced with a bioprosthetic valve. Histological examination of the valve that was removed was performed, and the findings were consistent with a diagnosis of infectious endocarditis. Possibly due to the administration of antibiotics, bacterial culture of the valve was negative. The 16S rRNA gene amplification and sequencing performed with the valvular tissue as described above provided a sequence identical to that obtained from the strain and thus confirmed the presence of *C. valvarum* DNA (4, 5, 7). Bacterial DNA was extracted by using the MagNA Pure kit II (Roche, Mannheim, Germany), as described by the manufacturer.

The genus *Cardiobacterium*, with its sole species, *C. hominis*, was established in 1964 for a group of fastidious gram-negative bacteria (8, 12, 13) that were members of the HACEK group. Until 2004, *C. hominis* was the only *Cardiobacterium* species known to cause endocarditis (1, 2). In 2004, Han et al. identified a new *Cardiobacterium* species, which they named *C. valvarum*, as an agent of endocarditis (6). The bacterium was described as a fastidious gram-negative bacillus that grows better on sheep blood agar than on chocolate agar. In contrast to *C. hominis*, *C. valvarum* grows more slowly; is nonhemolytic on sheep blood agar; and does not utilize sucrose, maltose, or mannitol (6, 7). However, phenotypic tests may not always allow the two *Cardiobacterium* species to be distinguished. In such cases, genotypic identification should be performed.

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Here, we report on the isolation of a *Cardiobacterium* species distinct from *C. hominis* from a patient with endocarditis. Characterization of the organism by a genotypic method identified it as *C. valvarum*. The source of this bacterium is likely the oral flora, as is the case for *C. hominis* (7). In the scientific literature, 64 cases of *C. hominis* endocarditis have been reported (3, 9, 11, 14, 15). The lack of early recognition of *C. valvarum* reflects its rarity. To the best of our knowledge, two clinical reports of endocarditis caused by *C. valvarum* have been reported in the literature (6, 8). Including our patient, the three patients presented with an insidious endocarditis, with large destructive vegetations necessitating valvular replacement (6, 8). Our patient was febrile, in contrast to the other two published cases. All three patients had a congenital bicuspid aortic valve. The history of recent dental manipulation in the three patients confirmed that the source of *C. valvarum* was probably oral, as is the case for *C. hominis*. In our experience, *Cardiobacterium* species are the rarest of the HACEK group of bacteria that cause infectious endocarditis (2). In our series, of a total of 427 cases of definite infectious endocarditis, according to the modified Duke criteria (10), 9 were caused by the HACEK group of bacteria. Of these, one case was caused by *C. hominis*, which was initially identified by biochemical tests and confirmed by 16S rRNA gene sequencing analysis (11), and one was caused by *C. valvarum*. Thus, physicians should be aware that *C. valvarum* is a potential agent of infectious endocarditis.

Nucleotide sequence accession number. The sequence of the *C. valvarum* isolate recovered in this study has been deposited in GenBank under accession number DQ174272.

All authors have read and approved the revised version of the manuscript and do not have any conflict of interest related to this research.

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