The clinical picture of *Ochrobactrum anthropi* infection is not well described because the infection is rare in humans and identification of the pathogen is difficult. We present a case of *O. anthropi* bacteremia that was initially misidentified as *Ralstonia paucula* and later identified by 16S rRNA sequencing and recA analysis.

**CASE REPORT**

An 85-year-old man was admitted to our hospital to receive transcatheter arterial chemoembolization (TACE). He had liver cirrhosis (Child–Pugh score A) and hepatocellular carcinoma (HCC) caused by hepatitis C virus infection. His medical history included repeated radio frequency ablation and a total of nine TACE procedures for the treatment of HCC. He had also experienced urinary bladder and ureteral carcinoma.

The patient was free from any complications; however, he suddenly developed high fever (39°C), chills, and rigors 12 days after TACE. Physical examination did not reveal any significant findings, but laboratory testing showed a highly inflammatory state: his white blood cell count was 17,700/mm³, and his C-reactive protein level was 4.5 mg/dl. Urine examination was normal, and whole-body computed tomography revealed no particular pathogenic lesion. An echocardiogram was not performed. Oral cefcapene pivoxil was prescribed for 1 week based on the suspicion of some forms of infection relating to TACE.

Two sets of blood cultures were obtained at the time of high fever. Of these four bottles, two different aerobic bottles became positive for Gram-negative rods after an incubation period of 36 h. However, the patient’s condition and laboratory measurements improved promptly, and he was discharged on day 16 without distinct diagnosis. Later, the organism was identified as *Ralstonia paucula* by the Microscan walkaway system (Siemens) with a concordance rate of 99.9%. Susceptibility testing showed the organism to be sensitive to imipenem, meropenem, amikacin, minocycline, and colistin but resistant to non-lactose-fermenting bacillus previously known as "Achromobacter group Vd" (12). Most cases of human disease due to this pathogen have been reported to occur in clinical samples (9).

Of the clinically relevant species, *O. anthropi* is becoming increasingly recognized as a potentially problematic, opportunistic, and nosocomial pathogen (10, 11). *O. anthropi* is an aerobic, oxidase-positive, urease-positive, Gram-negative, motile, non-lactose-fermenting bacillus previously known as "Achromobacter group Vd" (12). The genus *Ochrobactrum* currently comprises 9 species: to date, only 3 species, *O. anthropi*, *O. intermedium*, and *O. pseudintermedium*, have been reported as a cause of infective endocarditis (13–18). However, this organism has also been reported as a cause of infective endocarditis (10, 19, 20), pancreatic abscess (21), panniculitis (22), endophthalmitis (23), urinary tract infection (24), meningitis (25), pelvic abscess (26), and osteomyelitis (27). Infection is most commonly, although not exclusively, seen in immunocompromised patients, such as those with debilitating illnesses or malignancy (13, 14, 19, 26, 28–30). Opportunistic infections and nosocomial outbreaks of *O. anthropi* are being increasingly reported.

Yu et al. reported the clinical characteristics of 15 cases of *O. anthropi* bacteremia; this is the first case of *O. anthropi* bacteremia to be identified at our hospital. The patient responded well to the treatment and the antibiotic did not have to be changed.

The organism had been rarely encountered at our hospital, and therefore the sample was sent to Kochi University for further identification. The two samples derived from different blood cultures were examined separately. Blood samples were inoculated onto agar media and incubated at 28°C. Pale yellow colonies grew in almost the entire agar media and incubated at 28°C. Pale yellow colonies grew in agar media and incubated at 28°C. Almost the entire region of the recA partial sequences of isolated organisms are 100% identical to those of the *O. anthropi* cluster (Fig. 1). Subsequently, almost the entire region of the recA gene was amplified by colony PCR with a pair of primers (recA-BrucOchro-F, 5’-ATGTCTCAAA ATTICATTGCGAC-3’; recA-BrucOchro-R, AGCATCCTTCTCC GGTCCG-3’) and sequenced. Again, two colonies had the same sequences and were 100% identical to recA of several *O. anthropi* strains (Fig. 2), confirming that the organism is *O. anthropi*.

*Ochrobactrum spp.* belongs to the *Brucellaceae* and is known to be isolated from *Leguminosae* nodules (2, 3). Its name is derived from the Greek ochros, meaning pale yellow; this is the characteristic color of *Ochrobactrum* colonies. The organism has the potential to colonize an exceptionally wide variety of habitats (4–8). The genus *Ochrobactrum* currently comprises 9 species; to date, only 3 species, *O. anthropi*, *O. intermedium*, and *O. pseudintermedium*, have been reported to occur in clinical samples (9).

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anthropi bacteremia (31). They stated that all patients had severe underlying disease and manifested primary O. anthropi bacte-
ria without obvious focus; however, none of the patients died directly from the infection. Thus, although O. anthropi can be pathogenic in critically ill or immunocompromised patients, the organism is considered to be of relatively low virulence. However, the clinical picture of O. anthropi infection, especially bacteremia, has still not been well described. The reason is the difficulty of differentiating Ochrobactrum spp. from other organisms by physiological tests because of their high phenotypic similarity (32). To gain a better understanding of the clinical manifestations of O. anthropi infection, we need to be able to clearly identify the pathogen.

Commercially available test systems used in routine diagnosis are not suitable for species discrimination within the genus Ochro-

FIG 1 Phylogenetic tree of partial 16S rRNA nucleotide sequences (1,430 nucleotides) using neighbor-joining analysis.

FIG 2 Phylogenetic tree of partial recA nucleotide sequences (897 nucleotides) using neighbor-joining analysis.
In the present case, the pathogen in the present case was first misidentified as *R. paucula*. Although the biochemical properties of *O. anthropi* and *R. paucula* are similar, they have distinct differences, especially regarding malonic acid (MAL), the oxidation-fermentation test with glucose (OF/G), tobramycin (TO4), and colistin (23). The pathogen in the present case was resistant to various β-lactams except carbapenems, gentamicin, ciprofloxacin, levofloxacin, and sulfamethoxazole-trimethoprim. The patient was treated with an oral cephalosporin, to which the pathogen was later shown to be resistant, but he recovered well without any complications, presumably because of the low virulence of the organism. In fact, according to previous studies, immunocompetent patients with *O. anthropi* infection survived and experienced clinical cure without any long-term sequelae (26, 31), and 4 of 5 immunosuppressed patients (organ transplant recipients) with *O. anthropi* bacteremia experienced resolution of bacteremia without antibiotic administration (37).

We performed an environmental survey for *O. anthropi* in the ward to which the patient had been admitted; however, no environmental isolates matched the patient isolates. Therefore, we conclude that the patient had been colonized with the organism somewhere in his body, such as his throat or intestine, and his bacteremia resulted from bacterial translocation across the mucous membrane (38).

**Nucleotide sequence accession numbers.** Nucleotide sequences of 16S rRNA and *recA* have been deposited in DDBJ/EMBL/GenBank under the accession numbers AB778289 and AB778290.

**ACKNOWLEDGMENT**

We have no conflicts of interest to declare.

**REFERENCES**


