Herbaspirillum species bacteremia in a pediatric oncology patient

Edward D. Ziga  
Washington University School of Medicine in St. Louis

Todd Druley  
Washington University School of Medicine in St. Louis

Carey-Ann D. Burnham

Follow this and additional works at: https://digitalcommons.wustl.edu/open_access_pubs

Recommended Citation
https://digitalcommons.wustl.edu/open_access_pubs/2394

This Open Access Publication is brought to you for free and open access by Digital Commons@Becker. It has been accepted for inclusion in Open Access Publications by an authorized administrator of Digital Commons@Becker. For more information, please contact engeszer@wustl.edu.
Herbaspirillum Species Bacteremia in a Pediatric Oncology Patient

Edward D. Ziga, Todd Druley and Carey-Ann D. Burnham

Published Ahead of Print 25 August 2010.

Updated information and services can be found at:
http://jcm.asm.org/content/48/11/4320

REFERENCES

This article cites 7 articles, 4 of which can be accessed free at:
http://jcm.asm.org/content/48/11/4320#ref-list-1

CONTENT ALERTS

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: http://journals.asm.org/site/misc/reprints.xhtml
To subscribe to another ASM Journal go to: http://journals.asm.org/site/subscriptions/
**Herbaspirillum** Species Bacteremia in a Pediatric Oncology Patient

Edward D. Ziga,¹ Todd Druley,¹ and Carey-Ann D. Burnham¹,²*

Departments of Pediatrics¹ and Pathology & Immunology,² Washington University School of Medicine, St. Louis, Missouri 63110

Received 21 July 2010/Returned for modification 17 August 2010/Accepted 19 August 2010

**Herbaspirillum** species, an organism commonly found in soil, has only recently been linked to disease in humans. We report **Herbaspirillum** bacteremia in a 2-year-old female patient following a hematopoietic stem cell transplant for relapsed acute lymphoblastic leukemia.

**CASE REPORT**

We report the case of a 2-year-old female diagnosed with acute lymphoblastic leukemia (ALL) classified as high-risk due to MLL gene rearrangement. A double-lumen Broviac catheter was placed for intravascular access. The child went into clinical remission after standard five-drug induction chemotherapy, but cytogenetic analysis of her bone marrow following induction revealed the presence of persistent leukemic cells, conferring a risk for relapse. As a result, she underwent a matched, unrelated donor hematopoietic stem cell transplant (MUD HSCT). The child’s course of treatment was uncomplicated until posttransplant day 162, when she was admitted with a 2-day history of fever (maximum temperature, 103.5°F) and diarrhea. She presented to her local hospital emergency room, where she was found to be tachycardic and febrile. She received two intravenous normal saline fluid boluses and was empirically started on ceftriaxone (50 mg/kg of body weight) prior to transfer to our hospital.

On admission, the patient was hemodynamically stable, with an unremarkable physical examination. Admission laboratory results included a white blood cell (WBC) count of 3,400/mm³, with 83% neutrophils, 1% bands, 11% lymphocytes, 5% monocytes, an absolute neutrophil count of 2,822, and a hemoglobin level of 9.5 g/dl. She was empirically started on cefepime (50 mg/kg) administered every 8 h.

Two days later, an Isolator blood culture from the white central venous line lumen was still growing the same organism in a quantity too numerous to count. At this point, gentamicin (2.5 mg/kg/dose every 8 h) was added to the antibiotic therapy. Antibiotic therapy was changed to meropenem at a dose of 20 mg/kg every 8 h for a total of 7 days following the negative blood culture.

The Vitek 2 Gram-negative identification system identified the organism as Burkholderia cepacia complex. The corresponding Kirby-Bauer disk diffusion susceptibility testing showed that the isolate was colistin resistant (consistent with *B. cepacia*) but susceptible to piperacillin-tazobactam, ticarcillin-clavulanic acid, trimethoprim-sulfamethoxazole, meropenem, ceftazidime, gentamicin, amikacin, ciprofloxacin, and cefepime—a susceptibility pattern not consistent with that of *B. cepacia*. The isolate was then inoculated onto (i) the Remel Uni-N/F Tek plate for identification of oxidase-positive, nonfermenting Gram-negative bacilli, (ii) oxidation-fermentation polymyxin B-bacitracin-lactose (OFBPL) agar, and (iii) the BD Phoenix Gram-negative identification panel. The Phoenix panel identified the isolate as *Cupriavidus pauculus* and then on repeat testing as *Ochrobactrum anthropi*. The Uni-N/F Tek plate was positive for xylose, mannitol, urease, and *o*-nitrophenyl-β-D-galactopyranoside (ONPG). It was negative for hydrogen sulfide production, lactose, maltose, acetamide, esculin, DNase, and indole. The isolate was nonpigmented. The combination of the susceptibility pattern and the biochemical reactions was not compatible with any of the automated identifications.

DNA was extracted from a pure culture of the isolate using the BiOstic bacteremia DNA isolation kit (MoBio Laboratories, Inc., Carlsbad, CA). Amplification of the 16S rRNA gene was performed using the primers 27F (AGA GTT TGA TCC 99.9% identity (742/743 bp) with the GenBank “nr/nt” database and the Ribosomal Database Project and had 99.9% identity (742/743 nucleotides) with **Herbaspirillum** spp. The next-closest match was *Ralstonia* spp., with 97.0% sequence homology (720/743 nucleotides) to our isolate. The biochemical features of our isolate were consistent with what has been previously described for **Herbaspirillum** spp., namely, being oxidase positive and weakly catalase positive, in addition to being ONPG and urease positive (6, 7).

The patient’s central venous line was removed prior to discharge, and was not replaced, as this was her third line infection in 6 months, and it was almost 180 days after her stem cell infusion. The organisms associated with the previous infections were *Pseudomonas putida*, coagulase-negative *Staphylococcus*.
spp., and Candida parapsilosis, all of which were isolated 5 months prior to this admission.

Herbaspirillum species was first described about 25 years ago (1, 6) as a Gram-negative, rod-shaped member of the Beta-proteobacteria class. It is a nitrogen-fixing soil and plant bacterium previously not considered a human pathogen (1, 3). Its close phylogenetic and phenotypic resemblance to Burkholderia cepacia complex has often resulted in misidentification (2, 4). Although one of the earliest documented human infections with this organism was reported in 2005 from a wound isolate in a 49-year-old homeless man with a history of chronic liver disease (8), the advent of new technology has led to the reclassification as Herbaspirillum of previously identified and other, unclassified human isolates obtained as early as 1978 from infections of the ear, eye, knee, urine, oropharynx, gastrointestinal tract, blood, and respiratory tract (2). Between 2000 and 2007, the Burkholderia cepacia Research Laboratory and Repository at the University of Michigan, Ann Arbor, isolated Herbaspirillum from 28 sputum cultures and one blood isolate referred from 23 cystic fibrosis (CF) treatment centers in the United States; 19 (68%) of the isolates had been initially identified as Burkholderia (4). Recent theories about infections contributing to aortic aneurysms led to the isolation of multiple organisms, including Herbaspirillum species, from aneurismatic walls. Though this infectious etiology remains unproven, it is a cause for great concern (5). In light of the fact that automated systems will provide an identification for this organism (albeit an incorrect one), it is possible that this organism may be an underrecognized cause of opportunistic infection.

Although stem cell transplant recipients are prone to a wide spectrum of infections, Herbaspirillum species has not been previously described as a cause of infection in this patient population. It is uncertain how our patient was exposed to this soil-based organism, but she lives with her parents and grandparents on a large farm, and we speculate that she likely encountered the organism in that environment.

This case demonstrates the utility of sequence-based identification of organisms, especially those that are not in the databases of commercial identification systems or are not readily identifiable using conventional phenotypic methodology.

REFERENCES