

Letter to the editor

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Herbaspirillum huttiense pneumonia in a patient with essential thrombocythaemia

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Sir,

Herbaspirillum infection is a very rare cause of pneumonia. Although a few cases of *Herbaspirillum* infections in humans have been described [1-4], one only case of infection in a non-immunocompromised host has been reported [2].

The identification of this aetiology is clinically relevant. This strain appears identical to strains from *Burkholderia cepacia* complex (BCC), which are pathogens with different resistance profiles and different therapeutic implications. Thus, conventional identification methods cannot be used to identify *Herbaspirillum* [1-3,5], which may explain why it is so seldom described and perhaps often misidentified. It is expected that new methods of bacterial characterization (i.e., MALDI-TOF mass spectrometry) will enable the identification of this microorganism in clinical samples. To this end, it is necessary to be aware of the infection frequency and clinical characteristics. We present a new case of *Herbaspirillum* pneumonia, in a hospitalized patient suffering from essential thrombocythaemia (ET) but without evident immunocompromise.

A 59-year-old woman with deterioration of general condition presented with extensive aortic wall thrombosis and visceral and cerebral ischaemic lesions, establishing the diagnosis of JAK2+ essential thrombocythaemia and new onset diabetes mellitus. Anti-coagulant treatment was established, with progressive reduction of the aortic mural thrombus. Therefore, surgical treatment was ruled out. Upon admission, the patient presented no respiratory symptoms. After 10 days, she presented with dyspnoea, pulmonary infiltration and febrile syndrome, consistent with nosocomial pneumonia. The patient received empirical treatment with piperacillin-tazobactam and recovered completely once she had completed a cycle of antibiotic therapy.

Based on the suspicion of pneumonia, sputum culture, *Streptococcus pneumoniae* and *Legionella pneumophila* urinary antigens, blood cultures, urine culture and polymerase chain reaction for influenza A and B virus were performed. All results were negative except the sputum culture, which was positive after 24 hours. A pure culture of colonies with soft consistency was obtained and identified as *Herbaspirillum huttiense*/*H. aquaticum* by MALDI-TOF analysis. The identification was subsequently confirmed by 16S rRNA gene sequencing, which showed 99% similarity with *H. huttiense*. Antibiotic sensitivity was assessed by using the microdilution method (MicroScan WalkAway, Siemens). The isolate was sensitive to gentamicin, tobramycin, amikacin, cefepime, ceftazidime, piperacillin-tazobactam, ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole and imipenem.

This case study deals with *H. huttiense* pneumonia in a patient with ET, and our interest focuses on two aspects that we want to highlight. First, *Herbaspirillum* identification is not included in the databases of commercial identification systems such as MicroScan or Vitek 2. In addition, this strain looks the same as strains from BCC. Consequently, the commercially available microbial identification systems may misidentify the organism [1-3,5]. This is mainly because *Herbaspirillum* species and BCC share a close phylogenetic relationship as do other non-fermenting rods such as *Pseudomonas butanovora* [6]. However, the *Herbaspirillum* species show a different profile of antimicrobial susceptibility with respect to BCC, with the latter exhibiting higher resistance profiles. Therefore, when a bacterium is identified as BCC but is sensitive to all or most antibiotics, misidentification should be suspected in this microorganism. Currently, identification at the genus level is achieved through MALDI-TOF analysis; however, distinguishing *H. huttiense* and *H. aquaticum* species requires sequence-based identification of the 16S rRNA gene.

Second, in the context of pneumonia, the clinical significance deserves special attention. To our knowledge, *Herbaspirillum* species have only been isolated from respiratory

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samples of patients with cystic fibrosis, and its role is doubtful [7]. There is only one reported case of pneumonia with bacteraemia caused by *H. aquaticum*/*H. huttiense* in an immunocompetent adult [2]. Conversely, most infections have been reported in immunocompromised hosts [1], particularly those who have undergone haematopoietic stem cell transplant [3]. In our search of the available literature, we found no documented cases of *Herbaspirillum* pneumonia without bloodstream infections. There is one reported case of bacteraemia secondary to pneumonia in a patient with multiple myeloma [4] and one case of sepsis and pneumonia in a patient with lung cancer [1].

We find this case to be of interest because it describes a case of pneumonia caused by *H. huttiense* in a patient with ET, which is an uncommon myeloproliferative disorder. Further longitudinal studies are needed to establish whether the *Herbaspirillum* isolate obtained from cultures of sputum correspond to transient colonization or chronic infection. In addition, although there are currently only a limited number of reported cases, it is likely that new identification methods could facilitate its identification and lead to further cases of infection being recognized. In any case, immunocompromised patients colonized by opportunistic pathogens in the upper airway are at higher risk of pneumonia. Therefore, we emphasize the importance of including accurate identification systems such as MALDI-TOF and/or molecular techniques in diagnostic laboratories to improve the reliability of *Herbaspirillum* identification and to differentiate phylogenetic relatives. Such detailed levels of analysis should both enable appropriate treatment to be provided and establish the true prevalence of this potential opportunistic pathogen in human hosts.

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CONFLICT OF INTEREST

The author declare that they have no conflicts of interest

REFERENCES

1. Chemaly RF, Dantes R, Shah DP, Shah PK, Pascoe N, Mulanovich V, et al. Cluster an sporadic cases of *Herbaspirillum* species infections in patients with cancer. *Clin Infect Dis* 2015; 60: 48–54. PMID: 25216687.
2. Regunath H, Kimball J, Smith LP, Salzer W. Severe Community-Acquired Pneumonia with Bacteremia Caused by *Herbaspirillum aquaticum* or *Herbaspirillum huttiense* in a Immune-Competent Adult. *J Clin Microbiol* 2015; 53: 3086–8. PMID: 26179298.
3. Ziga ED, Druley T, Burnham C-AD. *Herbaspirillum* species bacteremia in a pediatric oncology patient. *J Clin Microbiol* 2010; 48:4320–4321. PMID: 20739483.
4. Suwantarant N, Adams LL, Romagnoli M, Carrol KC. Fatal case of *Herbaspirillum seropedicae* bacteremia secondary to pneumonia in an end-stage renal disease patient with multiple myeloma. *Diagn Microbiol Infect Dis* 2015; 82: 331–3. PMID: 25976156.
5. Pilker T, Uluer AZ, Marty FM, Yeh WW, Levison JH, Vandamme P, et al. Recovery of *Herbaspirillum* species from persons with cystic fibrosis. *J Clin Microbiol* 2008; 46:2774–2777. PMID: 18524958.
6. Tayeb LA, Lefevre M, Passet V, Diancourt L, Brisse S, Grimont PA. Comparative phylogenies of *Burkholderia*, *Ralstonia*, *Comamonas*, *Brevundimonas* and related organisms derived from *rpoB*, *gyrB* and *rrs* gene sequences. *Res Microbiol* 2008; 159: 169–77. PMID: 18280706.
7. Spilker T, Uluer AZ, Marty FM, Yeh WW, Levison JH, Vandamme P, et al. Recovery of *Herbaspirillum* species from persons with cystic fibrosis. *J Clin Microbiol* 2008; 46: 2774–7. PMID: 18524958.