Letter to the Editor

_Pantoea dispersa_ bacteremia caused by central line-associated bloodstream infection

Dear Editor,

Genus _Pantoea_ is a rare pathogen in clinical settings. Among seven species of the rare organism, _Pantoea agglomerans_ is the most prominent species in humans and clinical cases of _Pantoea dispersa_ infection have scarcely been described. First case was reported in Germany in a 71-year-old woman with respiratory infection,\(^1\) and recently, Mehar et al. described two neonatal cases in India.\(^2\) We herein report another clinical case of _P. dispersa_ infection from Japan.

A 64-year-old man with dilated cardiomyopathy, sick sinus syndrome and diabetes mellitus was admitted to our hospital for control of chronic heart failure. A central venous catheter (CVC) was inserted and a permanent pacemaker was embedded 10 days after admission. Approximately two months later, he suddenly had high fever with shivering. Blood cultures were obtained and the CVC was removed, suspecting central line-associated bloodstream infection. A Gram-negative rod was detected from both blood and catheter tip cultures, and the organism was identified as belonging to the genus _Pantoea_ by the Vitek2 system (bioMérieux, France) and rapid ID 32 system (bioMérieux, France). Finally, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis identified the isolate as _P. dispersa_ with a score value of 2.344. The pathogen was sensitive to ceftriaxone, cefepime, imipenem, gentamicyn, and levofloxacin, and administration of cefepime was initiated. A follow-up blood culture became positive again, and the pacemaker was removed with suspicion of pacemaker infection. The persistent bacteremia then disappeared. A total of four weeks of antibiotic therapy was completed without recurrence of infection.

Epidemiology and clinical features of _P. dispersa_ infection are still unknown due to its rarity and difficulty in accurate identification. For a more comprehensive understanding, bacterial identification should be accurately performed. However, due to the similarity in bacterial properties of species of the genus _Pantoea_, biochemical identification alone would not be appropriate and may even be misleading. For example, more than 10% of clinical isolates of _P. agglomerans_ were misidentified as species of the genus _Enterobacter_ by the VITEK MS system (bioMérieux, Marcy l’Etoile, France).\(^3\) In those two previous cases of _P. dispersa_ infection,\(^1,2\) API 50 CHE system and Vitek2 system were used, and thus, accuracy of the identification was not known. Usually, 16S rRNA gene sequencing is used for the reference of bacterial identification; however, nucleotide sequences of _P. dispersa_ have not been deposited in gene databases. Even if the sequence are known, results of analysis may not be correct; according to a recent report, only half of the clinical isolates of _P. agglomerans_ (9/18 cases) were identified correctly by 16S rRNA analysis.\(^4\)

We identified the pathogen by means of MALDI-TOF MS analysis. Although the clinical utility of MALDI-TOF MS analysis for accurate identification of genus _Pantoea_ is still unestablished, Richter et al.\(^4\) and Wensing et al.\(^5\) have reported its potential as a reliable method for the identification of the genus _Pantoea_. Misidentification based on biochemical properties of the organism might be a reason for the small number of clinical reports on _P. dispersa_ infection. As a new methodology, MALDI-TOF MS analysis is gradually prevailing and more clinical cases of _P. dispersa_ infection may be reported in the future.

Conflicts of interest

The authors declare no conflicts of interest.

REFERENCES


Hideharu Hagiya *, Fumio Otsuka
Department of General Medicine, Okayama University Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama, Japan

*Corresponding author at: Department of General Medicine, Okayama University Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, 2-5-1 Shikata-cho, Kitaku, Okayama 700-8558, Japan. E-mail address: e_dai_for_all@hotmail.com (H. Hagiya).

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