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LETTER TO THE EDITOR

Infections due to *Nocardia* species

Dear Editor,

Su et al[1] reported an unusual case of disseminated nocardiosis in the June 2011 issue of the *Journal of Microbiology, Immunology and Infection*. In that report, the authors described a case in which *Nocardia asteroides* was isolated from a thyroid abscess in a 70-year-old retired farmer and reported that the patient responded well to trimethoprim-sulfamethoxazole treatment. Although their findings are interesting, the methods the authors used to identify the isolate to the species level of the *Nocardia* genus were not shown in detail.

Morphologic and phenotypic characteristics are not adequate to identify some *Nocardia* species accurately. An accurate diagnosis can only be made based on the findings of advanced molecular methods, such as 16S rRNA gene sequencing, hsp65 gene sequencing, and multilocus sequence analysis using five loci (*gyrB*+16S+*secA1*+*hsp65*+*rpoB*).[2–4]

In our previous study we investigated the clinical presentations and microbiologic characteristics of various infections due to *Nocardia* species based on 16S rRNA sequence analysis.[5] In that study, 100 cases of nocardiosis were initially identified based on the results of conventional laboratory methods, including positive Gram staining (Gram-positive branching, beaded, filamentous bacilli), positive modified acid-fast staining results, colonial morphotypes, and biochemical reactions, including hydrolysis of casein, xanthine, hypoxanthine, and tyrosine. The preliminary results showed that 50 of the 100 nonduplicate isolates were *N brasiliensis*, 36 were *N asteroides*, 2 were *N farcinica*, and 12 were unidentified *Nocardia* species. All of those isolates were positively identified to the species level by 16S rRNA gene sequencing analysis.[5] Results of that molecular method revealed that 35 of the 36 isolates that had originally been identified as *N asteroides* by conventional tests were in fact non-*asteroides Nocardia* species, and that the majority of the isolates were *N cyriacigeorgica*, followed by *N farcinica*. Furthermore, we identified several rare pathogens including *N asiatica*, *N rhamnosiphila*, *N abscessus*, *N transvalensis*, *N elegans*, and *N carnea*. Moreover, we demonstrated that each *Nocardia* species had a distinct antimicrobial susceptibility profile.[6] For example, only 28 (47%) of 60 *N brasiliensis* isolates were susceptible to imipenem and all of the *N cyriacigeorgica* isolates ($n = 24$) were susceptible to imipenem. In addition, 57 (95%) of the 60 *N brasiliensis* isolates were susceptible to ceftriaxone and 9 (75%) of the 12 *N farcinica* isolates were resistant to ceftriaxone.[6]

In conclusion, molecular methods are essential for identifying bacteria in the *Nocardia* genus to the species level. Accurate identification of the causative pathogen is necessary so that clinicians can provide appropriate treatment.

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Chih-Cheng Lai
Department of Intensive Care Medicine, Chi-Mei Medical Center, Liouying, Tainan, Taiwan

Po-Ren Hsueh*
Departments of Laboratory Medicine and Internal Medicine, National Taiwan University Hospital, National Taiwan University College of Medicine, Taipei, Taiwan

*Corresponding author.
Departments of Laboratory Medicine and Internal Medicine, National Taiwan University Hospital, 7 Chung-Shan South Road, Taipei 100, Taiwan.
E-mail address: hsporen@ntu.edu.tw

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