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OBJECTIVES

Nocardia are found worldwide as usual members of soil, dust and stagnant water microbiota playing an active role in the organic material decomposition. Although most species are free-living saprophytes some are opportunistic pathogens that cause nocardiosis in humans. The most frequent clinical manifestation of nocardiosis are respiratory infections but *Nocardia* can also be found infecting the central nervous system, skin and other localizations. The aim of this work was to describe four *Nocardia* species firstly isolated in clinical specimens that previously had been described only as native soil microbiota.

METHODS

All *Nocardia* isolates collected at Donostia University Hospital (San Sebastian, northern Spain) between January 1998 and November 2013 were identified at species level by sequencing a 1140- bp fragment of 16sRNA gene and of the *hsp 65* and *secA1* genes. Sequences were compared with sequences of other *Nocardia* isolates available at Genbank (www.ncbi.nlm.nih.gov/genbank/) and in leBIBI (www.pbil.univ-lyon1.fr/bibi) databases.

RESULTS

Overall, 226 clinical isolates were collected from 164 different patients being 219 (98.2%) from respiratory samples. Twenty four different *Nocardia* species were identified, 20 (83.3%) of which had been previously described as causing humans disease. All were patients with corticosteroid chronic treatments considering them immunocompromised. However, there were nine clinical isolates obtained from respiratory specimens belonging to four species, *Nocardia albobflava*, *Nocardia cerradoensis*, *Nocardia gamkensis* and *Nocardia jiangxiensis* that had been formerly described only isolated from soil microbiota of different geographic locations (China, Brazil, and South Africa). There were 9 isolates of these four *Nocardia* species from 6 different patients; three men and three women. All samples were from respiratory origin. *Nocardia cerradoensis* was isolated in 3 different patients causing two episodes of COPD exacerbation and one episode of bronchiectasis. One patient had four episodes of *Nocardia albobflava* maintained during 11 months, causing within this time two episodes of pneumonia and two episodes of COPD exacerbation. The other two patients had one episode of *Nocardia gamkensis* and *Nocardia jiangxiensis* respectively, as a cause of COPD exacerbation and bronchiectasis, respectively.

CONCLUSIONS

The development of molecular techniques for *Nocardia* identification is increasing the number of species causing clinical disease. At our knowledge, this is the first evidence in the literature of the isolation of *N. albobflava*, *N. cerradoensis*, *N. gamkensis*, and *N. jiangxiensis* as opportunistic human pathogens.

* After the deadline for abstracts in October was published in December of 2013 an article of an isolate in a clinical specimen of *N. gamkensis* in Brazil.

REFERENCES

Baio PVP, Ramos JN, Santos LSd, Soriano MF, Ladeira EM, et al. (2013) Molecular Identification of *Nocardia* Isolates from Clinical Samples and an Overview of Human Nocardiosis in Brazil. PLoS Negl Trop Dis 7(12): e2573.



Figure 1. Natural environment of *Nocardia cerradoensis* and *Nocardia gamkensis*