

Nocardia neocaledoniensis as Rare Cause of Spondylodiscitis

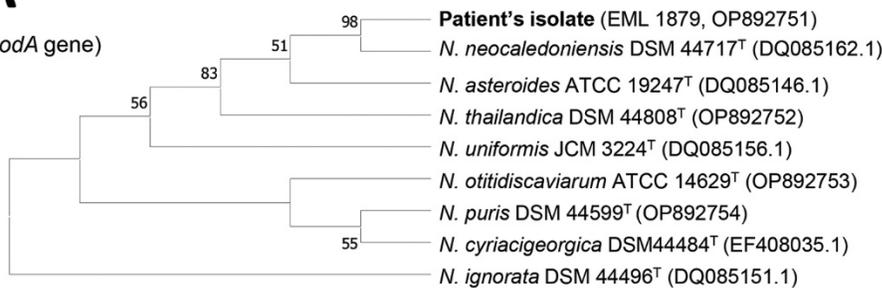
Appendix

Appendix Table. Primers used in this study for the DNA sequencing

Gene and primers	Sequences (5' →3')	Reference
16S rRNA		(1,2)
VIV8F	AGAGTTTGATCMTGGCTCAG	
V1V8R	GGGCGGWTGTACAAGGC	
V3V4F	CGGCCAGACTCCTACGGGAGGCAGCA	
V3-V4R	GCGTGGACTACCAGGTATCTAATCC	
Noc1F	GCTTAACACATGCAAGTCG	
Noc2R	GAATTCAGTCTCCCCTG	
<i>sodA</i>		(3)
SODF	CACCAYWSCAAGCACCA	
SODR	CCTTGACGTTCTGGTACTG	
<i>secA1</i>		(4)
M13F	GTAAAACGACGACCAGGACAGYAGTGGATGGGYCGSGTGCACCG	
M13R	CAGGAAACAGCTATGCGGCGGACGATGTAGTCCTTGTC	

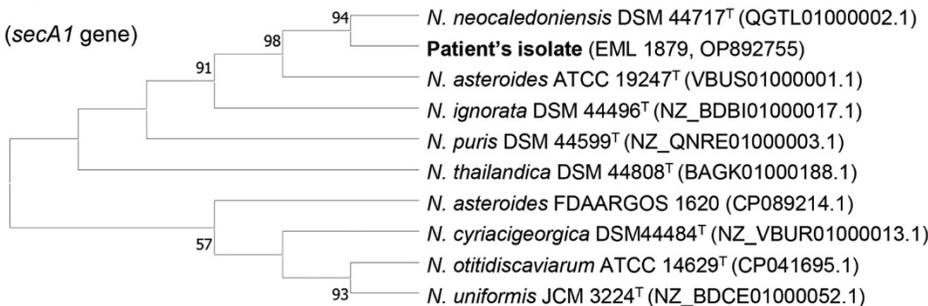
A

(*sodA* gene)



B

(*secA1* gene)



Appendix Figure. Alignment of 386 bp of the *sodA* (A) and 468 bp of the *secA1* genes (B) of the patient's isolate (strain EML 1879) with the *sodA* and *secA1* genes sequences of a set of reference strains of *Nocardia* species according to the Sánchez-Herrera's instructions (5). The evolutionary history

was inferred using the Neighbor-Joining method, Kimura's two-parameter model and bootstrap of 1000. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed.

References

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