

Supplementary Material

Genomic Virulence Features of two novel species, *Nocardia barduliensis* sp. nov. and *Nocardia gipuzkoensis* sp. nov., isolated from patients with chronic pulmonary diseases

Imen Nouioui ^{1,*}, Carlos Cortés-Albayay ², Meina Neumann-Schaal ¹, Diego Vicente ³, Gustavo Cilla ³, Hans-Peter Klenk ⁴, Jose María Marimón ³, Maria Ercibengoa ^{3,*}

¹ Leibniz Institute DSMZ–German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany; imen.nouioui@dsmz.de; meina.neumann-schaal@dsmz.de

² Laboratory of Microbial Complexity and Functional Ecology, Antofagasta Institute, University of Antofagasta, Antofagasta, Chile; c.j.cortesbt@gmail.com;

³ Biodonostia, Infectious Diseases Area, Respiratory Infection and Antimicrobial Resistance Group; Osakidetza Basque Health Service, Donostialdea Integrated Health Organisation, Microbiology Department, 20014 San Sebastian, Spain; diego.vicentearza@osakidetza.eus; carlosgustavosantiago.cillaeguiluz@osakidetza.eus; josemaria.marimonortizdez@osakidetza.eus; maria.ercibengoaarana@osakidetza.eus (M.E)

⁴ School of Natural and Environmental Sciences, Newcastle University, NE1 7RU Newcastle upon Tyne, United Kingdom; hans-peter.klenk@newcastle.ac.uk

* Correspondence: imen.nouioui@dsmz.de (I.N); maria.ercibengoaarana@osakidetza.eus (M.E)

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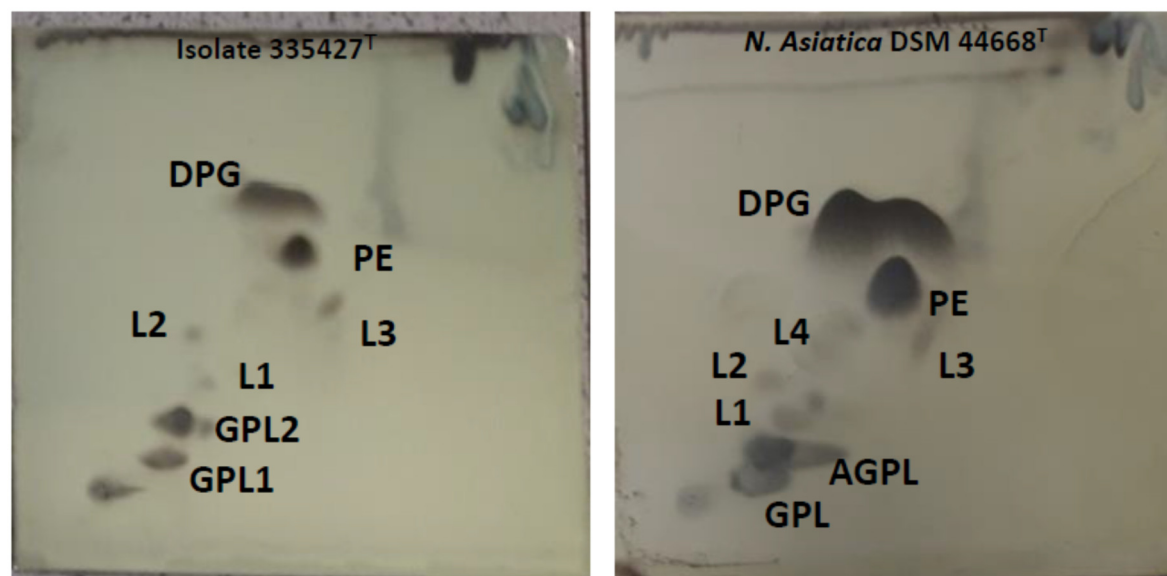


Figure S1. Two-dimensional TLC plates of polar lipids extracted from strains 335427^T and DSM 44668^T sprayed using molybdatophosphoric acid (Sigma P1518). AGPL, aminoglycophospholipid; DPG, diphosphatidylglycerol; GPL, glycophospholipid; L, lipid; PE, phosphatidylethanolamine. Solvent 1: chloroform: methanol: distilled water (65:25:4 v/v/v); Solvent 2: chloroform: glacial acetic acid: methanol: distilled water (80:12:15:4 v/v/v/v)

Table S1. Fatty acid profiles of isolates 335427^T and 234509^T and their closest phylogenetic neighbors. Only fatty acids more than 4% are listed.

Fatty acids	% of total composition			
	Isolate 335427 ^T	<i>N. asiatica</i> DSM 44668 ^T	Isolate 234509 ^T	<i>N. abscessus</i> DSM 44432 ^T
Summed feature 3 (C _{16:1} 7c/C _{16:1} ω6c)	14.7	17.8	4.5	12.9
C _{16:0}	21.4	43.6	10.0	33.8
C _{16:1} ω9c	-	-	6.2	-
C _{18:0}	25.4	-	-	9.5
C _{18:0} 10 methyl	15.0	16.5	-	10.9
C _{18:0} 1 ω7c	-	-	4.2	-
C _{18:1} ω9c	16.6	15.6	70.0	24.0
C _{19:0} anteiso	6.00	-	-	-

Table S2. Experimentally verified virulence genes on human and *Mus musculus* present in the genome sequences of isolates 335427^T and 234509^T.

Pathogenic gene	Function	Isolate		Isolate	
		Identity (%)	E-value	Identity (%)	E-value
<i>hrp1</i> (<i>Rv2626c</i>)	hypoxic response protein 1	50	6,00E-45	50,3	6E-46
<i>erm</i> (37) (<i>Rv1988</i>)	Probable 23S rRNA methyltransferase Erm (37)	35,7	2E-23	35,2	8E-18
<i>anxa1</i>	Immune response	24,5	2,00E-05	24,2	1,00E-16
<i>stf3</i>	PAPS-dependent sulfotransferase Stf3	28,02	4,00E-18	67,7	5E-130
<i>dosR</i> (<i>devR</i>)	Two-Component Regulatory Systems	79,9	R2-123	79,4	2E-122
<i>tcrX</i>	Probable transcriptional regulatory protein TcrX	54,9	2E-83	54,5	2E-88
<i>tcrY</i>	Probable sensor histidine kinase TcrY	43,4	2E-74	43,2	5,00E-73
<i>trcS</i>	Two component sensor histidine kinase TrcS	39,5	1E-39	41,8	2,00E-54
<i>kdpD</i>	Sensor protein KdpD	31,1	2E-23	30,1	2,00E-11
<i>kdpE</i>	Transcriptional regulatory protein KdpE	41,3	1E-54	80,8	2,00E-136

<i>Rv3213c</i>	Possible SOJ/para-related protein	43,8	7E-67	43,8	7,00E-67
<i>pepN</i>	Probable aminopeptidase N PepN (Lysyl aminopeptidase) (LYS-AP) (Alanine aminopeptidase)	73,1	0E+00	72,7	0
<i>Rv1773c</i>	Probable transcriptional regulatory protein	30,8	9E-19	32,6	5,00E-20
<i>umaA1</i>	S-adenosylmethionine-dependent methyltransferase UmaA	33,3	3E-41	33	1,00E-41
<i>alkB</i> (Rv3252c)	Probable transmembrane alkane 1-monooxygenase AlkB (Alkane 1-hydroxylase) (Lauric acid omega-hydroxylase) (Omega-hydroxylase) (Fatty acid omega-hydroxylase) (Alkane hydroxylase-rubredoxin)	69	0	68	0
<i>cmaA2</i>	Cyclopropane mycolic acid synthase 2	32,6	5E-42	33,1	2,00E-39
<i>fadB4</i>	Probable NADPH quinone oxidoreductase FadB4 (NADPH:quinone reductase) (zeta-crystallin)	66,3	1E-160	67	4,00E-161
<i>pknH</i>	Serine/threonine-protein kinase PknH	60	1,00E-104	59,2	2,00E-103
<i>hspX</i>	Alpha-crystallin	39,2	3,00E-18	38,2	2,00E-17
<i>Rv3167c</i>	Probable transcriptional regulatory protein	35,8	2,00E-23	37,2	9,00E-39

(Probably TetR-family)					
<i>glpX</i>	Fructose-1,6-bisphosphatase class 2	81,5	0E+00	82	0
<i>tap</i> (Rv1258c)	Multidrug efflux pump Tap	26,5	1E-06	26	3,00E-10
<i>mmpL11</i>	transmembrane transport protein	30	6E-74	32	9,00E-72
<i>espL</i>	ESX-1 secretion-associated protein EspL	38,4	5E-04	34,3	1,00E-05
<i>ppk2</i> (Rv3232c)	Polyphosphate:GDP phosphotransferase	29,8	4,00E-31	32	4,00E-32
<i>Rv0104</i>	Uncharacterized protein Rv0104	25,6	2,00E-06	26,2	1,00E-06
<i>Rv3404c</i>	dTDP-4-amino-4,6-dideoxyglucose formyltransferase	31,4	1,00E-12	31,5	8,00E-13
<i>mt3774</i> (CcsX)	Thioredoxin-related protein	41	6E-44	40,2	5,00E-45
<i>cnpB</i> (cpdA)	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	40,5	7,00E-59	41,5	6,00E-63
<i>lpqS</i>	Lipoprotein LpqS	34,2	7E-07	28,1	1,00E-06
<i>pptT</i>	Phosphopantetheinyl transferase PptT (CoA:APO-[ACP]panthetheinephosphotransferase) (CoA:APO-[acyl-carrier protein]panthetheinephosphotransferase)	56,7	8E-85	55,4	7,00E-82

<i>Rv0574c</i>	Probable polyglutamine synthesis accessory protein Rv0574c	63	2,00E-84	60,2	6,00E-153
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