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Identification of 2 Novel Species, *Mycobacterium novusgordoniae* and *M.* *shingordoniae*

Appendix

Case Descriptions

Case MN1

A 61-year-old female patient with familial hypercholesterolemia presented with a 1-month history of cough and hemoptysis. She was diagnosed with *Mycobacterium avium* pulmonary disease after multiple sputum cultures tests. She was treated with rifampin, ethambutol, and clarithromycin, which resolved the hemoptysis and achieved negative culture conversion. At 62 years old, an unidentified mycobacterium was detected by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) in a sputum acid-fast bacilli culture test.

Case MN2

A 65-year-old male with a history of pulmonary tuberculosis successfully treated with multi-drug therapy at the age of 60 resented with hemoptysis and was diagnosed with simple pulmonary aspergilloma, for which he received itraconazole. Treatment was discontinued after stabilization, and the patient remained clinically stable for several years. Acid-fast bacilli

cultures were consistently negative for a long time. However, at 72 years old, *Mycobacterium gordonae* was once detected using MALDI-TOF-MS. Chest computed tomography (CT) revealed bilateral apical cavities, scattered nodular shadows, and bronchiectasis; however, there was no significant progression over time, and his symptoms were mild and stable. At 73 years old, he was transferred to another hospital.

Case MS2

A 57-year-old male patient with no notable medical history, initially diagnosed with *M. avium* pulmonary disease during a routine health check, presented with an abnormal chest radiograph. He was treated with rifampin, ethambutol, and clarithromycin; however, disease progression with hemoptysis and worsening CT findings led to lingular segment resection. Postoperatively, sputum cultures were negative and antibiotics were discontinued.

At 69 years old, he developed a productive cough. Chest radiography and CT revealed atelectasis in the right upper lobe. *M. avium* and *Mycobacterium abscessus* subsp. *massiliense* were detected once. Subsequently, at 70 years old, an unidentified mycobacterium was detected by MALDI-TOF-MS in a sputum acid-fast bacilli culture test. Chronic airway infection was thought to have obstructed and narrowed the bronchi postoperatively. Airway clearance therapy with erythromycin and expectorants was initiated, which improved the atelectasis. Since then, no acid-fast bacilli have been detected and the patient's condition has remained stable.

Case MS3

A 76-year-old man with a history of peptic ulcer, glaucoma, and hypertension was referred to our hospital. Chest radiography revealed an abnormal chest shadow. CT showed a calcified nodule, infiltrates, and linear opacities in the middle lobe. Sputum tests for acid-fast bacilli and anti-GPL-core IgA antibody were negative. Considering the progressive enlargement

of the nodule, bronchoscopy was performed at 77 years old; however, no malignancy or mycobacterial infection was detected. The patient was clinically diagnosed with non-tuberculous mycobacterial pulmonary disease and erythromycin therapy was initiated, resulting in improvement of the radiographic findings. At 79 years old, an unidentified mycobacterial species was detected in the sputum cultures. The patient remained stable and no treatment was administered.

Methods

WGS Analysis

WGS analysis was performed using MinION (Oxford Nanopore Technologies, Oxford, UK) and MGISEQ-2000RS (MGI Tech, Shenzhen, People's Republic of China). Genome assembly for the MN1 and MS1–2 strains was performed using flye 2.9 (1) for long reads obtained from MinION, and sequencing errors were corrected with pilon 1.22 using short reads obtained from MGISEQ-2000RS. For MN2 and MS3, WGS analysis was performed using MGISEQ-2000RS (MGI Tech, Shenzhen, People's Republic of China), and genome assemblies were obtained using Unicycler v.0.5.0 (2).

Calculation and species identification using average nucleotide identity (ANI) value

Sequencing reads were assembled using flye 2.9 with default options (1). The assembled sequences were evaluated for the average nucleotide identity using FastANI (3) with “–fragLen 1000” option against 404 assemblies of *Mycobacterium* comprising 214 identified spp., 13 sub-spp., and 177 not identified spp.

References

1. Kolmogorov M, Yuan J, Lin Y, Pevzner PA. Assembly of long, error-prone reads using repeat graphs. Nat Biotechnol. 2019;37:540–6. [PubMed https://doi.org/10.1038/s41587-019-0072-8](https://doi.org/10.1038/s41587-019-0072-8)
2. Wick RR, Judd LM, Gorrie CL, Holt KE. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLOS Comput Biol. 2017;13:e1005595. [PubMed https://doi.org/10.1371/journal.pcbi.1005595](https://doi.org/10.1371/journal.pcbi.1005595)
3. Jain C, Rodriguez-R LM, Phillippy AM, Konstantinidis KT, Aluru S. High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nat Commun. 2018;9:5114. [PubMed https://doi.org/10.1038/s41467-018-03473-4](https://doi.org/10.1038/s41467-018-03473-4)

Appendix Table 1. Sampling dates for whole-genome sequencing of *Mycobacterium novusgordoniae* and *M. shingordoniae* strains

Isolate	Sampling dates
MN1 (TY813)	20210330
MN2	20221025
MS1 (TY814)	20201014, 20210707, 20220316
MS2 (TY815)	20220208, 20220325
MS3	20220830

Appendix Table 2. Reference sequence list of average nucleotides identifying mycobacteria species

Scientific name	NCBI RefSeq accession no.
<i>Mycobacterium ahvazicum</i>	GCF_022370835.1
<i>Mycobacterium alsense</i>	GCF_016592155.1
<i>Mycobacterium angelicum</i>	GCF_000015305.1
<i>Mycobacterium aquaticum</i>	GCF_002102265.1
<i>Mycobacterium arosiense</i>	GCF_010731755.1
<i>Mycobacterium asiaticum</i>	GCF_000382405.1
<i>Mycobacterium attenuatum</i>	GCF_002356495.1
<i>Mycobacterium avium</i>	GCF_010731935.1
<i>Mycobacterium avium</i> subsp. <i>avium</i>	GCF_000373905.1
<i>Mycobacterium avium</i> subsp. <i>hominissuis</i>	GCF_002982225.1
<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>	GCF_000262165.1
<i>Mycobacterium basiliense</i>	GCF_000364405.1

Scientific name	NCBI RefSeq accession no.
<i>Mycobacterium bohemicum</i>	GCF_012223425.1
<i>Mycobacterium botniense</i>	GCF_900141695.1
<i>Mycobacterium bouchedurhonense</i>	GCF_000419295.1
<i>Mycobacterium bourgelatii</i>	GCF_002148195.1
<i>Mycobacterium branderi</i>	GCF_015689175.1
<i>Mycobacterium canettii</i>	GCF_010731795.1
<i>Mycobacterium celatum</i>	GCF_002102185.1
<i>Mycobacterium colombiense</i>	GCF_010728155.1
<i>Mycobacterium conspicuum</i>	GCF_010723575.1
<i>Mycobacterium cookii</i>	GCF_010731735.1
<i>Mycobacterium crocinum</i>	GCF_010731815.2
<i>Mycobacterium decipiens</i>	GCF_002086455.1
<i>Mycobacterium diernhoferi</i>	GCF_000353205.1
<i>Mycobacterium dioxanotrophicus</i>	GCF_000709305.1
<i>Mycobacterium doricum</i>	GCF_000523635.1
<i>Mycobacterium europaeum</i>	GCF_000523975.1
<i>Mycobacterium florentinum</i>	GCF_010728525.1
<i>Mycobacterium fragae</i>	GCF_022370755.1
<i>Mycobacterium frederiksbergense</i>	GCF_000455205.1
<i>Mycobacterium gastrii</i>	GCF_000455125.1
<i>Mycobacterium genavense</i>	GCF_000620625.1
<i>Mycobacterium goodii</i>	GCF_010723415.1
<i>Mycobacterium gordonae</i>	GCF_022374895.1
<i>Mycobacterium grossiae</i>	GCF_002104675.1
<i>Mycobacterium hemophilum</i>	GCF_010731855.1
<i>Mycobacterium heckeshornense</i>	GCF_022179545.1
<i>Mycobacterium heidelbergense</i>	GCF_001570465.1
<i>Mycobacterium helveticum</i>	GCF_010731295.1
<i>Mycobacterium heraklionense</i>	GCF_001245615.1
<i>Mycobacterium hodleri</i>	GCF_001570425.1
<i>Mycobacterium holsaticum</i>	GCF_900078665.2
<i>Mycobacterium innocens</i>	GCF_002086915.1
<i>Mycobacterium interjectum</i>	GCF_019645835.1
<i>Mycobacterium intermedium</i>	GCF_010731875.1

Scientific name	NCBI RefSeq accession no.
<i>Mycobacterium intracellulare</i>	GCF_010731895.1
<i>Mycobacterium intracellulare</i> subsp. <i>chimaera</i>	GCF_002101785.1
<i>Mycobacterium intracellulare</i> subsp. <i>intracellulare</i>	GCF_000972905.1
<i>Mycobacterium intracellulare</i> subsp. <i>yongonense</i>	GCF_000972935.1
<i>Mycobacterium kansasii</i>	GCF_001021385.1
<i>Mycobacterium koreense</i>	GCF_003112775.1
<i>Mycobacterium kubicae</i>	GCF_008329645.1
<i>Mycobacterium kyogaense</i>	GCF_001050035.1
<i>Mycobacterium kyorinense</i>	GCF_001050015.1
<i>Mycobacterium lacus</i>	GCF_002086715.1
<i>Mycobacterium lehmannii</i>	GCF_001414075.1
<i>Mycobacterium lentiflavum</i>	GCF_001414095.1
<i>Mycobacterium leprae</i>	GCF_017876775.1
<i>Mycobacterium lepromatosis</i>	GCF_001644575.1
<i>Mycobacterium liflandii</i>	GCF_010731535.1
<i>Mycobacterium malmoense</i>	GCF_013466425.1
<i>Mycobacterium mantenii</i>	GCF_001440005.1
<i>Mycobacterium marinum</i>	GCF_001440085.1
<i>Mycobacterium marseillense</i>	GCF_001440125.1
<i>Mycobacterium montefiorensis</i>	GCF_001440105.1
<i>Mycobacterium mungi</i>	GCF_001440135.1
<i>Mycobacterium nebraskense</i>	GCF_001440155.1
<i>Mycobacterium neglectum</i>	GCF_001440185.1
<i>Mycobacterium neumannii</i>	GCF_001440205.1
<i>Mycobacterium noviomagense</i>	GCF_001440225.1
<i>Mycobacterium novum</i>	GCF_001440245.1
<i>Mycobacterium numidiamassiliense</i>	GCF_001440265.1
<i>Mycobacterium orygis</i>	GCF_001440275.1
<i>Mycobacterium ostraviense</i>	GCF_001440305.1
<i>Mycobacterium palauense</i>	GCF_001426545.1
<i>Mycobacterium pallens</i>	GCF_001428895.1
<i>Mycobacterium palustre</i>	GCF_002101935.1
<i>Mycobacterium paraense</i>	GCF_001545925.1
<i>Mycobacterium paraffinicum</i>	GCF_015708165.1

Scientific name	NCBI RefSeq accession no.
<i>Mycobacterium paragordoniae</i>	GCF_902509475.1
<i>Mycobacterium paraintracellulare</i>	GCF_001307545.1
<i>Mycobacterium parascrofulaceum</i>	GCF_000277125.1
<i>Mycobacterium paraseoulense</i>	GCF_000157895.3
<i>Mycobacterium paraterrae</i>	GCF_003253775.1
<i>Mycobacterium parmense</i>	GCF_021696875.1
<i>Mycobacterium persicum</i>	GCF_001583415.1
<i>Mycobacterium pseudokansasii</i>	GCF_013349145.1
<i>Mycobacterium pseudoshottsii</i>	GCF_001499905.1
<i>Mycobacterium rhizamassiliense</i>	GCF_001499965.1
<i>Mycobacterium riyadhense</i>	GCF_000195955.2
<i>Mycobacterium rufum</i>	GCF_001632805.1
<i>Mycobacterium saskatchewanense</i>	GCF_010727945.1
<i>Mycobacterium scrofulaceum</i>	GCF_001722335.1
<i>Mycobacterium senegalense</i>	GCF_002102175.1
<i>Mycobacterium senriense</i>	GCF_002101675.1
<i>Mycobacterium seoulense</i>	GCF_019645855.1
<i>Mycobacterium sherrisii</i>	GCF_003609695.1
<i>Mycobacterium shigaense</i>	GCF_002101775.1
<i>Mycobacterium shimoidei</i>	GCF_002086735.1
<i>Mycobacterium shinjukuense</i>	GCF_010727605.1
<i>Mycobacterium shottsii</i>	GCF_002250655.1
<i>Mycobacterium simiae</i>	GCF_002116635.1
<i>Mycobacterium simulans</i>	GCF_010727125.1
<i>Mycobacterium</i> sp. 012931	GCF_009936235.1
<i>Mycobacterium</i> sp. 1081908.1	GCF_000613245.1
<i>Mycobacterium</i> sp. 1100029.7	GCF_001049355.1
<i>Mycobacterium</i> sp. 1164966.3	GCF_010727725.1
<i>Mycobacterium</i> sp. 1165178.9	GCF_900078685.2
<i>Mycobacterium</i> sp. 1165196.3	GCF_010726955.1
<i>Mycobacterium</i> sp. 1245111.1	GCF_010728925.1
<i>Mycobacterium</i> sp. 1245499.0	GCF_005670605.1
<i>Mycobacterium</i> sp. 1245801.1	GCF_022374935.1
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Scientific name	NCBI RefSeq accession no.
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<i>Mycobacterium</i> sp. 1423905.2	GCF_001044255.1
<i>Mycobacterium</i> sp. 1465703.0	GCF_019456655.1
<i>Mycobacterium</i> sp. 1482292.6	GCF_000723385.1
<i>Mycobacterium</i> sp. 1554424.7	GCF_000184435.1
<i>Mycobacterium</i> sp. 155	GCF_002982215.1
<i>Mycobacterium</i> sp. 20KCMC460	GCF_001044245.1
<i>Mycobacterium</i> sp. 3519A	GCF_022374915.1
<i>Mycobacterium</i> sp. 4858	GCF_001552715.1
<i>Mycobacterium</i> sp. 852002–10029_SCH5224772	GCF_010722995.1
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<i>Mycobacterium</i> sp. CnD-18-1	GCF_001667105.1
<i>Mycobacterium</i> sp. DBP42	GCF_001667115.1
<i>Mycobacterium</i> sp. DL440	GCF_001667425.1
<i>Mycobacterium</i> sp. DL592	GCF_001667145.1
<i>Mycobacterium</i> sp. E1214	GCF_001667155.1

Scientific name	NCBI RefSeq accession no.
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<i>Mycobacterium</i> sp. E1747	GCF_001667075.1
<i>Mycobacterium</i> sp. E183	GCF_001667505.1
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<i>Mycobacterium</i> sp. E342	GCF_001667015.1
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<i>Mycobacterium</i> sp. E802	GCF_001666955.1
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<i>Mycobacterium</i> sp. H4Y	GCF_001954135.1
<i>Mycobacterium</i> sp. IDR2000157661	GCF_001954195.1
<i>Mycobacterium</i> sp. IEC1808	GCF_001954215.1
<i>Mycobacterium</i> sp. IS-1264	GCF_001954275.1

Scientific name	NCBI RefSeq accession no.
<i>Mycobacterium</i> sp. IS-2888	GCF_001953975.1
<i>Mycobacterium</i> sp. IS-836	GCF_001954045.1
<i>Mycobacterium</i> sp. ITM-2016-00316	GCF_900157385.1
<i>Mycobacterium</i> sp. ITM-2016-00318	GCF_900157375.1
<i>Mycobacterium</i> sp. IWGMT90018-18076	GCF_900157365.1
<i>Mycobacterium</i> sp. JS623	GCF_001652545.1
<i>Mycobacterium</i> sp. M1	GCF_010730575.1
<i>Mycobacterium</i> sp. MAC_011194_8550	GCF_001673155.1
<i>Mycobacterium</i> sp. MAC_080597_8934	GCF_001669335.1
<i>Mycobacterium</i> sp. MAG1	GCF_001665395.1
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<i>Mycobacterium</i> sp. MYCO198283	GCF_001854525.1
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<i>Mycobacterium</i> sp. NS-7484	GCF_002101585.1
<i>Mycobacterium</i> sp. OAS707	GCF_009729375.1
<i>Mycobacterium</i> <i>spongiae</i>	GCF_001942625.1
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<i>Mycobacterium</i> sp. PS03-16	GCF_001886515.1
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<i>Mycobacterium</i> sp. PYR15	GCF_001984215.1
<i>Mycobacterium</i> sp. QGD 101	GCF_002982275.1
<i>Mycobacterium</i> sp. Root135	GCF_002043095.1
<i>Mycobacterium</i> sp. Root265	GCF_000497265.2
<i>Mycobacterium</i> sp. shizuoka-1	GCF_900176255.2
<i>Mycobacterium</i> sp. SM1	GCF_009729395.1
<i>Mycobacterium</i> sp. SP-6446	GCF_008329605.1
<i>Mycobacterium</i> sp. 'sulfur cave'	GCF_008329585.1
<i>Mycobacterium</i> sp. TKK-01-0059	GCF_008329535.1
<i>Mycobacterium</i> sp. UM_11	GCF_002592005.1
<i>Mycobacterium</i> sp. UM_3	GCF_002723835.1
<i>Mycobacterium</i> sp. UM_CSW	GCF_002245535.1

Scientific name	NCBI RefSeq accession no.
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<i>Mycobacterium</i> sp. <i>UM_WGJ</i>	GCF_002335685.1
<i>Mycobacterium</i> sp. <i>URHB0044</i>	GCF_900240945.1
<i>Mycobacterium</i> sp. <i>WUMAC-025</i>	GCF_900240975.1
<i>Mycobacterium</i> sp. <i>WUMAC-067</i>	GCF_900292015.1
<i>Mycobacterium</i> sp. <i>WY10</i>	GCF_002968285.1
<i>Mycobacterium</i> sp. <i>Y57</i>	GCF_002968335.1
<i>Mycobacterium</i> sp. <i>YC-RL4</i>	GCF_010729665.1
<i>Mycobacterium stomatepiae</i>	GCF_000328565.1
<i>Mycobacterium syngnathidarum</i>	GCF_003408705.1
<i>Mycobacterium szulgai</i>	GCF_010729305.1
<i>Mycobacterium talmoniae</i>	GCF_003851485.1
<i>Mycobacterium terramassiliense</i>	GCF_002101875.1
<i>Mycobacterium timonense</i>	GCF_003254575.1
<i>Mycobacterium triplex</i>	GCF_002219285.1
<i>Mycobacterium tuberculosis</i>	GCF_003284965.1
<i>Mycobacterium tuberculosis</i> subsp. <i>tuberculosis</i>	GCF_002101555.1
<i>Mycobacterium tuberculosis</i> variant <i>africanum</i>	GCF_900566075.1
<i>Mycobacterium tuberculosis</i> variant <i>bovis BCG</i>	GCF_900566055.1
<i>Mycobacterium tuberculosis</i> variant <i>bovis</i>	GCF_900566065.1
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<i>Mycobacterium tuberculosis</i> variant <i>microti</i>	GCF_000164135.1
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<i>Mycobacterium vicinigordoniae</i>	GCF_003855255.1
<i>Mycobacterium virginense</i>	GCF_010726505.1
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<i>Mycobacterium xenopi</i>	GCF_005924235.1
<i>Mycobacteroides abscessus</i>	GCF_004570325.1
<i>Mycobacteroides abscessus</i> subsp. <i>abscessus</i>	GCF_005222675.1
<i>Mycobacteroides abscessus</i> subsp. <i>bolletii</i>	GCF_005938675.2

Scientific name	NCBI RefSeq accession no.
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<i>Mycobacteroides chelonae</i>	GCF_000613185.1
<i>Mycobacteroides franklinii</i>	GCF_014195125.1
<i>Mycobacteroides immunogenum</i>	GCF_014195195.1
<i>Mycobacteroides salmoniphilum</i>	GCF_014195025.1
<i>Mycobacteroides saopaulense</i>	GCF_007096635.1
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<i>Mycobacteroides</i> sp. <i>H002</i>	GCF_009729275.1
<i>Mycobacteroides</i> sp. <i>H003</i>	GCF_009729315.1
<i>Mycobacteroides</i> sp. <i>H054</i>	GCF_009729305.1
<i>Mycobacteroides</i> sp. <i>H063</i>	GCF_009729185.1
<i>Mycobacteroides</i> sp. <i>H070</i>	GCF_009729215.1
<i>Mycobacteroides</i> sp. <i>H072</i>	GCF_009729205.1
<i>Mycobacteroides</i> sp. <i>H079</i>	GCF_009729195.1
<i>Mycobacteroides</i> sp. <i>H092</i>	GCF_009729175.1
<i>Mycobacteroides</i> sp. <i>H101</i>	GCF_009729075.1
<i>Mycobacteroides</i> sp. <i>H110</i>	GCF_009729095.1
<i>Mycobacteroides</i> sp. <i>HXVII</i>	GCF_009729085.1
<i>Mycobacteroides</i> sp. <i>HXXIII</i>	GCF_009729105.1
<i>Mycobacteroides</i> sp. <i>LB1</i>	GCF_000026445.2
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<i>Mycolicibacillus trivialis</i>	GCF_003584745.1
<i>Mycolicibacter algericus</i>	GCF_014873705.1
<i>Mycolicibacter arupensis</i>	GCF_011745145.1
<i>Mycolicibacter engbaekii</i>	GCF_011694515.1
<i>Mycolicibacter hiberniae</i>	GCF_014202335.1
<i>Mycolicibacter icosiummassiliensis</i>	GCF_015710575.1
<i>Mycolicibacterium agri</i>	GCF_013404075.1
<i>Mycolicibacterium aichiense</i>	GCF_021183725.1
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<i>Mycolicibacterium arabiense</i>	GCF_018326285.1

Scientific name	NCBI RefSeq accession no.
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<i>Mycolicibacterium aubagnense</i>	GCF_019668465.1
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<i>Mycolicibacterium bacteremicum</i>	GCF_020217805.1
<i>Mycolicibacterium baixiangningiae</i>	GCF_000974705.1
<i>Mycolicibacterium boenickei</i>	GCF_010729895.1
<i>Mycolicibacterium brisbanense</i>	GCF_000878195.1
<i>Mycolicibacterium brumae</i>	GCF_017352375.1
<i>Mycolicibacterium canariasense</i>	GCF_017948465.1
<i>Mycolicibacterium celeriflavum</i>	GCF_018361265.1
<i>Mycolicibacterium chitae</i>	GCF_018455725.1
<i>Mycolicibacterium chlorophenolicum</i>	GCF_910591625.1
<i>Mycolicibacterium chubuense</i>	GCF_002086275.1
<i>Mycolicibacterium conceptionense</i>	GCF_019148985.1
<i>Mycolicibacterium confluentis</i>	GCF_020172665.1
<i>Mycolicibacterium cosmeticum</i>	GCF_020172685.1
<i>Mycolicibacterium duvalii</i>	GCF_022317005.1
<i>Mycolicibacterium elephantis</i>	GCF_021654635.1
<i>Mycolicibacterium fallax</i>	GCF_020181615.1
<i>Mycolicibacterium farcinogenes</i>	GCF_020181635.1
<i>Mycolicibacterium flavescens</i>	GCF_020181595.1
<i>Mycolicibacterium fluoranthenivorans</i>	GCF_021213805.1
<i>Mycolicibacterium fortuitum</i>	GCF_021916785.1
<i>Mycolicibacterium fortuitum</i> subsp. <i>acetamidolyticum</i>	GCF_022179425.1
<i>Mycolicibacterium fortuitum</i> subsp. <i>fortuitum</i>	GCF_022557175.1
<i>Mycolicibacterium gadium</i>	GCF_021648845.1
<i>Mycolicibacterium gilvum</i>	GCF_022348025.1
<i>Mycolicibacterium hassiacum</i>	GCF_022348085.1
<i>Mycolicibacterium helvum</i>	GCF_022348005.1
<i>Mycolicibacterium hippocampi</i>	GCF_010730355.1
<i>Mycolicibacterium houstonense</i>	GCF_023015925.1
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<i>Mycolicibacterium iranicum</i>	GCF_900417275.1

Scientific name	NCBI RefSeq accession no.
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<i>Mycolicibacterium litorale</i>	GCF_000559085.1
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<i>Mycolicibacterium lutetiense</i>	GCF_010731115.1
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<i>Mycolicibacterium mageritense</i>	GCF_002086635.1
<i>Mycolicibacterium malmesburyense</i>	GCF_015482805.1
<i>Mycolicibacterium mengxianglii</i>	GCF_002982335.1
<i>Mycolicibacterium monacense</i>	GCF_900078675.2
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<i>Mycolicibacterium mucogenicum</i>	GCF_002086515.1
<i>Mycolicibacterium murale</i>	GCF_002086285.1
<i>Mycolicibacterium neoaurum</i>	GCF_021183785.1
<i>Mycolicibacterium neworleansense</i>	GCF_000069185.1
<i>Mycolicibacterium nivoides</i>	GCF_010722915.1
<i>Mycolicibacterium novocastrense</i>	GCF_000526915.1
<i>Mycolicibacterium obuense</i>	GCF_010725725.1
<i>Mycolicibacterium parafortuitum</i>	GCF_002086695.1
<i>Mycolicibacterium peregrinum</i>	GCF_019456675.1
<i>Mycolicibacterium phlei</i>	GCF_900108565.1
<i>Mycolicibacterium phocaicum</i>	GCF_001552315.1
<i>Mycolicibacterium poriferae</i>	GCF_010731595.1
<i>Mycolicibacterium psychrotolerans</i>	GCF_002101885.1
<i>Mycolicibacterium pulveris</i>	GCF_022370635.1
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<i>Mycolicibacterium rutilum</i>	GCF_010726645.1
<i>Mycolicibacterium sarraceniae</i>	GCF_010726085.1
<i>Mycolicibacterium sediminis</i>	GCF_010725485.1
<i>Mycolicibacterium septicum</i>	GCF_010728325.1
<i>Mycolicibacterium setense</i>	GCF_010725885.1
<i>Mycolicibacterium smegmatis</i>	GCF_010730055.1
<i>Mycolicibacterium</i> sp. 018_SC-01_001	GCF_004924335.1
<i>Mycolicibacterium</i> sp. BK556	GCF_002086125.1

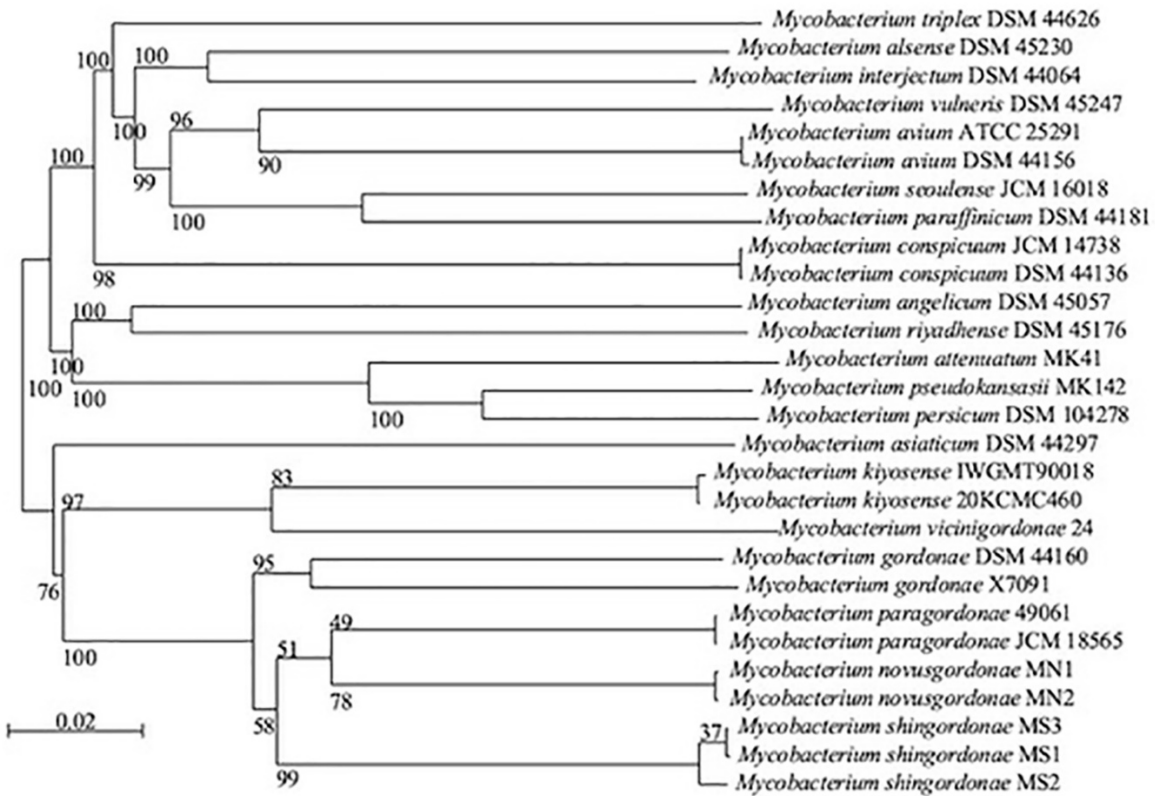
Scientific name	NCBI RefSeq accession no.
<i>Mycolicibacterium</i> sp. BK607	GCF_000805385.1
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<i>Mycolicibacterium</i> sp. CBMA 213	GCF_010728725.1
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<i>Mycolicibacterium</i> sp. CBMA 247	GCF_010731615.1
<i>Mycolicibacterium</i> sp. CBMA 293	GCF_002102065.1
<i>Mycolicibacterium</i> sp. CBMA 294	GCF_010731635.1
<i>Mycolicibacterium</i> sp. CBMA 295	GCF_000379865.1
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<i>Mycolicibacterium</i> sp. CBMA 360	GCF_002101845.1
<i>Mycolicibacterium</i> sp. CBMA 361	GCF_002101735.1
<i>Mycolicibacterium</i> sp. CH28	GCF_006864685.1
<i>Mycolicibacterium</i> sp. CR10	GCF_001021505.1
<i>Mycolicibacterium</i> sp. F2034L	GCF_010730745.1
<i>Mycolicibacterium</i> sp. GESEQ-9	GCF_001907675.1
<i>Mycolicibacterium</i> sp. GF69	GCF_010727475.1
<i>Mycolicibacterium sphagni</i>	GCF_002104765.1
<i>Mycolicibacterium</i> sp. NCC-Tsukiji	GCF_010731775.1
<i>Mycolicibacterium</i> sp. OfavD-34-C	GCF_002086115.1
<i>Mycolicibacterium</i> sp. P1-18	GCF_002102025.1
<i>Mycolicibacterium</i> sp. P9-22	GCF_005670685.2
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<i>Mycolicibacterium</i> sp. PAM1	GCF_010731655.1
<i>Mycolicibacterium</i> sp. S2-37	GCF_002101965.1
<i>Mycolicibacterium</i> sp. TY66	GCF_001499835.1
<i>Mycolicibacterium</i> sp. TY81	GCF_900232995.1
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<i>Mycolicibacterium stelleriae</i>	GCF_010727325.1

Scientific name	NCBI RefSeq accession no.
<i>Mycolicibacterium thermoresistibile</i>	GCF_002086165.1
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<i>Mycolicibacterium tusciae</i>	GCF_002086775.1
<i>Mycolicibacterium vaccae</i>	GCF_002356315.1
<i>Mycolicibacterium vanbaalenii</i>	GCF_010731695.1
<i>Mycolicibacterium vinylchloridicum</i>	GCF_002086795.1
<i>Mycolicibacterium wolinskyi</i>	GCF_002102155.1
<i>Mycolicibacter kumamotonensis</i>	GCF_002101815.1
<i>Mycolicibacter longobardus</i>	GCF_000253375.1
<i>Mycolicibacter minnesotensis</i>	GCF_004014805.1
<i>Mycolicibacter nonchromogenicus</i>	GCF_001605725.1
<i>Mycolicibacter senuensis</i>	GCF_010723305.1
<i>Mycolicibacter sinensis</i>	GCF_010731575.1
<i>Mycolicibacter</i> sp. MYC017	GCF_004014795.1
<i>Mycolicibacter</i> sp. MYC098	GCF_000214155.1
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<i>Mycolicibacter</i> sp. MYC123	GCF_002101705.1
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<i>Mycolicibacter terrae</i>	GCF_012396425.1

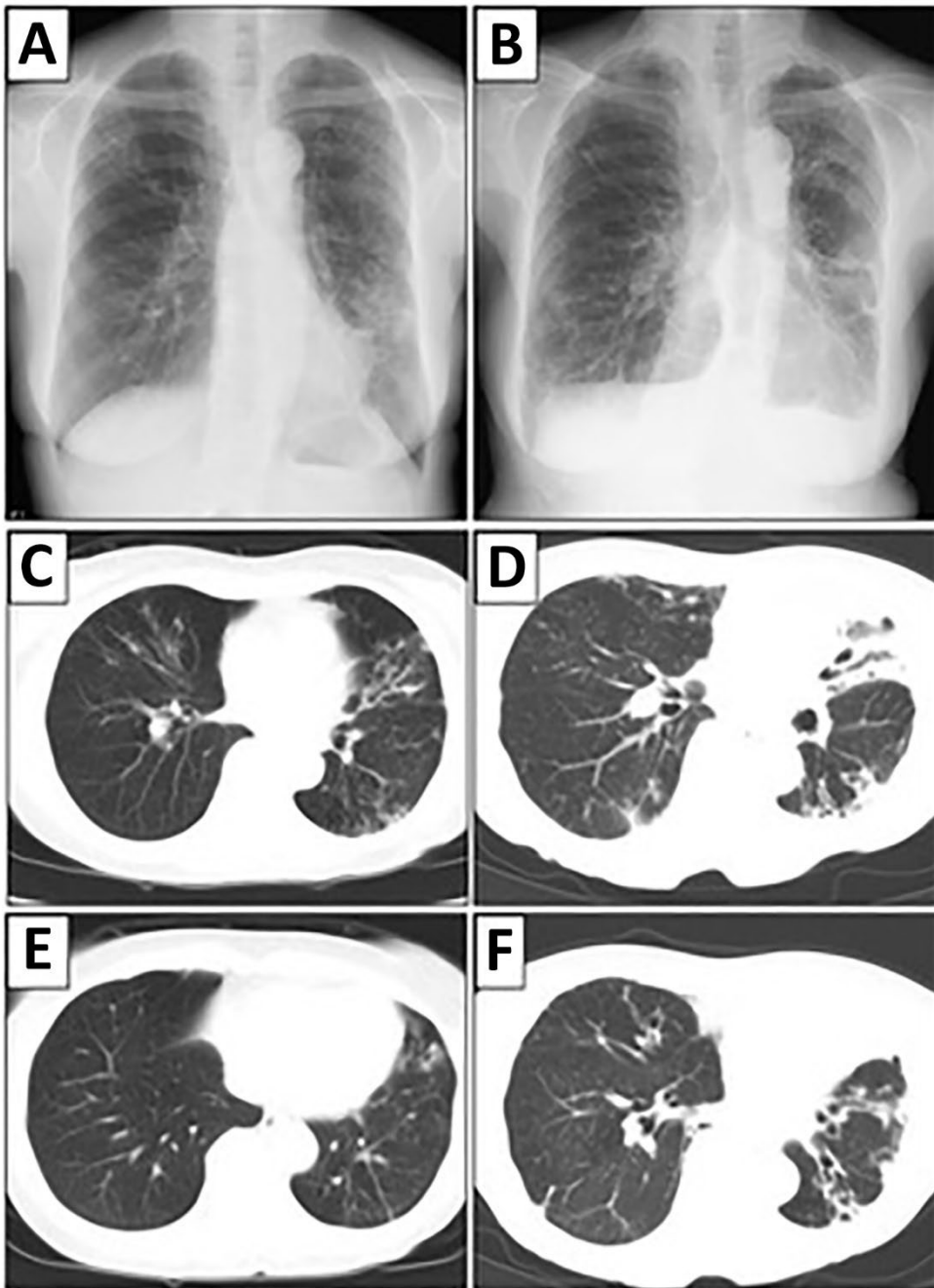
Appendix Table 3. Antimicrobial drug susceptibility data for the new *Mycobacterium gordonae*-clade species

Drug	MN1	MN2	MS1	MS2	MS3
Clarithromycin	0.5*	0.5	>32	1	0.5
Streptomycin	4	8	8	8	4
Kanamycin	4	4	16	8	8
Amikacin	2	4	8	8	8
Ethambutol	1	0.5	0.5	0.5	2
Rifampin	0.5	0.5	1	0.5	1
Levofloxacin	0.5	2	1	1	2
Ethionamide	16	16	16	16	16

*MIC; µg/mL



Appendix Figure 1. Whole-genome sequence based phylogenetic tree generated with TYGS. Tree inferred with FastME 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d5. The numbers above branches are GBDP pseudo-bootstrap support values >60% from 100 replications, with an average branch support of 91.8%, demonstrating the robustness of the inferred relationships. The tree was rooted at the midpoint.



Appendix Figure 2. Chest x-ray (A, B) and computed tomography (C, D, E, F), at age 68 (A, C, E), and at age 80 (B, D, F) are presented. The images revealed progressive worsening of centrilobular nodules and bronchiectasis in the middle and bilateral lower lobes.