

Table 1: 5'-16S rDNA (16S) and internal transcribed spacer (ITS) sequenced *Mycobacterium* species included in the RIDOM database

Species	Strain	Sequevar/serovar	16S/ ITS
<i>Mycobacterium abscessus</i> (T) ^a	DSM 44196 (ATCC 19977) ^b		+/+
" <i>M. acapulcensis</i> "	ATCC 14473		+/-
<i>M. abscessus</i>	DSM 43493		+/+
<i>M. africanum</i> (T)	ATCC 25420	subtype I	+/+
<i>M. africanum</i>	AHI ^d 15/99	subtype II	+/+
<i>M. africanum</i>	AHI 123/99	subtype II	+/-
<i>M. africanum</i>	AHI 128/99	subtype II	+/+
<i>M. agri</i> (T)	ATCC 27406		+/-
<i>M. agri</i>	ATCC 27407		+/-
<i>M. aichiense</i> (T)	DSM 44147 (ATCC 27280)		+/-
<i>M. alvei</i> (T)	DSM 44176 (ATCC 51304)		+/-
<i>M. asiaticum</i> (T)	DSM 44297 (ATCC 25276)		+/-
<i>M. aurum</i> (T)	DSM 43999 (ATCC 23366)		+/-
<i>M. austroafricanum</i> (T)	DSM 44191 (ATCC 33464)		+/-
<i>M. avium</i> subsp. <i>avium</i> (T)	DSM 44156 (ATCC 25291)	serovar 2, sequevar I/Mav A	+/+
<i>M. avium</i> subsp. <i>avium</i>	ATCC 35767	serovar 4, sequevar I/Mav A	+/+
<i>M. avium</i> subsp. <i>avium</i>	ATCC 35774	serovar 9, sequevar I/Mav D	+/+
<i>M. avium</i> subsp. <i>avium</i>	ATCC 35765	serovar 10, sequevar I/Mav B	+/+
<i>M. avium</i> subsp. <i>avium</i>	DSM 43216	sequevar II/Mav A	+/+
<i>M. avium</i> subsp. <i>paratuberculosis</i> (ST) ^a	DSM 44133 (ATCC 19698)	sequevar I/Mav A	+/+
<i>M. avium</i> subsp. <i>paratuberculosis</i> (ST) ^a	ATCC 700535	sequevar I	+/-
<i>M. avium</i> subsp. <i>silvaticum</i> (ST)	DSM 44175 (ATCC 49884)	sequevar I/Mav A	+/+
<i>M. bohemicum</i> (T)	DSM 44277		+/-
<i>M. bohemicum</i>	DSM 44408		+/-
<i>M. botniense</i> (T)	ATCC 700701		+/-
<i>M. bovis</i> subsp. <i>bovis</i> (T)	ATCC 19210		+/+
<i>M. bovis</i> subsp. <i>bovis</i>	DSM 43990 (ATCC 27289)	BCG	+/+
<i>M. bovis</i> subsp. <i>caprae</i> (ST)	CIP 105776		+/+
<i>M. branderi</i> (T)	ATCC 51789		+/-
<i>M. brumae</i> ⁸ (T)	DSM 44177 (ATCC 51384)		+/-
<i>M. celatum</i> (T)	DSM 44243 (ATCC 51131)		+ ^c /+
<i>M. chelonae</i> ¹ (T)	DSM 43804 (ATCC 35752)	sequevar I/Mche A	+/+
<i>M. chelonae</i>	DSM 43217 (ATCC 19236)	sequevar I	+/-
<i>M. chelonae</i>	DSM 43484 (ATCC 19536)	sequevar I/Mche B	+/+
<i>M. chelonae</i>	S385 ^m	sequevar II/Mche C	+/+
<i>M. chitae</i> (T)	ATCC 19627		+/-
<i>M. chlorophenicum</i> (T)	DSM 43826 (ATCC 49826)		+/-
<i>M. chubuense</i> (T)	DSM 44219 (ATCC 27278)		+/-
<i>M. confluentis</i> (T)	DSM 44017 (ATCC 49920)		+/-
<i>M. conspicuum</i> (T)	DSM 44136 (CIP 105165)		+/-
<i>M. cookii</i> (T)	DSM 43922 (ATCC 49103)		+/-
<i>M. diernhoferi</i> (T)	DSM 43524 (ATCC 19340)		+/-
<i>M. duvalii</i> (T)	DSM 44244 (ATCC 43910)		+/-
" <i>M. engbackii</i> "	ATCC 27353		+/-
" <i>M. engbackii</i> "	S280		+/-
<i>M. fallax</i> (T)	DSM 44179 (ATCC 35219)		+/-
<i>M. farcinogenes</i> (T)	DSM 43637 (ATCC 35753)		+/+
<i>M. farcinogenes</i>	DSM 43646		+/+
<i>M. flavescens</i> (T)	DSM 43991 (ATCC 14474)	sequevar I/Mfla A	+/+
<i>M. flavescens</i>	DSM 43531	sequevar II/Mfla B	+/+
<i>M. flavescens</i>	DSM 44430 (S318)	sequevar II	+/-
<i>M. flavescens</i>	S523	sequevar II	+/-
" <i>M. fluoroanthenvorans</i> "	DSM 44346		+/-
<i>M. fortuitum</i> subsp. <i>acetamidolyticum</i> (ST)	DSM 44220 (ATCC 35931)	sequevar I/Mfo B	+/+

<i>M. fortuitum</i> subsp. <i>acetamidolyticum</i>	ATCC 43266	sequevar I/Mfo B	+/+
<i>M. fortuitum</i> subsp. <i>fortuitum</i> (T)	DSM 46621 (ATCC 6841)	sequevar I/Mfo A	+/+ ^c
<i>M. fortuitum</i>	ATCC 49403	3rd biovariant complex (sorbitol +)	
		sequevar II/Mfo C	+/+ ^c
<i>M. fortuitum</i>	ATCC 49934	3rd biovariant complex (sorbitol +)	
		sequevar II	+/-
<i>M. fortuitum</i>	ATCC 49404	3rd biovariant complex (sorbitol -)	
		sequevar III/Mfo D	+/+ ^c
<i>M. fortuitum</i>	ATCC 49939	3rd biovariant complex (sorbitol -)	
		sequevar III	+/-
<i>M. fortuitum</i>	S312	sequevar III	+/-
<i>M. fortuitum</i>	S358	sequevar IV	+/-
<i>M. fortuitum</i>	DSM 43075 (IMRU 681)	sequevar V	+/-
<i>M. gadium</i> (T)	DSM 44077 (ATCC 27726)		+/-
<i>M. gastris</i> (T)	DSM 43505 (ATCC 15754)		+/+
<i>M. gastris</i>	DSM 43506		-/+
<i>M. genavense</i>	Wue ⁿ Tb268/96		+/-
<i>M. gilvum</i> (T)	ATCC 43909		+/-
<i>M. gilvum</i>	DSM 9487		+/-
<i>M. goodii</i> (T)	ATCC 700504		+/-
<i>M. gordonae</i> (T)	DSM 44160 (ATCC 14470)	sequevar I/Mgo A	+/+
<i>M. gordonae</i>	DSM 43212 (ATCC 35756)	sequevar II/Mgo B	+/+
<i>M. gordonae</i>	Bo ^s 4994/99	sequevar II	+/-
<i>M. gordonae</i>	Bo 11340/99	sequevar III/Mgo C	+/+
<i>M. gordonae</i>	Bo 10681/99	sequevar IV/Mgo D	+/+
<i>M. gordonae</i>	Bo 9411/99	sequevar V/Mgo E	+/+
<i>M. haemophilum</i> (T)	ATCC 29548		+/-
<i>M. hassiacum</i> (T)	DSM 44199 (ATCC 700660)		+/-
<i>M. heckeshornense</i> ²²	Wue 0687/99	100% similarity search match with <i>M. heckeshornense</i> [GenBank accession AF174290]	+/-
<i>M. heckeshornense</i> ²²	Bo 7644/99		+/-
<i>M. heidelbergense</i> (T)	ATCC 51253		+/-
<i>M. hiberniae</i> (T)	DSM 44241 (ATCC 49874)		+/-
<i>M. hodleri</i> (T)	DSM 44183 (CIP 104909T)		+/-
<i>M. interjectum</i> ^u (T)	ATCC 51457		+/-
<i>M. intermedium</i> (T)	DSM 44049 (ATCC 51848)		+/-
<i>M. intracellulare</i> (T)	DSM 43223 (ATCC 13950)	serovar 16, sequevar I/Min A	+/+
<i>M. intracellulare</i>	DSM 44161 (ATCC 23068)	sequevar I/Min A	+/+
<i>M. intracellulare</i>	ATCC 35762	serovar 12, sequevar I/Min A	+/+
<i>M. intracellulare</i>	ATCC 35847	serovar 7, sequevar II/MAC E	+/+
<i>M. intracellulare</i>	ATCC 35770	serovar 18, sequevar III/MAC D	+/+
<i>M. intracellulare</i>	S348	sequevar III/MAC J	+/+
<i>M. intracellulare</i>	S346	sequevar III/MAC K	+/+
<i>M. intracellulare</i>	S350	sequevar IV/MAC L	+/+
<i>M. intracellulare</i>	ATCC 35772	serovar 19, sequevar V	+/-
<i>M. intracellulare</i>	S247	sequevar V/MAC A	+/+
<i>M. kansasii</i> (T)	DSM 44162 (ATCC 12478)	sequevar I/Mka A	+/+
<i>M. kansasii</i>	DSM 43495 (IMET 10659)	sequevar I/Mka A	+/+
<i>M. kansasii</i> ^x	Paris ¹ I	sequevar I	+/-
<i>M. kansasii</i>	S221	sequevar II	+/-
<i>M. kansasii</i>	Bo 539/99	sequevar III/Mka C	+/+
<i>M. kansasii</i>	S536	sequevar III/Mka C	+/+
<i>M. kansasii</i> ^y	DSM 43221	sequevar IV/Mka D	+/+
<i>M. kansasii</i> ^y	DSM 43507	sequevar IV/Mka D	+/+
<i>M. kansasii</i> ^y	S233	sequevar IV/Mka D	+/+
<i>M. kansasii</i>	Bo 10492/98	sequevar V/Mka E	+/+
<i>M. kansasii</i> ^x	Paris V	sequevar V	+/-
<i>M. kansasii</i>	DSM 44431 (S522)	sequevar VI-1/Mka F	+/+
<i>M. kansasii</i> ^x	Bo 5160/97	sequevar VI-2/Mka F	+/+
<i>M. kansasii</i>	Bo 8875/99	sequevar VI-3/Mka F	+/+

<i>M. komossense</i> (T)	DSM 44078 (ATCC 33013)		+/-
" <i>M. lacticola</i> "	DSM 43270 (ATCC 12297)		+/-
<i>M. lentiflavum</i> (T)	DSM 44418 (ATCC 51985)	sequevar I	+/-
<i>M. leprae</i> ^x	AHI 1104/96		+/-
<i>M. lepraemurium</i> ^x	LRC ^k	Hawaiian material	+/+
<i>M. lepraemurium</i> ^x	AgR ^e	feline leprosy material	+/-
<i>M. madagascariense</i> (T)	ATCC 49865		+/-
<i>M. mageritense</i> (T)	CIP ^h 104973		+/-
<i>M. malmoense</i> (T)	DSM 44163 (ATCC 29571)		+/-
<i>M. malmoense</i>	DSM 44053		+/-
<i>M. marinum</i> (T)	DSM 44344 (ATCC 927)		+/+
<i>M. marinum</i>	DSM 43518		+/+
<i>M. microti</i> (T)	ATCC 19422 (DSM 44155)		+/+
<i>M. moriokaense</i> (T)	DSM 44221 (ATCC 43059)		+/-
<i>M. mucogenicum</i> (T)	ATCC 49650		+/-
<i>M. murale</i> (T)	DSM 44340		+/+ ^c
<i>M. neoaurum</i> (T)	DSM 44074 (ATCC 25795)		+/-
<i>M. nonchromogenicum</i> (T)	DSM 44164 (ATCC 19530)		+/-
<i>M. nonchromogenicum</i>	ATCC 25142		+/-
<i>M. nonchromogenicum</i>	S264		+/-
<i>M. novocastrense</i> (T)	DSM 44203		+/+ ^c
<i>M. obuense</i> (T)	DSM 44075 (ATCC 27023)		+/-
<i>M. obuense</i>	ATCC 27023		+/-
" <i>M. paraffinicum</i> "	DSM 44181 (ATCC 12670)		+/-
<i>M. parafortuitum</i> (T)	DSM 43528 (ATCC 19686)	sequevar I	+/-
<i>M. parafortuitum</i>	DSM 43526 (S513)	sequevar II/Mpa B	+/+
<i>M. peregrinum</i> ^v (T)	ATCC 14467 (DSM 43271)	Mpe A	+/+ ^c
<i>M. peregrinum</i>	ATCC 700686	Mpe B	+/+ ^c
<i>M. peregrinum</i>	S254	Mpe C	+/+
<i>M. peregrinum</i>	S334		+/-
" <i>M. petroleophilum</i> "	DSM 44182 (ATCC 21497)		+/-
<i>M. phlei</i> (T)	DSM 43239 (ATCC 11758)	Mphle A	+/+
<i>M. phlei</i>	S271	Mphle B	+/+
<i>M. porcinum</i> (T)	DSM 44242 (ATCC 33776)		+/+
<i>M. porcinum</i>	ATCC 33775		+/+
<i>M. poriferae</i> (T)	ATCC 35087		+/-
<i>M. pulveris</i> (T)	DSM 44222 (ATCC 35154)		+/-
<i>M. rhodesiae</i> ^w (T)	DSM 44223 (ATCC 27024)		+/+
<i>M. scrofulaceum</i> (T)	DSM 43992 (ATCC 19981)	Mscro A	+/+
<i>M. scrofulaceum</i>	S343	Mscro B	+/+
<i>M. senegalense</i> (T)	DSM 43656 (ATCC 35796)		+/+
<i>M. senegalense</i>	DSM 43231		+/+
<i>M. senegalense</i> ^{z1}	DSM 43655 (S113)		+/-
<i>M. septicum</i> (T)	DSM 44393 (ATCC 700731)		+/+
<i>M. shimoides</i> (T)	DSM 44152 (ATCC 27962)		+/-
" <i>M. shinshuense</i> "	ATCC 33728		+/-
<i>M. simiae</i> (T)	DSM 44165 (ATCC 25275)	sequevar I	+/-
<i>M. simiae</i>	ATCC 15080	sequevar II/Msi E	+/+
<i>M. smegmatis</i> (T)	DSM 43756 (ATCC 19420)		+/-
<i>M. sphagni</i> (T)	ATCC 33027		+/-
<i>M. sphagni</i>	ATCC 33026		+/-
<i>M. szulgai</i> (T)	DSM 44166 (ATCC 35799)		+/-
<i>M. terrae</i> (T)	DSM 43227 (ATCC 15755)	sequevar I	+/-
<i>M. terrae</i>	DSM 43541	sequevar II	+/-
<i>M. terrae</i>	S281	sequevar III	+/-
<i>M. thermoresistibile</i> (T)	DSM 44167 (ATCC 19527)		+/-
<i>M. tokaiense</i> (T)	ATCC 27282		+/+
<i>M. triplex</i> (T)	ATCC 700071		+/-
<i>M. triviale</i> (T)	DSM 44153 (ATCC 23292)		+/-
<i>M. triviale</i>	S354		+/-
<i>M. tuberculosis</i> (T)	ATCC 27294		+/+
<i>M. tuberculosis</i>	ATCC 25177		+/+

<i>M. tusciae</i> (T)	DSM 44338		+/-
<i>M. ulcerans</i> (T)	ATCC 19423 (DSM 44154)	ITM type 2/Mul A	+/+
<i>M. ulcerans</i>	ITM ^d 5114	ITM type 3/Mul B	+/+
<i>M. vaccae</i> (T)	DSM 43292 (ATCC 15483)		+/-
<i>M. wolinskyi</i> (T)	ATCC 700010		+/-
<i>M. xenopi</i> (T)	DSM 43995 (ATCC 19250)	sequevar I/Mxe A	+/+
<i>M. xenopi</i>	S88	sequevar II/Mxe B	+/+
<i>M. xenopi</i>	S91	sequevar III/Mxe C	+/+
<i>M. xenopi</i>	DSM 44169 (ATCC 19971)	sequevar II or III (due to one ambiguity)	+/-

^a (T) designates the type strain of this species and (ST) – designates the type strain of this subspecies.

^b (Culture collection number), identical strain in another culture collection.

^c Sequence only obtainable by subcloning of PCR products.

^d AHI, Armauer Hansen Institut, Würzburg, Germany.

^e AgR, Geoff de Lisle, AgResearch, Wallaceville Animal Research Centre, Upper Hutt - New Zealand.

^f ATCC, American Type Culture Collection, Manassas, USA..

^g Bo, Elvira Richter, Nationales Referenzzentrum für Mykobakterien, Forschungszentrum Borstel, Germany.

^h CIP, La Collection de l'Institut Pasteur, Paris, France.

ⁱ DSM, Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany.

^j IFT, Françoise Portaels, Institute of Tropical Medicine, Department of Microbiology, Antwerpen, Belgium.

^k LRC, Yoshiko Kashiwabara, Leprosy Research Center, Tokyo, Japan.

^l Paris, Veronique Vincent, Laboratoire de Reference des Mycobacteries, Institut Pasteur, Paris, France.

^m S, Andreas Roth, Institut für Mikrobiologie und Immunologie, Lungenklinik Heckeshorn, Berlin, Germany.

ⁿ Wue, Institut für Hygiene und Mikrobiologie, Universität Würzburg, Würzburg, Germany.

^s *M. brumae* DSM 44177 (T) from DSM checked with identical strain ATCC 51384 (T) ordered from ATCC.

^t *M. chelonae* DSM 43804 (T) from DSM checked with identical strain ATCC 35752 (T) ordered from ATCC.

^u *M. interjectum* ATCC 51457 (T) from ATCC checked with identical strain DSM 44064 (T) ordered from DSM.

^v *M. peregrinum* ATCC 14467 (T) from ATCC checked with identical strain DSM 43271 (T) ordered from DSM.

^w *M. rhodesiae* DSM 44223 (T) from DSM checked with identical strain ATCC 27024 (T) ordered from ATCC.

^x Only as DNA available (no culture).

^y According to ITS-RFLP [11], a *M. gastri* Mga B subtype (A. Roth, personal communication).

^{z1} According to ITS-RFLP [11], a *M. fortuitum* sequevar RFLP pattern VIII (A. Roth, personal communication).

^{z2} This species was recently validly published [61], type strain is DSM 44428.

The following GenBank sequences were also analysed and included in the RIDOM database:

16S rDNA: *M. doricum* (GenBank accession: AF264700, strain: DSM 44339); *M. immunogenum* (AJ011771, MN 3744); *M. kubicae* (AF133902, ATCC 700732 (T)); *M. lentiflavum* (X80770, ATCC 51988) sqv. II; "M. monacense" (AF107039, B9-21-178); "M. tilburgii" (Z50172, tilburgii strain).

ITS: *M. avium* subsp. *avium* (GenBank accession: L07857, sequevar: Mav C, strain: 6194); *M. avium* subsp. *avium* (L07858, Mav D, 17584-286); *M. avium* subsp. *avium* (Z46422, Mav E, c1505); *M. intracellulare* (Z46423, Min B, D71040); *M. intracellulare* (Z46424, Min C, D40135); *M. intracellulare* (Z46425, Min D, D70257); *M. intracellulare* (L07848, MAC B, 12645); *M. intracellulare* (L07849, MAC C, 23393); *M. intracellulare* (L07853, MAC F, 5154 O'Connor); *M. intracellulare* (L15620, MAC H); *M. intracellulare* (Z46421, MAC I, D40469); *M. kansasii* ([40], Mka B); *M. simiae* (Y14186, Msi A, ATCC 25275); *M. simiae* (Z46426, Msi B, C13383); *M. simiae* (Y14187, Msi C, S142); *M. simiae* (Y14188, Msi D, S136); *M. triviale* (X99221, Mtri A, ATCC 23292).

The following culture collection strains were also sequenced (16S rDNA) but were "wrong" and therefore **not** included in the RIDOM database: DSM 44218, DSM 44135, DSM 44277 (later replaced against the original strain by the depositor), DSM 43219, DSM 43074, DSM 44245, and DSM 44064.

The following GenBank sequences were also analysed but **not** included in the RIDOM database:

16S rDNA: "M. anthracenicum" (GenBank accession: Y15709); "M. buckleii" (AF000225); "M. canettii" (AJ007315, strain 217/94); "M. columbarii" (AJ001220); *M. elephantis* (AJ010747, DSM 44368 (T)); *M. heckeshornense* (AF174290, DSM 44428 (T)); "M. isoniaciini" (X80768, INA-I); "M. ratisbonense" (AF055331); "M. sydneyiensis" (AF101243).

ITS: "M. habana" (X74056, TMC 5135); "M. lufu" (X74055).