

## Twelve conserved DNA regions studied

Isolates	5' region of 16S rDNA (448 bp)	23S rDNA (3,112 bp)	ITS (216 bp)	<i>gyrA</i> (549 bp)	<i>hsp65</i> (401 bp)	<i>argH</i> (533 bp)	<i>cya</i> (513 bp)	<i>glpK</i> (554 bp)	<i>gnd</i> (494 bp)	<i>pgm</i> (559 bp)	<i>pta</i> (673 bp)	<i>purH</i> (598 bp)
INCQS 00594	GU143891 <sup>a</sup>	GU143886	EU117206	GU131159	EU117205	JQ582469	JQ582470	JQ582577	JQ582471	JQ582592	JQ582600	JQ582608
<i>Mycobacterium bolletii</i>	AY859681	GU143888.2	AM421291	GU131161	EU266576	FJ609780	FJ609784	FJ609781	FJ609783	HM371394	HM371395	HM371396
<i>Mycobacterium massiliense</i> B 67 <sup>b</sup>	AY593980	GU143887	AM421292	GU131160	EU266578	FJ609785	FJ609789	FJ609786	FJ609788	HM371391	HM371392	HM371393
IAL 002 <sup>c</sup>	-	-	-	JQ582585	EU220417	-	-	JQ582578	-	JQ582593	JQ582601	JQ582609
IAL 014 <sup>c</sup>	-	-	-	JQ582586	-	-	-	JQ582579	-	JQ582594	JQ582602	JQ582610
IAL 028 <sup>c</sup>	-	-	-	JQ582587	-	-	-	JQ582580	-	JQ582595	JQ582603	JQ582611
P7 <sup>d</sup>	FJ590460	-	-	JQ582588	-	-	-	JQ582581	-	JQ582596	JQ582604	JQ582612
P13 <sup>d</sup>	FJ590460	-	-	JQ582589	FJ536241	-	-	JQ582582	-	JQ582597	JQ582605	JQ582613
P13 <sup>d</sup>	FJ590466	-	-	JQ582590	FJ536247	-	-	JQ582583	-	JQ582598	JQ582606	JQ582614
P53 <sup>d</sup>	-	-	-	JQ582591	-	-	-	JQ582584	-	JQ582599	JQ582607	JQ582615
P3 <sup>d</sup>	-	-	-	-	FJ536237	-	-	-	-	-	-	-
P4 <sup>d</sup>	-	-	-	-	FJ536238	-	-	-	-	-	-	-
P5 <sup>d</sup>	-	-	-	-	FJ536239	-	-	-	-	-	-	-
P6 <sup>d</sup>	FJ590459	-	-	-	FJ536240	-	-	-	-	-	-	-
P8 <sup>d</sup>	FJ590461	-	-	-	FJ536242	-	-	-	-	-	-	-
P9 <sup>d</sup>	FJ590462	-	-	-	FJ536243	-	-	-	-	-	-	-
P10 <sup>d</sup>	FJ590463	-	-	-	FJ536244	-	-	-	-	-	-	-
P11 <sup>d</sup>	FJ590464	-	-	-	FJ536245	-	-	-	-	-	-	-
P12 <sup>d</sup>	FJ590465	-	-	-	FJ536246	-	-	-	-	-	-	-
P14 <sup>d</sup>	FJ590467	-	-	-	FJ536248	-	-	-	-	-	-	-
P15 <sup>d</sup>	FJ590468	-	-	-	FJ536249	-	-	-	-	-	-	-
B66 <sup>b</sup>	-	-	-	-	EU220418	-	-	-	-	-	-	-
B62 <sup>b</sup>	-	-	-	-	EU220419	-	-	-	-	-	-	-
B60 <sup>b</sup>	-	-	-	-	EU220420	-	-	-	-	-	-	-

sequences were aligned using CLUSTALW Multiple Alignment program (Thompson et al. 1994) included in BioEdit package version 7.0.5.3 (Hall 1999) for identification of single nucleotide polymorphisms (SNPs) present exclusively in INCQS 00594. Sizes of the analyzed fragments are in parenthesis. Exclusive SNPs of INCQS 00594 were not found in 23S rDNA, *argH*, *cya* and *gnd* and the internal transcribed sequence (ITS) region after alignment with two type strains. Alignment of the 5' region of 16S rDNA and *hsp65* sequences of INCQS 00594 and sequences available in GenBank has not evidenced exclusive SNPs for discrimination of the epidemic strain. *glpK* and *pta* could represent other targets to differentiate the epidemic strain. *a*: GenBank accession; *b*: Viana-Niero et al. (2008); *c*: Matsumoto et al. (2011); *d*: da Costa et al. (2009); -: not analyzed.

## Primers used for polymerase chain reaction and sequencing of conserved DNA regions

Genes	Primers	Sequences 5'-3'	Temperature (°C)	References
23S rDNA	Spl	ACCTCCTTTCTAAGGAGCACC	64	Roth et al. (2000)
	23S-1R	CCCAAAGCCTATATATTCAGC	60	
	23S-2F	AGCCTCGGGGAGCTGCCAACC	72	
	23S-2R	GAGGCTTTGACGGATTGTAGG	64	
	23S-3F	ACTCTCTAGTGACCGATAGCG	64	
	23S-3R	AGTTTGGCTGACGTCAGTAAC	62	
	23S-4F	ATTTAGGTGCAGCGTCGCGTG	66	
	23S-4R	AAGTTTCTCACTTGCCTGTCG	62	
	23S-5F	AGGGGAGCGTCTGCACCCAG	72	
	23S-5R	CGAAGTTACGGGGGTATTTTG	62	
	23S-6F	TATGCTGCCAAGAAAAGCCTC	62	
	23S-6R	TGTCCCTGGACCGGATATACG	66	
	23S-7F	TGTGAAGCAGGCACGCCAGTG	68	
	23S-7R	GTCCCGTCTCTCGTACTAG	68	
	23S-8R	GTGGAGTGTGGTCGTCAAATG	62	
	<i>gyrA</i>	GyrA-F	GCCGTCGACCGCATCGAACCG	72
GyrA-R		GTTGTCCAACGCCAGTAGAC	66	
<i>argH</i>	ARGHF	GACGAGGGCGACAGCTTC	60	Macheras et al. (2009)
	ARGHSR1	GTGCGCGAGCAGATGATG	58	
<i>cya</i>	ACF	GTGAAGCGGGCCAAGAAG	58	Macheras et al. (2009)
	ACSR1	AACTGGGAGGCCAGGAGC	60	
<i>glpK</i>	GLPKSF1	AATCTCACCGGCGGTGTC	58	Macheras et al. (2009)
	GLPKSFR2	GGACAGACCCACGATGGC	60	
<i>gnd</i>	GNDF	GTGACGTCGGAGTGGTTGG	62	Macheras et al. (2009)
	GNDSR1	CTTCGCCTCAGGTCAGCTC	62	
<i>pgm</i>	PGMSF1	CCATTTGAACCCGACCGG	58	Macheras et al. (2011)
	PGMSR2	GTGCCAACGAGATCCTGCG	62	
<i>pta</i>	PTASF1	GATCGGGCGTCATGCCCT	60	Macheras et al. (2011)
	PTASR2	ACGAGGCACTGCTCTCCC	60	
<i>purH</i>	PURHSF1	CGGAGGCTTACCCTGGA	60	Macheras et al. (2011)
	PURHSR2	CAGGCCACCGCTGATCTG	60	