

Table 1. Concordance rates of the nucleotide sequence for *hsp65* and *rpoB* among the present strain and the related mycobacteria

Organism	Concordance rates with the present strain	
	<i>hsp65</i> (607 bp)	<i>rpoB</i> (603 bp)
<i>Mycobacterium marinum</i> ATCC927	99.34%	99.69%
<i>Mycobacterium ulcerans</i> Agy99 (Africa)	99.34%	99.85%
<i>Mycobacterium ulcerans</i> subsp. <i>shinshuense</i> ATCC33728	100%	100%

Table 2. Comparison of the nucleotide sequence of 16S rRNA region among the related mycobacteria

Organism	The nucleotide sequences of 16S rRNA for differentiation			
	492	1247	1288	1449-1451 ^b
<i>Mycobacterium marinum</i> ATCC927 ^a	TGG <u>A</u> GAA	GGT <u>A</u> CAA	TAA <u>A</u> GCC	ACCC --- TTTG
<i>Mycobacterium ulcerans</i> 112509 ^a	TGG <u>A</u> GAA	GGT <u>G</u> CAA	TAA <u>C</u> GCC	ACCC <u>TTTT</u> TTTG
<i>Mycobacterium ulcerans</i> subsp. <i>shinshuense</i> ^a	TGG <u>G</u> GAA	GGT <u>G</u> CAA	TAA <u>G</u> GCC	ACCC --- TTTG
The present strain	TGG <u>G</u> GAA	GGT <u>G</u> CAA	TAA <u>G</u> GCC	ACCC --- TTTG

^a Nucleotides reported in references 15-18.

^b Hyphens indicate gaps.