TABLE 2. Genes used for the MLST scheme with primers used for amplification

Gene	Primer sets [a] (5' → 3')	Tm (°C)	Amplicon size (bp)	Gene fragment [b] size (bp)
nusA	P1 GCCTGCAAGA**R**CCCGACAAG P2 GTCCAT**S**GCGTGCTTGTCTTC	59	795	355
rpoB	P1 TGCC**M**TGGAACGG**Y**TACAAC P2 GGCCAG**R**TA**S**ACCTTGATCATCTT	57	791	413
eno	P1 ATGCCCGTGCC**S**ATGATGAA P2 TCAGGGTGCCGATCTGGTTG	57	613	214
gltB	P1 TGCAACCGGGCAAGATGTT P2 TCGGACACGATCAGGATGTT	57	685	241
lepA	P1 CTA**Y**AACCTGAACCTGATCGACAC P2 GCGACTT**S**GGCGTGAACAC	57	524	347
nuoL	P1 CATGCACCA**YR**ACCAGGACAT P2 CGCGAACGCGTAGTGATAGATG	56	880	230
nrdA	P1 GAACTGGATTCCCGACCTGTTC P2 TTCGATTTGACGTACAAGTTCTGG	56	954	449

[a] Standard mixed oligonucleotide bases for primer sequences are listed in bold

[b] Sequence length used in MLST analysis for each locus