Leptospira pathogenic sps MLST protocol

Gene	Primer Sequence (5’→3’)	Tm (°C)	Size (bp)	Allele size (bp)	
				MLST_2	MLST_3
Adenylate Kinase (adk)	F: GGGCTGGAAAAGGTACACAA R: ACGCAAGCTCCTTTTGAATC	58	531	430	429
	F2-ACATTATCTTCATGGGACCTCC R2- TTACACAAGCTCCCTTTGAAT	54	557		
Isocitarate dehydrogenase (icdA)	F: GGGACGAGATGACCAGGAT R:CTTTTTTGAGATCCGCAGCTTT	58	674	557	555
Lipoprotein L32 (LipL32)	F:ATCTCCGTTGCACTCTTTGC R:ACCATCATCATCATCGTCCA	58	474	450	450
Lipoprotein L41 (LipL41)	F:TAGGAAATTGCGCAGCTACA R:GCATCGAGAGGAATTAACATCA	58	520	493	492
UDP-N-acetylglucosamine pyrophosphorylase (glmU)	F:AGGATAAGGTCGCTGTGGTA R:AGTTTTTTTCCGGAGTTTCT	46	650	444	-
NAD(P) transhydrogenase subunit alpha (pntA)	F:TAGGAAARATGAAACCRGGAAC R:AAGAAGCAAGATCCACAAYTAC	46	621	525	-
Rod shape-determining protein rodA (mreA)	F:GGCTCGCTCTYGACGGAAA R:TCCRTAACTCATAAAMGACAAAGG	46	719	435	-
16S ribosomal RNA (rrs2)	F-CATGCAAGTCAAGCGGAGTA R-AGTTGAGCCCGCAGTTTTC	58	541	-	450
Pre-protein Translocase SecY subunit (secY)	F-ATGCCGATCATTTTTGCTTC R-CCGTCCCTTAATTTTAGACTTCTTC R2-CCTTCCTTTAATTTTAGACTTTTTC	58 54	549	-	501

* Same primers were used for sequencing

References:

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