

Appendix Table. Genes analyzed by PCR and primers used, for group C streptococci, from 8 dairy herds, Portugal

Primer	Sequence (5' ? 3')	Expected product, bp	Reference
Prophage-associated virulence determinants			
Pyrogenic exotoxins			
<i>ssa</i> (forward)	GTGTAGAATTGAGGTAATTG	706	(6)
<i>ssa</i> (reverse)	TAATATAGCCTGTCTCGTAC		
<i>speA</i> (forward)	CTTAAGAACCAAGAGATGGC	200	(6)
<i>speA</i> (reverse)	ATAGGCTTTGGATAACATCG		
<i>speC</i> (forward)	CATCTATGGAGGAATTACGC	246	(6)
<i>speC</i> (reverse)	TGTGCCAATTTGATTCTGC		
<i>speH</i> (forward)	AGATTGGATATCACAGG	416	(6)
<i>speH</i> (reverse)	CTATTCTCTCGTTATTGG		
<i>speI</i> (forward)	AAGGAAAATAAATGAAGGTCCGCCAT	217	(7)
<i>speI</i> (reverse)	TCGCTTAAAGTAATACCTCCATATGAATTCTTT		
<i>speJ</i> (forward)	ATCTTTCATGGGTACG	535	(6)
<i>speJ</i> (reverse)	TTTCATGTTTATTGCC		
<i>speK</i> (forward)	TATCGCTTGCTCTATACTACTGAGAGT	233	(7)
<i>speK</i> (reverse)	CCAAACTGTAGTATTTTCATCCGTATTA		
<i>speL</i> (forward)	GGACGCAAGTTATTATGGATGCTCA	460	(7)
<i>speL</i> (reverse)	TAAATAAGTCAGCACCTTCTCTTTCTC		
<i>speM</i> (forward)	GCTTTAAGGAGGAGGAGTTGATATTTATGCTCTA	411	(7)
<i>speM</i> (reverse)	CAAAGTGACTTACTTTACTCATATCAATCGTTTC		
DNase 1			
<i>spd1</i> (forward)	CCCTTCAGGATTGCTGTCAT	400	(8)
<i>spd1</i> (reverse)	ACTGTTGACGCAGCTAGGG		
Phospholipase A2e			
<i>slaA</i> (forward)	CTCTAATAGCATCGGCTACGC	440	(8)
<i>slaA</i> (reverse)	AATGGAAAATGGCACTGAAAG		
Composite transposon			
Tn 1207.3/F10394.4 RJ* (forward)	CGAGGAGTTAGTATGGAAAC	473	(9)
Tn 1207.3/F10394.4 RJ* (reverse)	CCCATAATAGGCAACTGGTCTCCAGC		
Tn 1207.3/F10394.4 LJ* (forward)	TCTTCGCCGCATAAACCCCTATC	453/6,807†	(9)

Tn 1207.3/F10394.4 LJ* (reverse)	CCTTTGACCAATGAAGTGACCTTT		
Antimicrobial drug resistance determinants			
Macrolide resistance			
<i>mef(A)</i> (forward)	GACCAAAAGCCACAATTGTGGA	1,432	(10)
<i>mef(A)</i> (reverse)	CCTCCTGTCTATAATCGCATG		
<i>erm(A)</i> [subclass <i>erm(TR)</i> ] (forward)	CCCGAAAAATACGCAAAATTCAT	590	(10)
<i>erm(A)</i> [subclass <i>erm(TR)</i> ] (reverse)	CCCTGTTTACCCATTTATAAACG		
<i>erm(B)</i> (forward)	GGAGTGATACATGAACAAAATA	531	(10)
<i>erm(B)</i> (reverse)	TTCTTTTAGTAACGTGTAACCTT		
Tetracycline resistance			
<i>tet(M)</i> (forward)	TGGAATTGATTTATCAACGG	1,080	(10)
<i>tet(M)</i> (reverse)	TTCCAACCATACAATCCTTG		
<i>tet(O)</i> (forward)	AACTTAGGCATTCTGGCTCAC	515	(11)
<i>tet(O)</i> (reverse)	TCCCCTGTTCCATATCGTCA		
<i>tet(T)</i> (forward)	AAGGTTTATTATATAAAAGTG	169	(12)
<i>tet(T)</i> (reverse)	AGGTGTATCTATGATATTTAC		
<i>tet(W)</i> (forward)	GAGAGCCTGCTATATGCCAGC	168	(12)
<i>tet(W)</i> (reverse)	GGGCGTATCCACAATGTTAAC		
<i>tet(Q)</i> (forward)	TTATACTTCCCTCCGGCATCG	904	(11)
<i>tet(Q)</i> (reverse)	ATCGGTTTCGAGAAATGCCAC		
<i>tet(S)</i> (forward)	GAAAGCTTACTATACAGTAGC	169	(12)
<i>tet(S)</i> (reverse)	AGGAGTATCTACAATATTTAC		
<i>tet(L)</i> (forward)	TCGTTAGCGTGCTGTCATTC	267	(11)
<i>tet(L)</i> (reverse)	GTATCCCACCAATGTAGCCG		
<i>tet(K)</i> (forward)	TCGATAGGAACAGCAGTA	169	(11)
<i>tet(K)</i> (reverse)	CAGCAGATCCTACTCCTT		
Lincosamide resistance			
<i>lin(B)</i> (forward)	CCTACCTATTGTTTGTGGAA	925	(13)
<i>lin(B)</i> (reverse)	ATAACGTTACTCTCCTATTC		
M protein			
<i>emm</i> (forward)	TATT(C/G)GCTTAGAAAATTA	Variable	‡
<i>emm</i> (reverse)	GCAAGTTCTTCAGCTTGT		

\*RJ, right junction; LJ, left junction.

‡The expected ampicon size was 454 bp according to the reported organization of the Tn1207.3 element or 6,807 bp according to the reported sequence of F10394.4 (9).

‡[www.cdc.gov/ncidod/biotech/strep/M-ProteinGene\\_typing.htm](http://www.cdc.gov/ncidod/biotech/strep/M-ProteinGene_typing.htm)