

Supplementary Material

Detection of *cfr*-positive MRSA CC398 in a pig farmer in Spain

Table S1. Primer pairs used for the molecular typing and detection of antimicrobial resistance genes, mutations and virulence determinants in the *S. aureus* isolate.

Target gene	Primer sequence (5'-3')	Amplicon size (bp)	Reference
Antimicrobial resistance			
<i>mecA</i>	F: GGGATCATAGCGTCATTATTC R: AACGATTGTGACACGATAGCC	527	1
<i>mecB</i>	F: TTAACATATACACCCGCTTG R: TAAAGTTCATTAGGCACCTCC	527	2
<i>mecC</i>	F: GCTCCTAATGCTAATGCA R: TAAGCAATAATGACTACC	304	3
<i>blaZ</i>	F: CAGTTCACATGCCAAAGAG R: TACACTCTTGGCGGTTTC	772	4
<i>lnu(A/A')</i>	F: GGTGGCTGGGGGGTAGATGTATTAAGTGG R: GCTTCTTTTGAAATACATGGTATTTTTCGATC	322	5
<i>lnu(B)</i>	F: CCTACCTATTGTTTGTGGAA R: ATAACGTTACTCTCCTATTC	944	6
<i>lsa(B)</i>	F: TGCCGAAGCCATGTTACCGTCC R: CGGTTAGACCAACCAGCCGAACG	396	7
<i>vga(A)</i>	F: AGTGGTGGTGAAGTAACACG R: GGTTCATACTCAATCGACTGAG	1264	8
<i>tet(K)</i>	F: TTAGGTGAAGGGTTAGGTCC R: GCAAATCATTCCAGAAGCA	697	9
<i>tet(L)</i>	F: CATTTGGTCTTATTGGATCG R: ATTACACTTCCGATTTCGG	456	
<i>tet(M)</i>	F: GTTAAATAGTGTCTTGGAG	576	

	R: CTAAGATATGGCTCTAACAA		
<i>fexA</i>	F: GTACTTGTAGGTGCAATTACGGCTGA R: CGCATCTGAGTAGGACATAGCGTC	1272	10
<i>fexB</i>	F: TTCCCACTATTGGTGAAAGGAT R: GCAATTCCCTTTTATGGACGTT	816	11
<i>cat_{pC194}</i>	F: CGACTTTTAGTATAACCCACAGA R: GCCAGTCATTAGGCCTAT	570	
<i>cat_{pC221}</i>	F: ATTTATGCAATTATGGAAGTTG R: TGAAGCATGGTAACCATCAC	434	4
<i>cat_{pC223}</i>	F: GAATCAAATGCTAGTTTTAACTC R: ACATGGTAACCATCACATAC	283	
<i>ant(4')-Ia</i>	F: GCAAGGACCGACAACATTTTC R: TGGCACAGATGGTCATAACC	165	
<i>aac(6')-Ie-aph(2'')-Ia</i>	F: CCAAGAGCAATAAGGGCATA R: CACTATCATAACCACTACCG	220	12
<i>cfr</i>	F: TGAAGTATAAAGCAGGTTGGGAGTCA R: ACCATATAATTGACCACAAGCAGC	746	13
<i>cfr(B)</i>	F: TGAGCATATACGAGTAACCTCAAGA R: CGCAAGCAGCGTCTATATCA	293	14
<i>optrA</i>	F: AGGTGGTCAGCGAACTAA R: ATCA ACTGTTCCCATTC	1395	15
<i>poxA</i>	F: TCAATGCAGAGCAGGAAGCA R: GGTGGATTTACCGACACCGT	791	16
Mutations			
23S rRNA	F: GCGGTCGCCTCCTAAAAG	420	17

	R: ATCCCGGTCCTCTCGTACT		
L3 (<i>rplC</i>)	F: ACCCTGATTTAGTTCGCTCTA	799	18
	R: GTTGACGCTTTAATGGGCTTA		
L4 (<i>rplD</i>)	F: TCGCTTACCTCCTTAATG	1080	
	R: GGTGGAAACACTGTAAC TG		
L22 (<i>rplV</i>)	F: CAACACGAAGTCCGATTGGA	468	19
	R: GCAGACGACAAGAAAACAAG		
<i>gyrA</i>	F: AATGAACAAGGTATGACACC	222	20
	R: TACGCGCTTCAGTATAACGC		
<i>grlA</i>	F: ACTTGAAGATGTTTTAGGTGAT	559	
	R: TTAGGAAATCTTGATGGCAA		
Molecular typing			
<i>spa</i>	F: AGACGATCCTTCGGTGAGC	Variable	21
	R: GCTTTTGCAATGTCATTTACTG		
<i>arcC</i>	F: TTGATTACACCAGCGCGTATTGTC	456	
	R: AGGTATCTGCTTCAATCAGCG		
<i>aroE</i>	F: ATCGGAAATCCTATTTACATTC	456	
	R: GGTGTTGTATTAATAACGATATC		
<i>glpF</i>	F: CTAGGAACTGCAATCTTAATCC	465	22
	R: TGGTAAAATCGCATGTCCAATTC		
<i>gmk</i>	F: ATCGTTTTATCGGGACCATC	429	
	R: TCATTAAC TACAACGTAATCGTA		
<i>pta</i>	F: GTTAAAATCGTATTACCTGAAGG	474	
	R: GACCCTTTTGTTGAAAAGCTTAA		
<i>tpi</i>	F: TCGTTCATTCTGAACGTCGTGAA	402	

	R: TTTGCACCTTCTAACAATTGTAC		
<i>yquiL</i>	F: CAGCATACAGGACACCTATTGGC R: CGTTGAGGAATCGATACTGGAAC	516	
<i>agrI</i>	F: GTCACAAGTACTATAAGCTGCGAT R: ATGCACATGGTGCACATGC	440	
<i>agrII</i>	F: GTATTACTAATTGAAAAGTGCCATAGC R: ATGCACATGGTGCACATGC	572	
<i>agrIII</i>	F: CTGTTGAAAAAGTCAACTAAAAGCTC R: ATGCACATGGTGCACATGC	406	23
<i>agrIV</i>	F: CGATAATGCCGTAATACCCG R: ATGCACATGGTGCACATGC	656	
SCC _{mec} V	F: GAACATTGTTACTTAAATGAGCG R: TGAAAGTTGTACCCTTGACACC	325	24
Virulence			
<i>lukF/S-PV</i>	F: ATCATTAGGTAAAATGTCTGGACATGATCCA R: GCATCAAGTGTATTGGATAGCAAAAGC	443	5
<i>tst</i>	F: TTCACTATTTGTAAAAGTGTCAGACCCACT R: TACTAATGAATTTTTTTATCGTAAGCCCTT	180	
<i>eta</i>	F: ACTGTAGGAGCTAGTGCATTGT R: TGGATACTTTTGTCTATCTTTTTCATCAAC	190	25
<i>etb</i>	F: CAGATAAAGAGCTTTATACACACATTAC R: AGTGAACCTTATCTTTCTATTGAAAAACACTC	612	
Immune Evasion Cluster (IEC)			
<i>scn</i>	F: AGCACAAGCTTGCCAACATCG R: TTAATATTTACTTTTTAGTGC	257	26

<i>chp</i>	F: TTTACTTTTGAACCGTTTCCTAC R: CGTCCTGAATTCTTAGTATGCATATTCATTAG	366
<i>sak</i>	F: AAGGCGATGACGCGAGTTAT R: GCGCTTGGATCTAATTCAAC	223
<i>sea</i>	F: AGATCATTCGTGGTATAACG R: TTAACCGAAGGTTCTGTAGA	344
<i>sep</i>	F: AATCATAACCAACCGAATCA R: TCATAATGGAAGTGCTATAA	196

Table S2. Primer pairs used to determine the genetic environment of the *cfr* gene.

Primer	Sequence (5'-3')	Reference
cfrinv-F	TGACTCCCAACCTGCTTTATACTTCA	27
cfrinv-R	GCTGTTGTGGTCAATTATATGGT	
fexAinv-R	GACGCTATGTCCTACTCAGATGCG	
pSCFS7-F	GTACTGTAACCTGGACGAATATCTAC	
tnpB-2-F	GGAACAGTGATAAGCCGGATGAT	
tnpB-2-R	GAAGGTGTATCCTTCCAGTCATATC	
cfr-ent-1-F	CTGTCAATTTCTCAAACAG	
cfr-ent-1-R	ATTAATACGTCCTCTGAACG	This study
istAS-F	GAGATTGTGGAAAGGCTCAAGG	
istAS-R	TGTTCAAGCACTCCTTCATCGAC	
istBS-F	GAATTACGTCTTCCTGGCATCC	
istBS-R	GTAAGATGGGCCGATCATATTCA	
pSCFS3-F	GGTGGTGGAAAGATGAAGGTTTCAG	
pSCFS3-R	GTGAAGACCGCCAGTGAATAGGAC	

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