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Article

Clonal Lineages, Antimicrobial Resistance, and PVL Carriage of *Staphylococcus aureus* Associated to Skin and Soft-Tissue Infections from Ambulatory Patients in Portugal

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Table S1. Primers used in this study.

Target Gene	Primers	Nucleotide Sequence (5′-3′)	Amplicon Size (bp)	Reference
		***S. aureus* identification**		
nuc	nuc-1	TCAGCAAATGCATCACAAACAG	255	[1]
	nuc-2	CGTAAATGCACTTGCTTCAGG		
		MLST		
arcC	arcC_Fw	TTGATTCACCAGCGCGTATTGTC	456	[2]
	arcC_Rv	AGGTATCTGCTTCAATCAGCG		[3]
aroE	aroE_Fw	ATCGGAAATCCTATTTCACATTC	456	[3]
	aroE_Rv	GGTGTTGTATTAATAACGATATC		
glpF	glpF_Fw	CTAGGAACTGCAATCTTAATCC	465	[3]
	glpF_Rv	TGGTAAAATCGCATGTCCAATTC		
gmk	gmk_Fw	ATCGTTTTATCGGGACCATC	429	[3]
	gmk_Rv	TCATTAACTACAACGTAATCGTA		
pta	pta_Fw	GTTAAAATCGTATTACCTGAAGG	474	[3]
	pta_Rv	GACCCTTTTGTTGAAAAGCTTAA		
tpi	tpi_Fw	TCGTTCATTCTGAACGTCGTGAA	402	[3]
	tpi_Rv	TTTGCACCTTCTAACAATTGTAC		
yqiL	yqiL_Fw	CAGCATACAGGACACCTATTGGC	516	[3]
	yqiL_Rv	CGTTGAGGAATCGATACTGGAAC		
		Screening of resistance genes and mutations		
mecA	mecA_Fw	GGTCCCATTAACTCTGAAG	1040	[4]
	mecA_Rv	AGTTCTGCAGTACCGGATTTGC		
blaZ	blaZ_Fw	GATAAGAGATTTGCCTATGC	533	[5]
	blaZ_Rv	GCATATGTTATTGCTTGACC		
***erm*(A)**	erm(A)_Fw	AAGCGGTAAACCCCTCTGAG	442	[6]
	erm(A)_Rv	TCAAAGCCTGTCGGAATTGG		

bp: base pair; **Fw:** "forward"; **Rv:** "reverse".

Table S1. Primers used in this study.

Target Gene	PRIMERS	Nucleotide Sequence (5′-3′)	Amplicon Size (bp)	Reference
***erm*(B)**	erm(B)_Fw	TGGAACAGGTAAAGGGCATT	433	[7]
	erm(B)_Rv	TGTGGTATGGCGGGTAAGTT		
***erm*(C)**	erm(C)_Fw	TCGTAACTGCCATTGAAATA	348	[7]
	erm(C)_Rv	TCACTTTAGGTTTAGGATGAAA		
***msr*(A)**	msr(A)_Fw	GATTGTCCCAAGCCAGTAAA	445	This study
	msr(A)_Rv	GCCATTTGCACTTTAGGAGA		
***mph*(C)**	mph(C)_Fw	ATGACTCGACATAATGAAAT	900	[8]
	mph(C)_Rv	CTACTCTTTCATACCTAACTC		
***vga*(A)**	vga(A)_Fw	ACCCGAGACATCTTCACCAC	400	[9]
	vga(A)_Rv	GGAAATTGACGAGGGGAGA		
***vga*(C)**	vga(C)_Fw	ACGAATAAAGGGATCGAAGC	510	This study
	vga(C)_Rv	AGCACATGCACAGGTTTGTA		
***aac*(A)-*aph*(D)**	aacA-aphD_Fw	CAGAGCCTTGGGAAGATGAAG	348	[10]
	aacA-aphD_Rv	CCTCGTGTAATTCATGTTCTGGC		
aph*(3′)-*IIIa	aph(3′)-IIIa_Fw	CCGCTGCGTAAAAGATAC	609	[11]
	aph(3′)-IIIa_Rv	GTCATACCACTTGTCCGC		
***aad*D**	aadD_Fw	GGAAGCAGAGTTCAGCCATG	266	[12]
	aadD_Rv	TGCCTGCATATTCAAACAGC		
fusB	fusB_Fw	ATTCAATCGGAAACCTATAATGATA	292	[13]
	fusB_Rv	TTATATATTTCCGATTTGATGCAAG		
fusC	fusC_Fw	GATATTGATATCTCGGACTT	128	[14]
	fusC_Rv	AGTTGACTTGATGAAGGTAT		
fusA	fusA_Fw	TTTACCCTGAGTGTGTTCT	2250	[15]
	fusA_Rv	TACATTTAAGCTCACCTTGT		
	FusA_Int_A_F	CGCCAACTCACGTGAAGAAA	1025	
	FusA_Int_B_R	ATTGACCACGACCACCAGAT	1351	
	FusA_Int_C_R	TGCTTCACGTGCTTCTTCAG	639	
***qac*A/B**	qacA/B_Fw	GCTGCATTTATGACAATGTTTG	628	[16]
	qacA/B_Rv	AATCCCACCTACTAAAGCAG		
smr	smr_Fw	ATAAGTACTGAAGTTATTGGAAGT	285	[17]
	smr_Rv	TTCCGAAAATGTTTAACGAAACTA		
gyrA	gyrA_Fw	CCAGTGAAATGCGTGAATC	514	[18]
	gyrA_Rv	TGTGGTGGAATATTCGTTGC		
grlA	grlA_Fw	AGGTGATCGCTTTGGAAGA	501	[18]
	grlA_Rv	TGGTGGTATATCTGTCGCGTA		
Screening of PVL encoding genes and *agr* typing				
lukS-lukF	lukSF_Fw	CATTAGGTAAAATGTCTGG	431	This study
	lukSF_Rv	GCATCAACTGTATTGGAT		
agr locus	pan_agr_Fw	ATGCACATGGTGCACATGC		[19]
	agrI_Rv	GTCACAAGTACTATAAGCTGCGAT	439	
	agrII_Rv	TATTACTAATTGAAAAGTGCCATAGC	572	
	agrIII_Rv	GTAATGTAATAGCTTGTATAATAA-TACCCAG	321	
	agrIV_Rv	CGATAATGCCGTAATACCCG	657	

bp: base pair; **Fw:** "forward"; **Rv:** "reverse".

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