

Article

Phenotypic and molecular traits of *Staphylococcus coagulans* associated with canine skin infections in Portugal

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Table S1. Distribution of inhibition zone diameters of 21 antibiotics for the 27 *S. coagulans* studied

Cells are colored according to the breakpoints established by respective recommendations; S: green; I: yellow; R: red. * Breakpoint established by CLSI for staphylococci isolated from animals, document VET01S ED5 [1]; ** Breakpoint established by CLSI for staphylococci isolated from humans, document M100-S30 [2]; *** Breakpoint established by EUCAST [3].

Table S1. (Continuation). Distribution of inhibition zone diameters of 21 antibiotics for the 27 *S. coagulans* studied.

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Table S2. Distribution of inhibition zone diameters of six antibiotics with no breakpoint or epidemiological cut-off value for the 27 *S. coagulans* studied.

Table S3. Inhibition zone diameters of 27 antibiotics for the single *S. schleiferi* isolate studied.

Antibiotic	ZD (mm)	Antibiotic	ZD (mm)	Antibiotic	ZD (mm)	Antibiotic	ZD (mm)
Penicillin	11	Clindamycin	28	Chloramphenicol	28	Kanamycin	28
Oxacillin	19	Quinupristin - dalfopristin	29	Florfenicol	30	Neomycin	23
Enrofloxacin	15	Tetracycline	35	Trimethoprim - sulfamethoxazole	29	Apramycin	25
Pradofloxacin	26	Minocycline	34	Rifampicin	36	Bacitracin	20
Ciprofloxacin	17	Tigecycline	29	Gentamicin	25	Mupirocin	42
Moxifloxacin	25	Fusidic acid	17	Amikacin	28	Novobiocin	36
Erythromycin	30	Linezolid	34	Tobramycin	27		

ZD: inhibition zone diameter.



Table S4. Primers used in this study.

Target Gene	Primers	Nucleotide Sequence (5'-3')	Amplicon Size (bp)	Reference
<i>S. coagulans</i> and <i>S. schleiferi</i> identification				
<i>nuc</i>	nuc-fw	AATGGCTACAATGATAATCACTAA	526	[4]
	nuc-rv	CATATCTGTCTTCGGCGCG		
Screening of resistance genes and mutations				
<i>mecA</i>	mecA_Fw	GGTCCCATTAACTCTGAAG	1040	[5]
	mecA_Rv	AGTTCTGCAGTACCGGATTGCG		
<i>blaZ</i>	blaZ_Fw	GATAAGAGATTGCCTATGC	533	[6]
	blaZ_Rv	GCATATGTTATTGCTTGACC		
<i>erm(A)</i>	erm(A)_Fw	AAGCGGTAAACCCCTCTGAG	442	[7]
	erm(A)_Rv	TCAAAGCCTGTCGGAATTGG		
<i>erm(B)</i>	erm(B)_Fw	TGGAACAGGTAAAGGGCATT	433	[8]
	erm(B)_Rv	TGTGGTATGGCGGGTAAGTT		
<i>erm(C)</i>	erm(C)_Fw	TCGTAACTGCCATTGAAATA	348	[8]
	erm(C)_Rv	TCACTTAGGTTAGGATGAAA		
<i>msr(A)</i>	msr(A)_Fw	GATTGTCCCAAGCCAGTAAA	445	[9]
	msr(A)_Rv	GCCATTGCACCTTAGGAGA		
<i>mph(C)</i>	mph(C)_Fw	ATGACTCGACATAATGAAAT	900	[10]
	mph(C)_Rv	CTACTCTTCATACCTAAC		
<i>vga(A)</i>	vga(A)_Fw	ACCCGAGACATCTCACCA	400	[11]
	vga(A)_Rv	GGAAATTGACGAGGGGAGA		
<i>vga(C)</i>	vga(C)_Fw	ACGAATAAAGGGATCGAAGC	510	[9]
	vga(C)_Rv	AGCACATGCACAGGTTGTA		
<i>fusB</i>	fusB_Fw	ATTCAATCGAACCTATAATGATA	292	[12]
	fusB_Rv	TTATATATTCCGATTTGATGCAAG		
<i>fusC</i>	fusC_Fw	GATATTGATATCTCGGACTT	128	[13]
	fusC_Rv	AGTTGACTTGTGAAGGTAT		
<i>tet(K)</i>	tet(K)_Fw	GTAGCGACAATAGTAATAGT	361	[14]
	tet(K)_Rv	GTAGTGACAATAAACCTCCTA		
<i>tet(M)</i>	tet(M)_Fw	GTTAAATAGTGTCTGGAG	657	[15]
	tet(M)_Rv	CTAAGATATGGCTCTAACAA		
<i>tet(L)</i>	tet(L)_Fw	GTCGGTAATTGGGTTGTG	421	This study
	tet(L)_Rv	TGACAGCACGCTAACGATAA		
<i>grlA</i>	grlA_Fw	CAAGAGCGTGTTRCCT	300	This study
	grlA_Rv	CTGACTYAATTTCGCTTCAG		
<i>gyrA</i>	gyrA_Fw	ATGAGTGTATYGTRTCTCGT	261	This study
	gyrA_Rv	CATMGAACCRAAGTTACCTTG		

bp: base pair; **Fw:** "forward"; **Rv:** "reverse"; R: A + G; Y: C + T; M: A + C.

**Table S5.** Control strains used in the screening of antibiotic resistance genes.

Target Gene	Control strain	Reference	Target Gene	Control strain	Reference
<i>mecA</i>	<i>S. aureus</i> SM1	[16]	<i>vga(A)</i>	<i>S. epidermidis</i> FMV-51	[18]
<i>blaZ</i>	<i>S. aureus</i> SM1	[16]	<i>vga(C)</i>	<i>S. aureus</i> 49.1	[11]
<i>erm(A)</i>	<i>S. aureus</i> SM39	[8]	<i>fusB</i>	<i>S. epidermidis</i> FMV-97	[19]
<i>erm(B)</i>	<i>S. pseudintermedius</i> 4877/10	[17]	<i>fusC</i>	<i>S. epidermidis</i> FMV-34	[19]
<i>erm(C)</i>	<i>S. aureus</i> SM26	[8]	<i>tet(K)</i>	<i>S. epidermidis</i> ATCC12228	[20]
<i>msr(A)</i>	<i>S. epidermidis</i> FMV-51	[18]	<i>tet(M)</i>	<i>S. aureus</i> H4/09	[11]
<i>mph(C)</i>	<i>S. epidermidis</i> FMV-51	[18]	<i>tet(L)</i>	<i>S. aureus</i> 25.1	[11]

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