

## Supplementar Material

**Supplementary Table S1** – Details of the antimicrobial resistance among staphylococci isolated from dogs admitted to the ICU of HV-UFGM in Belo Horizonte, Minas Gerais, between August 2018 and April 2019.

Species	Isolate s	OXA/FO X	PEN	TET	SXT	ERI	CLI	RIF	CIP	GEN	ENO	CHL	NIT	MRS	MDR
<b>SIG</b>	<b>151</b> <b>(71.5</b> <b>%)</b>	<b>38</b> <b>(18%)</b>	<b>97</b> <b>(46%)</b>	<b>88</b> <b>(41.7</b> <b>%)</b>	<b>75</b> <b>(35.5</b> <b>%)</b>	<b>52</b> <b>(24.6</b> <b>%)</b>	<b>52</b> <b>(24.6</b> <b>%)</b>	<b>44</b> <b>(20.8</b> <b>%)</b>	<b>42</b> <b>(19.9</b> <b>%)</b>	<b>42</b> <b>(19.9</b> <b>%)</b>	<b>41</b> <b>(19.4</b> <b>%)</b>	<b>13</b> <b>(6.2%</b> <b>)</b>	<b>1</b> <b>(0.5%</b> <b>)</b>	<b>38</b> <b>(18.0</b> <b>%)</b>	<b>69</b> <b>(32.7</b> <b>%)</b>
<i>S. pseudintermedius</i>	150 (71.1%)	38 (18.0%)	96 (45.5%)	87 (41.2%)	75 (35.5%)	52 (24.6%)	52 (24.6%)	44 (20.8%)	42 (19.9%)	42 (19.9%)	41 (19.4%)	13 (6.2%)	1 (0.5%)	38 (18.0%)	69 (32.7%)
<i>S. delphini</i>	1 (0.5%)	0 (0.0%)	1 (0.5%)	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
<b>Non-SIG</b>	<b>60</b> <b>(28.4</b> <b>%)</b>	<b>14</b> <b>(6.6%)</b>	<b>25</b> <b>(11.8</b> <b>%)</b>	<b>22</b> <b>(10.4</b> <b>%)</b>	<b>19</b> <b>(9.0%)</b>	<b>24</b> <b>(11.4</b> <b>%)</b>	<b>22</b> <b>(10.4</b> <b>%)</b>	<b>6</b> <b>(2.8%)</b>	<b>15</b> <b>(7.1%)</b>	<b>10</b> <b>(4.7%)</b>	<b>15</b> <b>(7.1%)</b>	<b>3</b> <b>(1.4%</b> <b>)</b>	<b>3</b> <b>(1.4%</b> <b>)</b>	<b>19</b> <b>(9.0%)</b>	<b>23</b> <b>(10.9</b> <b>%)</b>
<i>S. aureus</i>	27 (12.8%)	4 (1.9%)	11 (5.2%)	10 (4.7%)	7 (3.3%)	9 (4.3%)	8 (3.8%)	3 (1.4%)	6 (2.8%)	5 (2.4%)	6 (2.8%)	2 (0.9%)	2 (0.9%)	4 (1.9%)	8 (3.8%)
<i>S. haemolyticus</i>	13 (6.2%)	2 (0.9%)	6 (2.8%)	5 (2.4%)	2 (0.9%)	6 (2.8%)	3 (1.4%)	1 (0.5%)	2 (0.9%)	1 (0.5%)	2 (0.9%)	0 (0.0%)	0 (0.0%)	7 (3.3%)	3 (1.4%)
<i>S. devriese</i>	4 (1.9%)	0 (0.0%)	2 (0.9%)	0 (0.0%)	0 (0.0%)	2 (0.9%)	2 (0.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	2 (0.9%)
<i>S. felis</i>	3 (1.4%)	3 (1.4%)	2 (0.9%)	2 (0.9%)	2 (0.9%)	2 (0.9%)	2 (0.9%)	1 (0.5%)	2 (0.9%)	2 (0.9%)	2 (0.9%)	0 (0.0%)	0 (0.0%)	2 (0.9%)	3 (1.4%)
<i>S. epidermidis</i>	3 (1.4%)	2 (0.9%)	0 (0.0%)	2 (0.9%)	3 (1.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.9%)	0 (0.0%)	2 (0.9%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	2 (0.9%)
<i>S. hominis</i>	3 (1.4%)	1 (0.5%)	2 (0.9%)	1 (0.5%)	2 (0.9%)	3 (1.4%)	2 (0.9%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	2 (0.9%)	2 (0.9%)
<i>S. simulans</i>	3	1	1	1	1	1	3	0	1	0	1	0	0	1	2

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	(1.4%)	(0.5%)	(0.5%)	(0.5%)	(0.5%)	(0.5%)	(1.4%)	(0.0%)	(0.5%)	(0.0%)	(0.5%)	(0.0%)	(0.0%)	(0.5%)	(0.9%)
<i>S. saprophyticus</i>	2 (1.0%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	0 (0%)	1 (0.5%)	1 (0.5%)	1 (0.5%)	0 (0%)	0 (0%)	1 (0.5%)	1 (0.5%)
<i>S. schleiferi</i> *	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
<i>S. equorum</i>	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total	211 (100%)	52 <sup>c</sup> (24.6%)	122 <sup>f</sup> (57.8%)	110 <sup>ef</sup> (52.1%)	94 <sup>de</sup> (44.5%)	76 <sup>d</sup> (36.0%)	74 <sup>d</sup> (35.0%)	50 <sup>c</sup> (23.7%)	57 <sup>c</sup> (27.0%)	52 <sup>c</sup> (24.6%)	56 <sup>c</sup> (26.5%)	16 <sup>b</sup> (7.6%)	4 <sup>a</sup> (1.9%)	57 (27.0%)	92 (43.6%)

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**Supplementar Table S2** - Antimicrobial resistance among *Staphylococcus aureus*, *S. pseudintermedius* and other staphylococci isolated from dogs admitted to the ICU of HV-UFGM in Belo Horizonte, Minas Gerais, between August 2018 and April 2019.

Species	Isolate s	OXA/FO X	PEN	TET	SXT	ERY	CLI	RIF	CIP	GEN	ENO	CHL	NIT	MRS	MDR
<i>S. pseudintermedius</i>	150 (100%)	38 (25.3%)	96 (64%)	87 (58%)	75 (50%)	52 (34.7%)	52 (34.7%)	44 (29.3%)	42 (28%)	42 (28%)	41 (27.3%)	13 (8.7%)	1 (0.7%)	38 (25.3%)	69 (46%)
<i>S. aureus</i>	27 (100%)	4 (14.8%)	11 (40.7%)	10 (37%)	7 (25.9%)	9 (33.3%)	8 (29.6%)	3 (11.1%)	6 (22.2%)	5 (18.5%)	6 (22.2%)	2 (7.4%)	2 (7.4%)	4 (14.8%)	8 (29.6%)
Other staphylococci species <sup>1</sup>	34 (100%)	10 (29.4%)	15 (44.1%)	13 (38.2%)	12 (35.3%)	15 (44.1%)	14 (41.2%)	3 (8.8%)	9 (26.5%)	5 (14.7%)	9 (26.5%)	1 (2.9%)	1 (2.9%)	5 (14.7%)	15 (44.1%)
<b>Total</b>	<b>211 (100%)</b>	<b>52<sup>c</sup> (24.6%)</b>	<b>122<sup>f</sup> (57.8%)</b>	<b>110<sup>ef</sup> (52.1%)</b>	<b>94<sup>de</sup> (44.5%)</b>	<b>76<sup>d</sup> (36%)</b>	<b>74<sup>d</sup> (35%)</b>	<b>50<sup>c</sup> (23.7%)</b>	<b>57<sup>c</sup> (27%)</b>	<b>52<sup>c</sup> (24.6%)</b>	<b>56<sup>c</sup> (26.5%)</b>	<b>16<sup>b</sup> (7.6%)</b>	<b>4<sup>a</sup> (1.9%)</b>	<b>57 (27%)</b>	<b>92 (43.6%)</b>

**Supplementary Table S3** - Total isolates, frequency, and staphylococcal species that had the *mecA* gene.

Species	Frequency among <i>mecA</i> <sup>+</sup> isolates	<i>mecA</i> <sup>+</sup> but CEF/OXA susceptibility
<i>S. pseudintermedius</i>	38/48 (79.2%)	0/38 (0.0%)
<i>S. haemolyticus</i>	7/48 (14.6%)	5/7 (71.4%)
<i>S. hominis</i>	1/48 (2.1%)	1/1 (100.0%)
<i>S. epidermidis</i>	1/48 (2.1%)	1/1 (100.0%)
<i>S. devriesei</i>	1/48 (2.1%)	1/1 (100.0%)
<b>Total</b>	<b>48/48 (100.0%)</b>	<b>8/48 (16.7%)</b>

**Supplementary Table S4** - Staphylococcal species and total isolates that showed phenotypic methicillin resistance profile (MRS).

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Species	Frequency (%)
<i>S. aureus</i>	4/9 (44.4%)
<i>S. felis</i>	2/9 (14.6%)
<i>S. hominis</i>	1/9 (11.1%)
<i>S. simulans</i>	1/9 (11.1%)
<i>S. saprophyticus</i>	1/9 (11.1%)
<b>Total</b>	<b>9/48 (100.0%)</b>

**Supplementary Table S5** – Breakpoints used to determine the breakpoints for oxacillin and cefotaxime for Staphylococcal species.

<i>Staphylococcus</i> species	Antimicrobial Zone Diameter Breakpoints	
	Oxacillin	Cefoxitin
<i>S. pseudintermedius</i> and <i>S. schleiferi</i>	R: ≤17 mm /S: ≥18 mm	NA
<i>S. aureus</i> and <i>S. lugdunensis</i>	NA	R: ≤21 mm /S: ≥22 mm
Other <i>Staphylococcus</i> species	NA	R: ≤24 mm /S: ≥25 mm

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**Supplementary Table S6:** Isolates and accession number of methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) isolated from nostril, axilla, and rectum from dogs admitted to the Intensive Care Unit of the Veterinary Hospital of the Federal University of Minas Gerais and from dogs diagnosed with MRSP infection in the same institution.

Isolate	Source (Body site)	Genome Accession	Reference
S5.1R	Colonization (Rectum)	SAMN32679007	This study
S32.4N	Colonization (Nostril)	SAMN32678995	
S32.1R	Colonization (Rectum)	SAMN32678987	
S53.9N	Colonization (Nostril)	SAMN32679010	
S10.1R	Colonization (Rectum)	SAMN32679008	
S16.4A	Colonization (Axilla)	SAMN32678988	
S54.4A	Colonization (Axilla)	SAMN32679004	
S54.3N	Colonization (Nostril)	SAMN32678993	
S53.6R	Colonization (Rectum)	SAMN32678992	
S57.4R	Colonization (Rectum)	SAMN32679001	
S17.6R	Colonization (Rectum)	SAMN32679009	
S53.3N	Colonization (Nostril)	SAMN32679002	
BR49	Infection	SAMN32679003	Vieira et al. (2022)
BR52		SAMN32678998	
BR65		SAMN32678989	
BR19		SAMN32679005	
BR89		SAMN32678991	
BR106		SAMN32678999	
BR81		SAMN32678990	
BR67		SAMN32678994	
BR130		SAMN32678997	
AC41		SAMN32678996	