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Exploring Efflux as a Mechanism of Reduced Susceptibility towards Biocides and Fluoroquinolones in *Staphylococcus pseudintermedius*

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Table S1. Distribution of MRSP, MSSP and MDR phenotypes among the *S. pseudintermedius* study collection (n=155).

<i>S. pseudintermedius</i> clinical strains	Number of strains (n/N) (%)	Reference
MRSP	48/155 (31.0%)	[1]
MRSP non-MDR	2/48 (4.2%)	
MRSP-MDR	46/48 (95.8%)	
MSSP	107/155 (69.0%)	
MSSP non-MDR	83/107 (77.6%)	
MSSP-MDR	24/107 (22.4%)	

MRSP: Methicillin-resistant *S. pseudintermedius*; MSSP: Methicillin-susceptible *S. pseudintermedius*; MDR: Multidrug resistant. Susceptibility profiles were interpreted according to guidelines VET01S (CLSI, 2020) (clindamycin, tetracycline, enrofloxacin, pradofloxacin) [2], M100-ED32 (CLSI, 2022) (penicillin, oxacillin, gentamicin, erythromycin, trimethoprim-sulfamethoxazole, chloramphenicol, rifampicin, ciprofloxacin, moxifloxacin) [3].

Table S2. Control strains used for the detection of plasmid-encoded efflux pump genes.

Target gene	Control strain	Reference
<i>qacA/B</i>	<i>S. aureus</i> SM39	[4]
<i>smr</i>	<i>S. aureus</i> SM52	[4,5]

Table S3. Primers used in this study.

Target gene	Primers	Nucleotide Sequence (5'-3')	Amplicon size (bp)	Reference
Detection of plasmid-encoded efflux pump genes				
<i>qacA/B</i>	<i>qacA/B_FW</i>	GCTGCATTTATGACAATGTTT	628	[6]
	<i>qacA/B_RV</i>	AATCCACCTACTAAAGCAG		
<i>smr</i>	<i>smr_FW</i>	ATAAGTACTGAAGTTATTGGAAGT	285	[7]
	<i>smr_RV</i>	TTCCGAAAATGTTTAACGAAACTA		
	<i>gyrB_RV</i>	GGATGCGGTTTTACCAGATA		

bp: Base pair; FW: Forward; RV: Reverse.

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