Antimicrobial resistance and AMR genes occurrence in Streptococcus suis

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Introduction

Diseases caused by *Streptococcus suis* are a significant economic concern for pig farms globally and have also zoonotic potential (1). Antimicrobials are commonly used to treat *S. suis* infections, and it is therefore essential to monitor antimicrobial resistance (AMR).

Materials and Methods

A total of 525 *S. suis* isolates were collected from diseased pigs on Czech farms between 2018 and 2022. Antimicrobial susceptibility testing (AST) was performed by determining the minimum inhibitory concentrations (MICs) using the microdilution broth method. In selected 173 isolates, genes encoding AMR were detected by searching the whole genome sequences using the ResFinder database.

Results

None of the isolates tested were resistant to ceftiofur, a very high level of susceptibility of *S. suis* isolates was also found to amoxicillin with clavulanic acid, sulfamethoxazole potentiated with trimethoprim, enrofloxacin and florfenicol. On the contrary, high levels of resistance were found to tetracycline, clindamycin, tilmicosin, tulathromycin and tiamulin (Fig. 1, Tab. 1). AMR genes were predominantly present for macrolides and lincosamides (*erm(B)*), tetracyclines (*tet(O)*) and aminoglycosides (*ant(6)-la*) (Tab. 2).

Figure 1. Percentage representation of susceptible, intermediate susceptible and resistant strains of *S. suis.* (n=525).

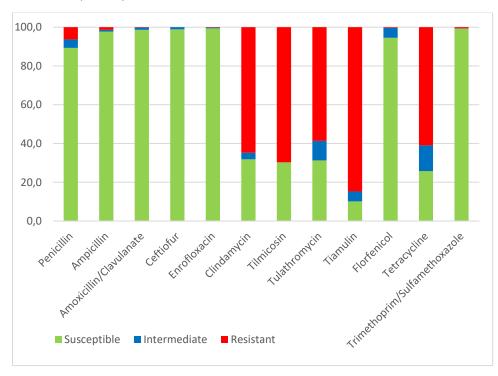


Table 1. MICs distribution for antimicrobials; percentages of susceptible, intermediately resistant, and resistant isolates, and MIC_{50} and MIC_{90} values in *S. suis* isolates

		MIC (mg/L)							S (%)	I (%)	R (%)	MIC ₅₀	MIC ₉₀						
	0,03	0,06	0,125	0,25	0,5	1	2	4	8	16	32	64	128	256	5 (%)	1(%)	п (%)	(mg/L)	(mg/L)
PEN	212	199	32	26	23	17	12	4		_					89,3	4,4	6,3	0,06	0,25
AMP	257	185	46	19	6	5	4	2	1			_			97,7	1,0	1,3	0,06	0,125
AMC				511	7	6	1								98,7	1,1	0,2	≤0,25	≤0,25
EFT			312	109	34	36	28	6				-			98,9	1,1	0,0	≤0,125	1
ENR		13	102	286	121	2	1				-				99,4	0,4	0,2	0,25	0,5
CLI			136	31	18	5	4	44	20	12	255				31,8	3,4	64,8	0,25	0,5
TIL						1	4	11	20	123	114	8	15	229	30,3	0,0	69,7	0,25	0,5
TUL						12	15	32	47	58	53	50	11	247	31,2	10,1	58,7	0,25	0,5
TIA				13	40	27	50	111	49	41	48	146	_	-	10,1	5,1	84,8	0,25	0,5
FFC					4	123	369	27		2					94,5	5,1	0,4	2	2
TET				99	36	70	24	5	17	48	194	32			25,7	13,3	61,0	2	32
SXT		398	78	34	8	3	1	3							99,2	0,2	0,6	≤0,06	0,125

S = Susceptible (green); I = Intermediate (blue); R = Resistant (orange); MIC = Minimal Inhibitory Concentration; Antimicrobial dilution ranges tested are outlined by black lines. The MIC_{50} and MIC_{90} values represent the lowest concentration (mg/L) inhibiting the growth of 50% and 90% of the isolates in the bacterial culture with a density of 10⁵ CFU/mL.

Antibiotic group	Percentage of the strains carrying AMR gene	Resistance genes (ResFinder database)	Percentage of strains carrying the gene		
		mef(A)	3.5		
Macrolides	54.9	msr(D)	2.9		
		erm(B)	53.8		
		erm(B)	53.8		
Lincosamides	57.2	Inu(B)	6.4		
Lincosamides	57.2	InuC	0.6		
		lsa(E)	5.8		
		tet(W)	4.6		
	66.5	tet(L)	0.6		
Totrogualingo		tet(44)	2.3		
Tetracyclines	88.5	tet(40)	3.5		
		tet(O)	49.1		
		tet(M)	12.7		
		ant(6)-la	15.6		
Aminoglygogidog	22.5	ant(6)-Ib	4.0		
Aminoglycosides	22.0	aph(3')-III	5.2		
		aac(6')-aph(2")	1.7		
Amphenicols	1.7	optrA	1.7		

Table 2. Antimicrobial resistance genes in S. suis isolates (n=173).

Discussion and Conclusion

Resistance to certain antimicrobials may be related to their high consumption in pig farms for the treatment of infections (2). The prevalence of AMR genes in our study is consistent with the results of phenotypic AST. However, the presence of AMR genes in the isolates did not always correspond to the AST results. This discrepancy is likely due to the presence of silent genes or, conversely, the presence of genes not identified by the available database.

Any use of antimicrobials must be well justified to increase the likelihood of treatment success and prevent the spread of resistence. This work was supported by grants RO0523 and TN02000017.

References:

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- 2. Vela (2005) Vet Microbiol 105, 143-147.