

Antimicrobial susceptibility of isolates from clinical outbreaks of porcine respiratory diseases

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1	Antimicrobial susceptibility of Actinobacillus pleuropneumoniae isolates from clinical
2	outbreaks of porcine respiratory diseases
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26	ABSTRACT
27	
28	Limited data regarding the susceptibility of Actinobacillus pleuropneumoniae to
29	antimicrobials has been published during recent years. Accordingly, the aim of the present
30	study was to investigate the distribution of MICs for the isolates of A. pleuropneumoniae
31	from diseased pigs in the Czech Republic between 2007 and 2009.
32	
33	A total of 242 isolates were tested for susceptibility to 16 antimicrobial agents by a broth
34	microdilution method. A low degree of resistance was observed for florfenicol (0.8 %),
35	amoxicillin and clavulanic acid (0.8 %), tilmicosin (1.2 %), tiamulin (1.7 %) and ampicillin
36	(3.3 %), whereas resistance to tetracycline was detected more frequently, 23.9 % of
37	isolates. Interestingly, resistance to florfenicol has not yet been reported in any study
38	investigating antimicrobial resistance of A. pleuropneumoniae. By PCR the presence of the
39	floR gene was confirmed in all florfenicol resistant isolates.
40	
41	Keywords: Antimicrobials; Minimal inhibition concentration; Pig; Pleuropneumonia
42	
43	INTRODUCTION
44	
45	Actinobacillus pleuropneumoniae is one of the main etiologic agents of contagious
46	bacterial diseases in swine. It causes pleuropneumonia, a severe contagious pulmonary
47	disease of pigs resulting in high morbidity and mortality worldwide (Sebunya et al., 1983).
48	

49	variations in anumicrootal use for the control of A. pieuropheumoniae infections from one
50	country to another and variations in methodology can contribute to evident differences in
51	antimicrobial susceptibility of A. pleuropneumoniae.
52	
53	In accordance with the recommendation of Schwarz et al. (2010) on the requirement of
54	application of the same methodology and interpretive criteria (which would allow for re-
55	evaluation of the original data if the interpretive criteria change over time), only a limited
56	number of recent studies were conducted with the use of microdilution method (Gutiérrez-
57	Martin et al., 2006; Matter et al., 2007; Godinho, 2008).
58	
59	Due to the fact that there is a lack of recent results obtained by A. pleuropneumoniae
60	testing for antimicrobial susceptibility which could be compared with results from
61	subsequent years, the purpose of the current study was to assess the distribution of the
62	minimum inhibition concentration (MIC) of 16 antimicrobial agents for A.
63	pleuropneumoniae isolates, using the broth microdilution method.
64	
65	This paper presents the results obtained by evaluation of the distribution of the MICs,
66	clinical resistance rates, and phenotypic drug resistance profiles for 242 isolates of A .
67	pleuropneumoniae from diseased pigs in the Czech Republic between 2007 and 2009.
68	Furthermore, presence of the <i>floR</i> gene was confirmed in florfenicol resistant isolates.
69	
70	MATERIALS AND METHODS
71	
72	Sampling
73	

74	All A. pleuropneumoniae isolates used in this study were derived from the lungs of
75	growing pigs (body weight from 18 to 50 kg) that died of acute respiratory diseases. The
76	isolates were obtained from 127 herds across the Czech Republic in 2007-2009.
77	Not more than one isolate of A. pleuropneumoniae from the same farm per six-month
78	period was included in the study. Isolates from animals that had been treated with
79	antimicrobials during the two weeks prior to sampling were not included in this study.
80	
81	Bacterial isolates
82	
83	Two hundred and forty-two isolates were isolated on Columbia blood agar plates, using a
84	strip of Staphylococcus aureus culture to display the positive CAMP reaction. After an
85	additional passage through Columbia chocolate agar, cultures were identified and
86	serotyped using serological and molecular techniques as described previously (Mittal et al.,
87	1983; Gram et al., 2000). All isolates were stored at -80 °C in vials containing 0.25 ml of
88	Foetal Bovine Serum Gold (PAA Laboratories GmbH, Austria) and 0.25 ml of Cation
89	Adjusted Mueller Hinton Broth II (CAMHB) (Becton, Dickinson and Company, USA).
90	
91	Antimicrobial susceptibility testing
92	
93	All A. pleuropneumoniae isolates were investigated for their in vitro susceptibility by the
94	microdilution broth method using veterinary fastidious medium (VFM) according to the
95	CLSI standard M31-A3 (CLSI, 2008). MIC-determinations were performed using a
96	commercially prepared microtitre plates (Trek Diagnostic Systems, East England and
97	Trios, Czech Republic). The antimicrobial agents tested and their dilution ranges are
98	shown in Table 1. In categorizing the MIC results, CLSI breakpoints of resistance for

swine respiratory disease pathogens were generally used (CLSI, 2008). The interpretive
criteria for A. pleuropneumoniae taken from a proposal of clinical breakpoints for
amoxicillin (Schwarz et al., 2008) were used for ampicillin and amoxicillin/clavulanic acid
and breakpoints of A. pleuropneumoniae for tulathromycin (Godinho, 2008) were
accepted. The breakpoints used are indicated in Table 1. A. pleuropneumoniae ATCC
27090 was used as reference strain for quality-control (QC) testing each batch of the plates
and lot of VFM. QC testing was also performed simultaneously in each series of
investigated isolates. The expected MIC values (CLSI, 2008) for the control strain were
established: tetracycline \leq 0.5 mg/L; gentamicin 8-16 mg/L;
trimethoprim/sulfamethoxazole $\leq 0.5/9.5$ mg/L; ceftiofur ≤ 0.5 mg/L; cefquinome ≤ 0.25
mg/L; tilmicosin 4-8 mg/L; tiamulin 8-16 mg/L; tulathromycin 16-32 mg/L; florfenicol
0.25-0.5 mg/L.

Polymerase chain reaction (PCR)

The primers for the detection of the *floR* gene were 5′ GCG ATA TTC ATT ACT TTG GC 3′ and 5′ TAG GAT GAA GGT GAG GAA TG 3′ (Faldynova et al., 2003). To obtain a template DNA, a loop of bacterial culture was re-suspended in 50 µl of water and boiled for 20 min. The suspension was spun for 1 min and 2 µl of the supernatant was used for the reaction. The PCR was carried out in 20 µl volumes using 10 pmol of each primer and PCR Master Mix (Qiagen, Germany). PCR cycling consisted of 35 cycles of 40 s at 95 °C, 45 s at 55 °C and 1 min at 72 °C. The amplification products were separated by electrophoresis in 1.5% agarose gel, stained with ethidium bromide and visualized under UV light.

124	Sequencing of the floR gene
125	
126	The PCR product obtained by amplification with primers covering the whole sequence of
127	the floR gene (5' ACC ACC ACA CGC CCC GCG TG 3' and 5' GAC GAC TGG CGA
128	CTT CTC GG 3') was cloned into pCR2.1-TOPO (Invitrogen, USA) according to the
129	manufacturer's instructions. The insert was then sequenced using the BigDye Terminator
130	v1.1 Sequencing Standard Kit (Applied Biosystems, USA) in ABI 310 Genetic Analyser
131	(Applied Biosystems, USA) with M13 forward and reverse primers. The sequences
132	obtained were compared at the GenBank web site using BLAST.
133	
134	RESULTS
135	
136	Results of susceptibility testing of 242 A. pleuropneumoniae isolates to 16 antimicrobial
137	agents between 2007 and 2009 presented as the MICs distribution data, MIC ₅₀ , MIC ₉₀
138	values and percentage of resistance are shown in Table 1.
139	
140	Based on the established MIC breakpoints, the 242 A. pleuropneumoniae isolates showed
141	low levels of antimicrobial drug resistance, except for tetracycline for which, on the
142	contrary, was frequent, i.e. in 58 (23.9 %) isolates. Resistance to florfenicol and tiamulin
143	was detected in two (0.8 %) and four (1.7 %) isolates, respectively. Regarding β -lactams,
144	low-levels of ampicillin and amoxicillin/clavulanic acid resistance were observed, in eight
145	(3.3 %) and two (0.8 %) isolates, respectively. Resistance to ceftiofur was not detected in
146	any isolate of A. pleuropneumoniae. With regard to macrolide resistance, a low-level
147	resistance to tilmicosin was exhibited by three (1.2 %) isolates, whereas resistance to
148	tulathromycin was not observed.

149	
150	The two A. pleuropneumoniae isolates exhibiting resistance (MIC 8 mg/L) to florfenicol,
151	were analysed for the presence of the floR gene. The presence of the floR gene was
152	confirmed in both isolates. In one of them, the DNA sequence was further confirmed by
153	DNA sequencing and obtained sequence was 99 % identical to Escherichia coli
154	florfenicol-resistance flo gene (accession number AF252855).
155	
156	Due to the fact that resistance breakpoints for swine bacterial respiratory pathogens are not
157	available for all antimicrobial agents tested, phenotypes of antimicrobial resistance profiles
158	for the isolates were constructed, taking into account ampicillin, amoxicillin and clavulanic
159	acid, ceftiofur, tulathromycin, tilmicosin, florfenicol, tetracycline and tiamulin (Table 2).
160	One hundred and seventy-three isolates (71.5 %) were fully susceptible to the selected
161	antimicrobial agents. The occurrence of resistance to at least one antimicrobial agent was
162	observed in 69 isolates (28.5 %), which were grouped into eight resistance profiles. The
163	most frequently occurring profile of resistance to one antimicrobial agent was found in 63
164	isolates (26.0 %) being followed - at a long interval - by 6 isolates (2.5 %) resistant to two
165	or three antimicrobial agents from two antimicrobial classes. Multidrug resistance to three
166	or more antimicrobial classes was not found among the isolates in the present study.
167	
168	Regarding serovar distribution of the isolates, the most prevalent were serovar 9 (93, 38.6
169	%) and serovar 2 (88, 36.4 %), followed by serovar 11 (23, 9.5 %) and a group of serovars
170	9 and 11 (26, 10.7 %), which could not be differentiated by either serological or molecular
171	techniques used. Serovars 3, 7, 8 and 12 were only represented by a small number of
172	isolates, in proportions equal or lower than 1.7 %. No correlation was detected between the
173	distributions of the resistances to antimicrobials and the serovars of A. pleuropneumoniae.

174	
175	DISCUSSION
176	
177	This study reports on the antimicrobial susceptibility to 16 antimicrobial agents in A.
178	pleuropneumoniae isolates collected from diseased pigs in Czech Republic between 2007
179	and 2009.
180	Based on the established MIC breakpoints, the 242 A. pleuropneumoniae isolates showed a
181	low level of resistance to antimicrobial agents, except for tetracycline. Following the
182	recommendation for the use of the same methodology and interpretive criteria because it
183	would allow for re-analysis of the original data if interpretive criteria changed (Schwarz et
184	al., 2010), three recent studies of susceptibility of A. pleuropneumoniae to antimicrobial
185	agents (Gutiérrez-Martin et al., 2006; Matter et al., 2007; Godinho, 2008) were suitable for
186	comparison with our data.
187	
188	In the first study (Gutiérrez-Martin et al., 2006), in vitro susceptibility of 11 antimicrobial
189	agents was determined for 229 A. pleuropneumoniae isolates collected in Spain between
190	1997 2004. Using equivalent breakpoints of resistance to amoxicillin (Schwarz et al.,
191	2008) and tetracycline for swine respiratory disease pathogens (CLSI, 2008) the
192	percentages of resistant Spanish isolates to tetracycline (85.6 %) and amoxicillin (27.9 %)
193	were much higher than those of tetracycline and ampicillin found in the present study.
194	
195	The second study (Matter et al., 2007) described in vitro susceptibility to 20 antimicrobial
196	agents in 83 A. pleuropneumoniae isolates collected in Switzerland between 2002 and
197	2004. Using equivalent currently accepted breakpoints, our study showed a close similarity
198	in the percentage of isolates resistant to ampicillin and tilmicosin. In contrast, the

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199	percentage of isolates resistant to amoxicillin/clavulanic acid (100 %) and tiamulin (10.8
200	%) was higher and the percentage of isolates resistant to tetracycline (8.4 %) was lower in
201	the Swiss study compared to the values obtained in the present study.
202	
203	In the third study (Godinho, 2008) in vitro susceptibility to tulathromycin was detected in
204	bacterial isolates obtained from field outbreaks of bovine and porcine respiratory disease in
205	a number of European countries between 2004 and 2006. Their MIC ₉₀ and MIC ₅₀ values
206	for tulathromycin against 53 A. pleuropneumoniae isolates were in accordance with those
207	of the present study.
208	
209	Whilst resistance to florfenicol was observed in two (1.2%) isolates, no resistance of A .
210	pleuropneumoniae to florfenicol has been reported for isolates tested so far by other
211	authors (Priebe and Schwarz, 2003; Gutierrez et al., 2006; Matter et al., 2007). A number
212	of genes, referred to in the published literature as pp-flo, omlA-like, floSt, flo, or floR,
213	mediate combined resistance of different bacterial species to chloramphenicol and
214	florfenicol. Despite their varying designations, these genes are closely related and show
215	96-100 % identity in their nucleotide sequences (Schwarz et al., 2004). The similar results
216	were obtained in this study. The presence of floR was confirmed in florfenicol resistant
217	isolates and 99 % identity of floR to Escherichia coli florfenicol-resistance flo gene was
218	detected.
219	
220	In conclusion, based on the MIC breakpoints, we have detected a new phenotype of
221	resistance to florfenicol and a low degree of resistance to other antimicrobials, with the
222	exception of tetracycline, among A. pleuropneumoniae isolates from the Czech Republic.
223	The <i>floR</i> gene was identified in florfenicol resistant isolates.

224	
225	CONFLICT OF INTEREST
226	
227	None of the authors have any relationship with any commercial entity that has interest in
228	the subject matter of this manuscript.
229	
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231	
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235	
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Table 1 MICs for 16 antimicrobial agents of the *Actinobacillus pleuropneumoniae* (n = 242) isolates identified in this study

Antimicrobial			Numb	oer o	f isol	ates w	vith M	IC of	(mg	<u>(/L)</u>			MIC ₅₀	MIC ₉₀	Percentage
agent	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	=		of resistance
Ampicillin			229	5	2	0	1	1	1	0	3		≤0.5	≤0.5	3.3
Amoxicillin/clavulanic acida			238	2	2	0	0	0	0	0			≤0.5	≤0.5	0.8
Ceftiofur			241	0	0	_1	0	0	0	0			≤0.5	≤0.5	0.0
Cefquinome		238	3	1	0	0	0	0	0				≤0.25	≤0.25	-
Tulathromycin			0	2	19	51	145	23	2	0			8	16	0.0
Tilmicosin				3	11	107	115	3	1	1	0	1	4	8	1.2
Chloramphenicol		197	23	6	3	4	4	3	2				≤0.25	0.5	-
Florfenicol		88	137	3	8	4	2	0	0				0.5	0.5	0.8
Oxolinic acid			190	14	4	5	9	7	7	3	3		≤0.5	8	-
Flumequine			211	4	4	13	4	0	2	4			≤0.5	2	-
Enrofloxacin	223	11	6	2	0	0	0	0					≤0.12	≤ 0.12	-
Tetracycline			153	31	10	11	6	8	13	6	4		≤0.5	16	24.0
Tiamulin			3	3	13	63	126	30	3	1			8	16	1.7
Gentamicin			17	34	94	79	13	1	0	1	3		2	4	-
Streptomycin				6	16	90	102	15	2	1	5	5	8	16	-
Trimethoprim/sulfamethoxazole ^b		215	6	9	6	3	1	0	2				≤0.25	0.5	

^a Amoxicillin and clavulanic acid in the ratio 2:1; test ranges are expressed as the amoxicillin concentration. ^b Trimethoprim and sulfamethoxazole in the ratio 1:19; test ranges are expressed as the trimethoprim concentration. The dilution ranges tested are those contained in the white area. Values above this range indicate MIC values higher than the highest concentration within the range. Values corresponding to the lowest concentration tested indicated MIC values lower or equal to the lowest concentration within the range. When available, breakpoints of resistance used are indicated with vertical black lines. Cross: No breakpoint for *A. pleuropneumoniae* is available.

Table 2
Resistance phenotypes of 242 *Actinobacillus pleuropneumoniae* isolates

Resistance phenotype	Number of	Number of
	antimicrobial agents	isolates
No antimicrobial resistance	0	173
TET	1	53
AMP	1	3
TIA	1	3
TIL	1	2
FFN	1	2
AMP + TET	2	3
TIL + TIA	2	1
AMP + AMC + TET	3	2
Total		242

Abbreviations: AMC, amoxicillin and clavulanic acid; AMP, ampicillin; FFN, florfenicol; TET, tetracycline; TIA, tiamulin; TIL, tilmicosin.