



**HAL**  
open science

## Distribution of integrons and SGI1 among antibiotic resistant isolates of animal origin

H. Havlickova, H. Hradecka, I. Bernardyova, I. Rychlik

► **To cite this version:**

H. Havlickova, H. Hradecka, I. Bernardyova, I. Rychlik. Distribution of integrons and SGI1 among antibiotic resistant isolates of animal origin. *Veterinary Microbiology*, 2008, 133 (1-2), pp.193. 10.1016/j.vetmic.2008.06.027 . hal-00532450

**HAL Id: hal-00532450**

**<https://hal.science/hal-00532450>**

Submitted on 4 Nov 2010

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## Accepted Manuscript

Title: Distribution of integrons and SGI1 among antibiotic resistant *Salmonella enterica* isolates of animal origin

Authors: H. Havlickova, H. Hradecka, I. Bernardyova, I. Rychlik



PII: S0378-1135(08)00252-6  
DOI: doi:10.1016/j.vetmic.2008.06.027  
Reference: VETMIC 4083

To appear in: *VETMIC*

Received date: 10-4-2008  
Revised date: 13-6-2008  
Accepted date: 26-6-2008

Please cite this article as: Havlickova, H., Hradecka, H., Bernardyova, I., Rychlik, I., Distribution of integrons and SGI1 among antibiotic resistant *Salmonella enterica* isolates of animal origin, *Veterinary Microbiology* (2007), doi:10.1016/j.vetmic.2008.06.027

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

1 Distribution of integrons and SGI1 among antibiotic resistant *Salmonella enterica* isolates of  
2 animal origin

3

4

5 Havlickova H.<sup>1</sup>, Hradecka H.<sup>1</sup>, Bernardyova I.<sup>2</sup>, Rychlik I.<sup>1\*</sup>

6

7

8

9 <sup>1</sup> Veterinary Research Institute, Hudcova 70, 621 00 Brno, Czech Republic

10

11 <sup>2</sup> State Veterinary Institute, Sidlistni 136, 165 03 Prague, Czech Republic

12

13

14

15

16 \* Corresponding author

17 Ivan Rychlik

18 Veterinary Research Institute

19 Hudcova 70

20 621 00 Brno

21 Czech Republic

22

23 phone +420 533331201

24 fax +420 541211229

25 Email: rychlik@vri.cz

**26 Abstract**

27 In *Salmonella enterica*, resistance to antibiotics can be caused by the presence of SGI1,  
28 transposons or conjugative plasmids. In this study we were interested in the relative  
29 contribution of these genetic elements to the antibiotic resistance of *S. enterica* isolates  
30 collected within a single year in the Czech Republic from animal sources. Altogether 123  
31 antibiotic-resistant isolates belonging to 16 different *S. enterica* serovars were classified into  
32 3 groups according to the presence of SGI1 and the presence of integrons. The first group  
33 consisted of 62 strains in which neither SGI1 nor class 1 integron was detected. A high  
34 diversity among serovars and resistance phenotypes was found in this group. The second  
35 group consisted of 56 strains positive for both the SGI1 and class 1 integron, out of which 55  
36 belonged to serovar Typhimurium and one to a nonmotile serovar [4,12] which harboured the  
37 SGI1-B variant. The third group comprised five strains which were positive for class 1  
38 integron but negative for the SGI1. Sequencing of the integrons in these isolates identified  
39 integron with *sat1* and *aadA1* gene cassettes in *S. Sandiego* and *S. Pullorum*, *dfrA1* and *aadA1*  
40 gene cassettes in *S. Typhimurium* integron, and *aadA21* gene cassette in *S. Braenderub* and *S.*  
41 *Zanzibar*.

42

**43 Keywords**

44 *Salmonella*, antibiotic resistance, SGI1, integron, plasmid

45

**46 Introduction**

47 The failure of bacterial disease treatment due to the antibiotic resistance of pathogenic  
48 microorganisms is a cause for concern for both the scientific community and the general  
49 public. Pathogenic microorganisms may become resistant to antibiotics in multiple ways. The  
50 two most extreme examples are point mutations in house-keeping genes leading to the

51 resistance phenotype or the horizontal acquisition of genes coding for antibiotic resistance. In  
52 *Salmonella enterica* (*S. enterica*), an example of the former case is the resistance to nalidixic  
53 acid which is most frequently associated with point mutations in the *gyrA* gene (Reyna et al.,  
54 1995). An example of the latter case is the appearance of multidrug resistant *S. Typhimurium*  
55 which acquired the *Salmonella* Genomic Island 1 (SGI1), part of which codes for resistance to  
56 antibiotics (Boyd et al., 2001).

57

58 In *S. enterica*, strains belonging to serovar Typhimurium are most frequently reported to be  
59 antibiotic resistant and within this serovar, one dominant lineage can be identified which is  
60 comprised of highly similar strains with the chromosomally located SGI1 (Boyd et al., 2001;  
61 Matiasovicova et al., 2007). Such strains were first recorded in the mid 1980's in the UK  
62 (Threlfall et al., 1994) and since that time they have spread throughout the whole world. Why  
63 this has happened is not fully understood but explanations regarding their increased virulence  
64 or ability of biofilm formation are being sought (Evans and Davies, 1996; Malcova et al.,  
65 2008). The remaining antibiotic resistant strains of *S. Typhimurium* are highly heterogenous  
66 and consist mainly of strains in which different conjugative R-plasmids can be found  
67 (Pezzella et al., 2004; Rodriguez et al., 2006; Vo et al., 2007).

68

69 Unlike some extensive studies, aim of our work was to analyse the relative frequency of  
70 different modes of antibiotic resistance in a collection of strains all isolated during a single  
71 year from animal sources from a relatively restricted geographic area. We therefore tested *S.*  
72 *enterica* strains which were submitted for confirmation of their antibiotic resistance to the  
73 National Reference Laboratory for Antibiotic Resistance in the Czech Republic over the  
74 course of a single year. This approach gave us a realistic view of the current situation among  
75 antibiotic resistant strains of *S. enterica* of animal origin in the Czech Republic regardless of

76 the serovar which, due to similarities in technologies of animal production, can be with a  
77 certain care generalised for the rest of Central Europe.

78

## 79 **Materials and Methods**

### 80 *Bacterial strains, serotyping and antibiotic susceptibility testing*

81 A total of 123 *Salmonella enterica* strains isolated from animal sources in the Czech Republic  
82 during year 2006 were included in this study. The strains were submitted to our laboratory by  
83 local diagnostic laboratories because of their resistance to one or more antibiotics. The strains  
84 originated from pigs (n=61), cattle (n=18), chickens (n=11), turkeys (n= 6) and from other  
85 animal or environmental sources (n=27) (for additional details see supplementary material).  
86 Isolated *Salmonella* were typed by agglutination with monovalent O and H anti-*Salmonella*  
87 sera (Bio-Rad, France), and classified into serotypes according to the Kauffman-White  
88 system. All isolates were tested by the disc diffusion method based on CLSI standards for  
89 sensitivity to the following 18 antibiotics (Oxoid Ltd., UK): ampicillin (A, 10 µg),  
90 amoxicillin/clavulanic acid (AMC, 30 µg), apramycin (APR, 15 µg), colistin (CT, 10 µg),  
91 cefotaxime (CTX, 30 µg), cephalothin (KF, 30 µg), ceftiofur (EFT, 30 µg), ciprofloxacin  
92 (CIP, 5 µg) chloramphenicol (C, 30 µg), enrofloxacin (ENR, 5 µg), gentamicin (G, 10 µg),  
93 kanamycin (K, 30 µg) nalidixic acid (NA, 30 µg), neomycin (N, 30 µg), streptomycin (S, 10  
94 µg), tetracycline (T, 30 µg), sulphonamides (Su, 300 µg) and trimethoprim (W, 5 µg).

95

### 96 *PCR detection of the left junction of SGI1 and class 1 integrons*

97 All the strains were tested for the presence of *Salmonella* genomic island 1 (SGI1) and class 1  
98 integrons. PCR for the detection of the left junction of SGI1 was carried out with the primer  
99 pair U7-L12 and LJ-R1 and the whole integron sequence was amplified using the 5CS and  
100 3CS primer pair described previously (Levesque et al., 1995; Boyd et al., 2002). PCR  
101 conditions we described previously (Faldynova et al., 2003).

102

103 *Sequencing of class 1 integrons*

104 To identify gene cassettes inside the class 1 integrons, the resulting PCR products were  
105 sequenced using a BigDye Terminator v3.1 Cycle Sequencing Kit according to the  
106 instructions of the manufacturer (Applied Biosystems). The extension products were  
107 separated and analysed by the ABI 310 Genetic Analyser (Applied Biosystems) and obtained  
108 sequences were BLAST compared with GenBank entries. The sequencing was performed for  
109 all strains which were different from *S. Typhimurium* displaying the ACSSuT or  
110 ACSSuT+Nal resistance phenotype and giving rise to 2 expected PCR products of 1009 and  
111 1197 bp after the 5CS-3CS PCR, or *S. Typhimurium* displaying the SSu resistance phenotype  
112 and giving rise to a single 1009 bp PCR product after the 5CS-3CS PCR. Such isolates were  
113 considered to contain either SGI1 or the SGI1-C variant of SGI1 (Boyd et al., 2002).

114

115 **Results**116 *Serotyping and antibiotic susceptibility testing*

117 The 123 antibiotic-resistant *Salmonella* isolates were assigned to 16 different *S. enterica*  
118 serovars including Typhimurium (n=93), Enteritidis (n=6), Infantis (n=5), Derby (n=4),  
119 Choleraesuis (n=2), Saintpaul (n=2) and Zanzibar (n=2). One isolates each was classified as  
120 belonging to the serovars Braenderub, Kentucky, Langeveld, Lomita, London, Ohio,  
121 Sandiego, Uppsala and a nonmotile serovar [4,12].

122

123 Resistance to streptomycin, ampicillin and sulphonamides was most frequently observed (in  
124 approx. 83 % of all isolates), followed by resistance to tetracycline (74 %) and  
125 chloramphenicol (54.5 %). The rates of resistances to nalidixic acid, trimethoprim and  
126 kanamycin were 13.8 %, 7.3 % and 4.1 %, respectively. Only 2 strains (1.6 %) were resistant

127 to neomycin or cefalotin. Resistance to apramycin, gentamicin or amoxycilin-clavulanic acid  
128 was always observed in a single isolate. Within the given collection of strains and the set of  
129 antibiotics used we never observed strains resistant to cefotaxime, ceftiofur, ciprofloxacin,  
130 colistin and enrofloxacin.

131

### 132 *PCR detection of the left junction of SGI1 and class 1 integrons*

133 Based on the two PCRs, the strains could be clustered into three groups. The first group  
134 consisted of 62 strains in which neither the left junction of SGI1 nor the class 1 integron was  
135 detected. A high diversity in serovars and resistance phenotypes was found in this group (see  
136 Table 1 and also electronic supplementary material). This type of antibiotic resistance was  
137 most frequently found in serovar Typhimurium (59.7 %). Although the isolates were resistant  
138 from 1 to 8 antibiotics, the most frequent type of resistance of non-SGI1 *S. Typhimurium* was  
139 characterised as ASSuT.

140

141 The second group consisted of 56 strains positive for both the left junction of SGI1 and the  
142 class 1 integron. Except for a single isolate of nonmotile *Salmonella* [4,12] isolated from a  
143 shark, all the strains in this group belonged to serovar Typhimurium. The nonmotile  
144 *Salmonella* [4,12] strain was resistant to ampicillin and sulphonamides and both these  
145 resistances were associated with the presence of the SGI1-B variant present downstream from  
146 the *thdF* gene.

147

148 The third group comprised five strains of serovars Braenderub (SSuT resistance phenotype),  
149 Sandiego (SSuT), Saintpaul (SSuT), Typhimurium (ASSuT+W+Apr) and Zanzibar (CSSuT)  
150 which were positive for the class 1 integron but negative for the left junction of SGI1. To

151 determine which of the antibiotic resistances were parts of the integrons, the 5CS-3CS PCR  
152 products were subjected to DNA sequencing.

153

#### 154 *Sequencing of class 1 integrons*

155 In the 5 strains in which the integrons were not part of the SGI1 and, *S. Sandiego* and *S.*  
156 *Saintpaul* harboured integrons with *sat1* and *aadA1* gene cassettes similar to the GenBank  
157 Ac.n. AM055748. *S. Typhimurium* harboured integron with *dfrA1* and *aadA1* gene cassettes  
158 similar to the GenBank Ac.n. DQ133164, and in *S. Zanzibar* and *S. Braenderub*, an *aadA21*  
159 containing integron similar to the GenBank Ac.n. AY171244 was found. All these gene  
160 cassettes were different from those usually found in different SGI1 variants further  
161 confirming the non-SGI1 nature of these integrons (Table 2).

162

#### 163 **Discussion**

164 The *S. enterica* isolates in this study were most frequently resistant to streptomycin,  
165 ampicillin and sulphonamides. Resistance to tetracycline and chloramphenicol were recorded  
166 slightly less frequently (Fig. 1). The dominant occurrence of these resistances is closely  
167 linked with the presence of the SGI1 and *S. Typhimurium*. Indeed, in 56 isolates with the  
168 ACSSuT type of resistance all belonged to the serovar *Typhimurium* and only 4 of them did  
169 not harbour the SGI1. Less frequent resistance to chloramphenicol can be explained by the  
170 detection of 19 strains without the SGI1 (18 isolates of serovar *Typhimurium* and a single  
171 isolate of serovar *Infantis*) which were resistant to ampicillin, streptomycin, sulphonamides  
172 and tetracycline. Isolates of *S. Typhimurium* exhibiting this type of resistance have already  
173 been recorded by other authors (Soler et al., 2006; Graziani et al., 2008).

174

175 Sixty two *S. enterica* isolates resistant to antibiotics were free of the SGI1 as well as  
176 integrons. The increased variation in serovars represented in this group indicated a recent  
177 horizontal acquisition of antibiotic resistance from different sources. It is possible that at least  
178 in some of the cases the resistance was encoded by conjugative plasmids which may transfer  
179 resistance to a single antibiotic (Hradecka et al., 2006) as well as multidrug resistance  
180 (Carattoli et al., 2001; Guerra et al., 2002).

181

182 The SGI1 and integrons were found in 56 isolates, 55 of which belonged to serovar  
183 Typhimurium. The only non-Typhimurium serovar harbouring the SGI1 was nonmotile  
184 *Salmonella* [4,12] with a SGI1-B variant (ASu type of antibiotic resistance). Although the  
185 SGI1 can be mobilised for conjugative transfer (Doublet et al., 2005), its dominant association  
186 with serovar Typhimurium and much less frequent presence in other serovars also suggests  
187 that the conjugational transfer of SGI1 is probably not a common event in the environment.

188

189 Five strains were positive for the presence of integrons but negative for the SGI1. Since these  
190 strains were all from different serovars, it is quite probable that the integrons were acquired  
191 by each of the isolates independently. All combinations of gene cassettes identified in our  
192 strain collection have already been described although the *sat1 aadA1* combination is found in  
193 *S. enterica* quite rarely (Guerra et al., 2000; Zhao et al., 2007).

194

195 Although antibiotic resistance testing is a relatively simple procedure, a detailed  
196 characterisation of genotypes of antibiotic resistant *S. enterica* by PCR targeted to the  
197 antibiotic resistance genes is quite laborious due to the extensive list of potential gene  
198 candidates (Faldynova et al., 2003). The last, rather indirect result of this study therefore is  
199 that by a combination of only two PCRs specific for the left junction of the SGI and the

200 presence of integrons, *S. enterica* isolates can be easily classified into 3 basic clusters. The  
201 sizes of the amplification products in 5CS-3CS PCR enabled the further characterisation of  
202 the field isolates and the selection of strains with unusual characteristics suitable for  
203 subsequent detailed analysis.

204

#### 205 **Acknowledgement**

206 This work has been supported by projects 1B44019 and MZE0002716201 of the Czech  
207 Ministry of Agriculture. The authors wish to acknowledge the excellent technical assistance  
208 of Michaela Dekanova and Neysan Donelli for English language corrections.

209

#### 210 **References**

211 Boyd, D., Cloeckaert, A., Chaslus-Dancla, E., Mulvey, M.R., 2002. Characterization of  
212 variant *Salmonella* genomic island 1 multidrug resistance regions from serovars Typhimurium  
213 DT104 and Agona. Antimicrob. Agents Chemother. 46, 1714-1722.

214

215 Boyd, D., Peters, G.A., Cloeckaert, A., Boumedine, K.S., Chaslus-Dancla, E., Imberechts, H.,  
216 Mulvey, M.R., 2001. Complete nucleotide sequence of a 43-kilobase genomic island  
217 associated with the multidrug resistance region of *Salmonella enterica* serovar Typhimurium  
218 DT104 and its identification in phage type DT120 and serovar Agona. J. Bacteriol. 183, 5725-  
219 5732.

220

221 Carattoli, A., Villa, L., Pezzella, C., Bordi, E., Visca, P., 2001. Expanding drug resistance  
222 through integron acquisition by IncFI plasmids of *Salmonella enterica* Typhimurium. Emerg.  
223 Infect. Dis. 7, 444-447.

224

225 Doublet, B., Boyd, D., Mulvey, M.R., Cloeckaert, A., 2005. The *Salmonella* genomic island 1  
226 is an integrative mobilizable element. *Mol. Microbiol.* 55, 1911-1924.

227

228 Evans, S., Davies, R., 1996. Case control study of multiple-resistant *Salmonella typhimurium*  
229 DT104 infection of cattle in Great Britain. *Vet. Rec.* 139, 557-558.

230

231 Faldynova, M., Pravcova, M., Sisak, F., Havlickova, H., Kolackova, I., Cizek, A.,  
232 Karpiskova, R., Rychlik, I., 2003. Evolution of antibiotic resistance in *Salmonella enterica*  
233 serovar typhimurium strains isolated in the Czech Republic between 1984 and 2002.

234 *Antimicrob. Agents Chemother.* 47, 2002-2005.

235

236 Graziani, C., Busani, L., Dionisi, A.M., Lucarelli, C., Owczarek, S., Ricci, A., Mancin, M.,  
237 Caprioli, A., Luzzi, I., 2008. Antimicrobial resistance in *Salmonella enterica* serovar  
238 Typhimurium from human and animal sources in Italy. *Vet. Microbiol.* 128, 414-418.

239

240 Guerra, B., Soto, S., Cal, S., Mendoza, M.C., 2000. Antimicrobial resistance and spread of  
241 class 1 integrons among *Salmonella* serotypes. *Antimicrob. Agents Chemother.* 44, 2166-  
242 2169.

243

244 Guerra, B., Soto, S., Helmuth, R., Mendoza, M.C., 2002. Characterization of a self-  
245 transferable plasmid from *Salmonella enterica* serotype typhimurium clinical isolates carrying  
246 two integron-borne gene cassettes together with virulence and drug resistance genes.

247 *Antimicrob. Agents Chemother.* 46, 2977-2981.

248

- 249 Hradecka, H., Kolackova, I., Karpiskova, R., Rychlik, I., 2006. An outbreak of human  
250 salmonellosis caused by ampicillin-resistant *Salmonella enterica* serovar Enteritidis PT13 in  
251 the Czech Republic. *Epidemiol. Infect.* 134, 737-740.
- 252
- 253 Levesque, C., Piche, L., Larose, C., Roy, P.H., 1995. PCR mapping of integrons reveals  
254 several novel combinations of resistance genes. *Antimicrob. Agents Chemother.* 39, 185-191.
- 255
- 256 Malcova, M., Hradecka, H., Karpiskova, R., Rychlik, I., 2008. Biofilm formation in field  
257 strains of *Salmonella enterica* serovar Typhimurium: Identification of a new colony  
258 morphology type and the role of SG11 in biofilm formation. *Vet. Microbiol.* 129, 360-6.
- 259
- 260 Matiasovicova, J., Adams, P., Barrow, P.A., Hradecka, H., Malcova, M., Karpiskova, R.,  
261 Budinska, E., Pilousova, L., Rychlik, I., 2007. Identification of putative ancestors of the  
262 multidrug-resistant *Salmonella enterica* serovar typhimurium DT104 clone harboring the  
263 *Salmonella* genomic island 1. *Arch. Microbiol.* 187, 415-424.
- 264
- 265 Pezzella, C., Ricci, A., DiGiannatale, E., Luzzi, I., Carattoli, A., 2004. Tetracycline and  
266 streptomycin resistance genes, transposons, and plasmids in *Salmonella enterica* isolates from  
267 animals in Italy. *Antimicrob. Agents Chemother.* 48, 903-908.
- 268
- 269 Reyna, F., Huesca, M., Gonzalez, V., Fuchs, L.Y., 1995. *Salmonella typhimurium gyrA*  
270 mutations associated with fluoroquinolone resistance. *Antimicrob. Agents Chemother.* 39,  
271 1621-1623.
- 272

- 273 Rodriguez, I., Martin, M.C., Mendoza, M.C., Rodicio, M.R., 2006. Class 1 and class 2  
274 integrons in non-prevalent serovars of *Salmonella enterica*: structure and association with  
275 transposons and plasmids. J. Antimicrob. Chemother. 58, 1124-1132.  
276
- 277 Soler, P., Gonzalez-Sanz, R., Bleda, M.J., Hernandez, G., Echeita, A., Usera, M.A., 2006.  
278 Antimicrobial resistance in non-typhoidal *Salmonella* from human sources, Spain, 2001-2003.  
279 J. Antimicrob. Chemother. 58, 310-314.  
280
- 281 Threlfall, E.J., Frost, J.A., Ward, L.R., Rowe, B., 1994. Epidemic in cattle and humans of  
282 *Salmonella typhimurium* DT 104 with chromosomally integrated multiple drug resistance.  
283 Vet. Rec. 134, 577.  
284
- 285 Vo, A.T., van Duijkeren, E., Fluit, A.C., Gaastra, W., 2007. A novel *Salmonella* genomic  
286 island 1 and rare integron types in *Salmonella* Typhimurium isolates from horses in The  
287 Netherlands. J. Antimicrob. Chemother. 59, 594-599.  
288
- 289 Zhao, S., McDermott, P.F., White, D.G., Qaiyumi, S., Friedman, S.L., Abbott, J.W., Glenn,  
290 A., Ayers, S.L., Post, K.W., Fales, W.H., Wilson, R.B., Reggiardo, C., Walker, R.D., 2007.  
291 Characterization of multidrug resistant *Salmonella* recovered from diseased animals. Vet.  
292 Microbiol. 123, 122-132.

293 **Figure legend**

294 Figure 1. Resistance to individual antibiotics among *S. enterica* strains isolated from animal  
295 sources in the Czech Republic during 2006. A, ampicillin; AMC, amoxicillin/clavulanic acid;  
296 APR, apramycin; C, chloramphenicol, G, gentamicin; K, kanamycin; KF, cefalotin; N,  
297 neomycin; NA, nalidixic acid; S, streptomycin; Su, sulphonamides; T, tetracycline; W,  
298 trimethoprim.

Accepted Manuscript

299 Table 1. Variability in serovars and antibiotic resistance patterns depending on the presence of  
 300 SGI1 or integrons

group	LJ <sup>&amp;</sup>	5CS	3CS <sup>&amp;</sup>	strains*	serovars*	resistance*
1	-	-		62	13	27
2	+	+		56	2	5
3	-	+		5	5	3

301

302 \* numbers indicate number of strains, serovars or different resistance patterns in each group

303 <sup>&</sup> result of particular PCR

304 Table 2. Integrons of *Salmonella enterica* as identified by DNA sequencing of 5CS-3CS PCR  
 305 products.

306

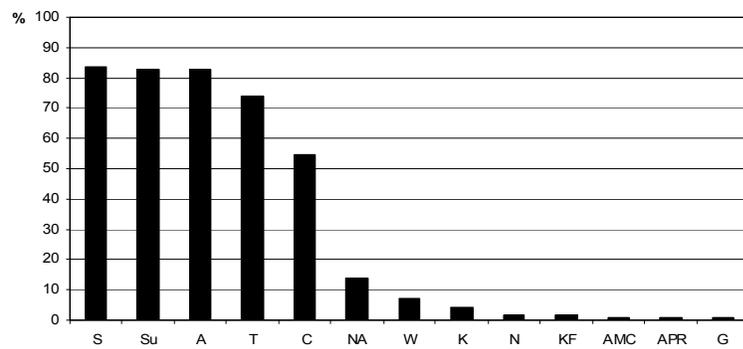
Serovar	Resistance phenotype	Presence of SGII	Array of gene cassettes	Origin
[4,12]	ASu	yes	<i>bla<sub>PSE-1</sub></i>	shark
Braenderub	SSuT	no	<i>aadA21</i>	chicken
Sandiego	SSuT	no	<i>sat1 aadA1</i>	turkey
Saintpaul	SSuT	no	<i>sat1 aadA1</i>	turkey
Typhimurium	ASSuT+W+Apr	no	<i>dfrA1 aadA1</i>	pig
Zanzibar	CSSuT	no	<i>aadA21</i>	turkey

307

308 A, ampicillin; Apr, apramycin; C, chloramphenicol; S, streptomycin; Su, sulphonamides; T,

309 tetracycline; W, trimethoprim

Fig 1. Havlickova et al. Distribution of integrons and SGI1 among antibiotic resistant Salmonella...



Accepted Manuscript