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1 **Prevalence, serovars, phage types and antibiotic susceptibilities of *Salmonella* strains isolated**
2 **from animals in the United Arab Emirates from 1996 to 2009**

3

4 S. Münch^a, P. Braun^b, U. Wernery^c, J. Kinne^c, M. Pees^d, A. Flieger^a, E. Tietze^a and W. Rabsch^{a*}

5 ^aDivision of Bacterial Infections and National Reference Centre for *Salmonella* and other Bacterial
6 Enteric Pathogens, Robert Koch Institute, Wernigerode Branch, Burgstr. 37, 38855 Wernigerode,
7 Germany

8 ^bInstitute for Food Hygiene, Veterinary Faculty, University of Leipzig, An den Tierkliniken 1, 04103,
9 Leipzig, Germany

10 ^cCentral Veterinary Research Laboratory, P.O. Box 597, Dubai, United Arab Emirates

11 ^dClinic for Birds and Reptiles, Veterinary Faculty, University of Leipzig, An den Tierkliniken 17,
12 04103 Leipzig

13 *Correspondence: E-mail: RabschW@rki.de, Tel: +49 3943 679 318,

14 Fax: +49 3943 679 207

15

16 **Abstract** The aim of this study was to give some insights into the prevalence, serovars, phage types
17 and antibiotic resistances of *Salmonella* from animal origin in the United Arab Emirates. Data on
18 diagnostic samples from animals (n= 20871) examined for *Salmonella* between 1996 and 2009 were
19 extracted from the databases of the Central Veterinary Research Laboratory in Dubai and from typed
20 strains (n= 1052) from the Robert Koch Institute, Wernigerode Branch in Germany and analysed for
21 general and animal specific trends. *Salmonella* were isolated from 1928 (9%) of the 20871 samples
22 examined. Among the 1052 typed strains, most were from camels (n= 232), falcons (n= 166), bustards
23 (n= 101) antelopes (n= 66) and horses (n= 63). The predominant serovars were *S. Typhimurium*
24 (25%), *S. Kentucky* (8%), followed by *S. Frintrop* (7%) and *S. Hindmarsh* (5%). When analysed by
25 animal species the most frequent serovars in camels were *S. Frintrop* (28%) and *S. Hinmarsh* (21%), in
26 falcons *S. Typhimurium* (32%), in bustards *S. Kentucky* (19%), in antelopes *S. Typhimurium* (9%)

27 and in horses *S. Typhimurium* (17%) and *S. Kentucky* (16%). Resistance of all typed *Salmonella*
28 strains (n= 1052) was most often seen to tetracycline (23%), streptomycin (22%), nalidixic acid (18%)
29 and ampicillin (15%). These data show trends in the epidemiology of *Salmonella* in different animal
30 species which can be used as a base for future prevention, control and therapy strategies.

31

32 **Keywords** *Salmonella*, serovars, phage types, antibiotic susceptibility, animal, UAE

33

34 **Introduction**

35 *Salmonellae* are one of the most important pathogens in both humans and animals worldwide, as
36 they cause gastrointestinal infections or septicaemia (Khakhria 1997). Over 2600 *Salmonella* serovars
37 are known (Guibourdenche et al. 2010) with a different host adaption and virulence (Rolle and Mayr
38 2007). Generally, the *Salmonella* prevalence differs between animal species (Goppee et al. 2000).
39 Many studies reported a high *Salmonella* prevalence in healthy and diseased wild and captive reptiles
40 (Dimow 1966; Hidalgo-Vila et al. 2007; Geue and Löschner 2002; Briones et al. 2004) and it is
41 thought that they are an important *Salmonella* reservoir. The epidemiology of salmonellosis is quite
42 complex since there are many routes of infection, for example from feed to animal, from animal to
43 animal (same or different species) or from human to animal (Williams 1975). For that reason, the
44 surveillance of *Salmonella* serovars and phage types is important for identifying outbreaks, for
45 discovering infection sources, and to carry out adequate prevention and control measures (Van
46 Duijkeren et al. 2002).

47 Although a large number of *Salmonella* serovars exist, most infections are only caused by a few
48 emerging serovars and phage types (Helms et al. 2005). Various authors have reported *S.*
49 *Typhimurium* as one of the most prevalent serovars in animals globally (Basu et al. 1965; Nabbut and
50 Jamal, 1970; Molla et al. 2002; Oolya et al. 2007; Institute of Medical and Veterinary Science, 2008;
51 Friedrich et al. 2010; Kidamemariam et al. 2010). For that reason and since it has a broad host
52 spectrum, the serovar *Typhimurium* is further subdivided by phage typing to identify its different

53 clones. In the last two decades, multidrug resistant *S. Typhimurium* DT 104 which has usually a
54 chromosomal encoded pentaresistance against ampicillin, chloramphenicol, streptomycin,
55 sulphonamides and tetracyclines spread internationally (Helms et al. 2005; Ridley and Threlfall 1998).
56 However, recently in Europe, DT193 was the most common found in humans with salmonellosis in
57 2007 (European Food Safety Authority 2009) and was also isolated from diagnostic samples isolated
58 from pigs and broiler chicken in Germany and Australia (Bundesinstitut für Risikobewertung 2011;
59 Institute of Medical and Veterinary Science 2009).

60 Apart from causing severe illness, there are concerns about the emergence of MDR *Salmonella*
61 strains (Oloya et al. 2007) because they reduce treatment options and can lead to treatment failures and
62 more severe illness in both animals and humans (Threlfall et al. 2003). Moreover, they are potential
63 donors of resistance genes to other pathogens or commensals in the gastrointestinal tract (McEwen and
64 Fedorka-Cray 2002). It is believed that the development of MDR bacteria was promoted by the use of
65 antimicrobial drugs in food animals (Rabsch et al. 2001). Fluoroquinolones and third generation
66 cephalosporins are drugs of choice in human invasive salmonellosis (World Health Organization
67 2005). Nevertheless, fluoroquinolones are also used for many indications in veterinary medicine.
68 Rotimi et al. (2008) reported the emergence of reduced susceptibility of ciprofloxacin (CIP) in
69 *Salmonella* isolates from diseased humans in the United Arab Emirates (UAE). *Salmonella* serovars
70 that have been associated with a high rate of ciprofloxacin resistant are *S. Typhimurium*, *S.*
71 *Choleraesuis* and *S. Schwarzengrund* (Olsen et al. 2001; Chiu et al. 2002, Casin et al. 2003). Recently,
72 the first CIP resistant *S. Kentucky* strain has been isolated from the stool of a French tourist with
73 gastroenteritis returning from Egypt, and later it emerged in different countries in Africa and Middle
74 East (Weill et al. 2006; Le Hello et al. 2011). As the CIP resistant *S. Kentucky* was detected in chicken
75 from Ethiopia, Morocco and Togo, it is believed that poultry is the reservoir of this strain (Le Hello et
76 al. 2011).

77 The United Arab Emirates are located in the southeast of Asia and have combined the
78 characteristics of both developed and developing countries (Rotimi et al. 2008). They are importing
79 domestic and exotic animals for food production, private wildlife collections or sport competitions as

80 well as, animal feed from Africa, Asia and Europe (Bailey et al. 2000a; Wernery and Wernery 2004).
81 Subsequently, that might play an important role as potential source for *Salmonella* infections for
82 humans and animals (D'Aoust 1994; Helms et al. 2005). Hence, the data from the UAE may have a
83 worldwide significance in the context of the distribution of *Salmonella* serovars, phage types, and
84 antimicrobial resistances in different animal species.

85 So far there have been only a few epidemiological studies about *Salmonella* infections in captive
86 falcons (Wernery et al. 1998; Gierse 2001), camels (Wernery and Makarem 1996; Wernery 1992;
87 Moore et al. 2002) and captive bustards (Bailey et al. 2000b) in the UAE but the actual situation of
88 *Salmonella* in above mentioned and other animal species is not known. Moreover, there is no
89 published information on the endemic phage types of *S. Typhimurium* and *S. Enteritidis* and the
90 epidemiology of antibiotic resistances in animals, except in bustards (Bailey et al. 1998). Therefore,
91 the aim of this retrospective study was to provide insight into the prevalence, serovars, phage types,
92 and antibiotic resistances of *Salmonella* in the UAE between 1996 and 2009.

93

94 **Materials and methods**

95 Study design

96 We conducted a retrospective data analysis among 20871 diagnostic samples from over 80 different
97 animal species from the UAE, which have been examined for *Salmonella* at the Central Veterinary
98 Research Laboratory (CVRL) in Dubai from January 1996 to June 2009. The different animal species
99 examined are shown in Supplement Table 1. The diagnostic materials examined were faeces and
100 different organs (liver, spleen, mesenteric lymph nodes, small intestine, kidney and lung) from healthy
101 and diseased animals. 1052 isolated *Salmonella* strains subtyped at the Robert Koch Institute (RKI),
102 Wernigerode Branch, Germany.

103

104

105 Data acquisition

106 Data on *Salmonella* serovars, phage types, and antimicrobial resistances from domestic and non
107 domestic animals in the UAE were obtained from the database of the RKI. Additionally, the
108 epidemiological data on *Salmonella* serovars was retrieved from the records of CVRL.
109 Epidemiological data extracted included age, sex, date of submission, animal species, and residence of
110 the animals. Furthermore, data on the total number of samples from different animal species, which
111 were screened for *Salmonella*, and the number of *Salmonella* positive samples were extracted from the
112 CVRL database. If there was a cluster (e.g., three or more *Salmonella* cases in the same animal species
113 caused by the same *Salmonella* strain), only one of these cluster strains was included into this data
114 analysis.

115

116 Collection of samples and isolation of *Salmonella*

117 Faecal specimens or swabs were sent to CVRL for microbiological diagnostic. Furthermore, at CVRL
118 about 15 g of organ samples (liver, spleen, mesenteric lymph nodes, small intestine, kidney and lung)
119 and 15 g faeces were taken during pathological examination of different animal species with sterile
120 instruments and collected in sterile petri dishes. Afterwards, about 10 g of each organ sample was cut
121 into small pieces with a sterile scalpel blade and put into 10 ml tetrathionate broth (Merck, Darmstadt,
122 Germany). About 3 g of the faecal samples were added into 10 ml of tetrathionate broth (Merck) and
123 incubated at 37 °C for 24 h. This was followed by spreading the enriched samples onto brilliant green-
124 phenol red-lactose-sucrose agar (Merck), MacConkey agar (Merck) and xylose-lysine-desoxycholate
125 agar (Oxoid, Basingstoke, England). After incubation at 37 °C for 24 h, the plates were examined for
126 the presence of *Salmonella* colonies. *Salmonella*-like colonies were tested biochemically with the API
127 20 E System (BioMérieux, Nürtingen, Germany). 1052 isolated *Salmonella* strains were sent to the
128 RKI.

129

130 Subspecies detection

131 The subspecies were determined at the RKI. For that, the *Salmonella* were suspended in 10 ml
132 nutrition broth (Difco, Detroit, USA). Afterwards 5 ml potassium cyanide (Merck), 5 ml lysine

133 (Merck, both layered with paraffin) and 5 ml malonate (Becton Dickinson, Heidelberg, Germany)
134 have been inoculated with 5 µl of the *Salmonella* suspension. Furthermore, Kligler iron Agar (Kligler,
135 1917; Heipha, Eppelheim, Germany) was inoculated and incubated together with the above nutrient
136 broth and biochemical substances at 37 °C for 18 h. On the next day, the Indol test was performed by
137 adding two drops of indol into the nutrition broth. All *Salmonella* strains were grouped into different
138 subspecies according to their biochemical reaction as reported by Farmer (1985).

139

140 Serotyping

141 Serotyping of the *Salmonella* species was performed by using the slide agglutination test with
142 polyvalent and monovalent antisera against the somatic (O-) and flagellar (H-) antigen (SIFIN, Berlin,
143 Germany). The serovars were named according to the White-Kauffmann-LeMinor scheme (Grimont,
144 2007).

145

146 Phage typing

147 Phage typing was done by using the standard technique as reported by Kühn (1973). Isolates which
148 did not react with any of the typing phages were designated as untypable (ut). Strains showing
149 untypical lysis pattern of any definitive type (DT) or provisional phage type (PTU) were named
150 RDNC (read with phages but does not conform to definite or provisional types).

151 *S. Typhimurium* strains were phage typed by the scheme of Anderson et al. (1977) with phages
152 obtained from the National *Salmonella* Reference Laboratory (NSRL), London, England. *S. Enteritidis*
153 phage typing was performed with the schemes from Ward et al. (1987) and Lászlo et al. (1985) with
154 phages obtained from the NRSL and Veterinary Medical Research Institute of the Hungarian
155 Academy of Sciences, Budapest, Hungary (Rabsch et al. 2007).

156

157 Antimicrobial susceptibility testing

158 Antimicrobial susceptibility testing was done by broth microdilution in agreement with document
159 58940-8 of the Deutsches Institut für Normung (DIN) (Deutsches Institut für Normung, 2004). Strains

160 were categorised as resistant according to clinical breakpoints recommended in DIN 58940-4
161 (Anonymus 2004).

162 The breakpoints for nalidixic acid (≥ 32), streptomycin (≥ 32) and kanamycin (≥ 32) are suitable for
163 epidemiological surveillance. The strain *Escherichia coli* ATCC[®] 25922 was used for quality
164 control. The following antimicrobials grouped according to their classes were tested: β -lactams
165 (penicillins): ampicillin (AMP), β -lactams (cephalosporins (2nd generation)): cefotiam (CTM),
166 cefoxitin (COX); β -lactams (cephalosporins (3rd generation)): cefotaxime (CTX), ceftazidime (CAZ);
167 quinolones: nalidixic acid (NAL), Fluroquinolones Ciprofloxacin (CIP), aminoglycosides
168 streptomycin (STR), kanamycin (KAN), gentamycin (GEN); Tetracyclines: oxytetracycline (OTE);
169 sulfonamides (SMZ); trimethoprim+sulfamethoxazole (SXT), Phenicols: chloramphenicol (CMP).
170 Details of the breakpoints for the 13 antimicrobials are presented in Table 6.

171 Multidrug resistance was defined as resistance to at least three or more antimicrobial classes (Centers
172 for Disease Control and Prevention, 2010).

173

174 **Results**

175 As shown in Table 1, 1928 (9%) of the total 20871 diagnostic samples from different animal
176 species were *Salmonella* positive. The animal species included camels, falcons, chicken, horses,
177 antelopes, bustards, pigeons, sheep/goats, quails, rheas/ostriches, stone curlews, cheetahs, reptiles, and
178 other animal species (Suppl. Table 1). *Salmonella* was most frequently detected in diagnostic samples
179 from reptiles (36%), followed by rheas/ostriches (30%), pigeons (26%), cheetahs (19%) bustards
180 (18%), and quails (15%). In contrast, the lowest prevalence was observed in falcon (6%), horses (4%),
181 sheep/goats (3%) and poultry (2%; Table 1).

182 1052 *Salmonella* isolates were typed, most were from camels (n=232), falcons (n=166), bustards
183 (n=101), antelopes (n=66), horses (n=63) and pigeons (n=51; Table 2). In total, 104 different serovars
184 were identified among all diagnostic *Salmonella* isolates. 98% were from *Salmonella enterica*

185 subspecies I and in total two percent belonged to the subspecies II, IIIa, IIIb and IV. However, among
186 36 reptile isolates 64% belonged to subspecies I, 14% to subspecies IV, 11% to as well IIIa as IIIb.

187 The ten most frequently detected *Salmonella* were *S. Typhimurium* (n=258), *S. Kentucky* (n=82),
188 *S. Frintrop* (n=73), *S. Hindmarsh* (n=55), *S. Enteritidis* (n=36), *S. Infantis* (n=29), *S. Newport* (n=25),
189 *S. Agona* (n=23), *S. Anatum* (n=21), *S. Meleagridis* (n=21), and *S. Amsterdam* (n=21; Table 2). For
190 camels, the most important serovars were *S. Frintrop* (n=65), *S. Hindmarsh* (n=48) and *S.*
191 *Typhimurium* (n=27); for falcons *S. Typhimurium* (n=53) and *S. Enteritidis* (n=13); for bustards *S.*
192 *Kentucky* (n=19) and *S. Typhimurium* (n=14); for horses *S. Typhimurium* (n=11) and *S. Kentucky*
193 (n=10); for pigeons *S. Typhimurium* (n=40); ostriches/nandus *S. Typhimurium* (n=23); for quails *S.*
194 *Typhimurium* (n=12); and finally, for poultry *S. Infantis* (n=6) and *S. Typhimurium* (n=6). A
195 comparison of serovars with the different animal species showed, that 90 % of all *S. Frintrop* isolates
196 (n=73) and 87 % of all *S. Hindmarsh* isolates (n=55) were from camels. In contrast, a broad host
197 spectrum was observed with *S. Typhimurium* and *S. Kentucky* isolates (Table 2 and Suppl. Table 1).
198 Figure 1 presents the distribution of the four most common serovars during the 14 years of the study.
199 Although the rate of isolation of *S. Typhimurium* decreased dramatically during the study, it still
200 dominated in all years except 2004, 2006, and 2007. *S. Hindmarsh* was the most common serovar in
201 2004 and 2006, and *S. Kentucky* in 2007. Serovar *Kentucky* isolates increased substantially between
202 2004 and 2007. Interestingly, *S. Frintrop* was first isolated in the year 2000 and *S. Hindmarsh* in 2001.

203 As presented in Table 3, *S. Typhimurium* was further analysed by phage typing. Among the 258 *S.*
204 *Typhimurium* strains, 25 different types were isolated; however, 20 strains were ut and 70 were
205 RDNC. The lyses patterns from the RDNC strains were heterogenic during the years of the study
206 period. Therefore, no new phage types were defined. Most of the *S. Typhimurium* strains belonged to
207 DT104 (n=29), DT193 (n=28), DT099 (n=27), and PTU (provisional type, untypable with the 34 basic
208 types of the new Callow scheme (Anderson et al. 1977)) 302 (n=18). Table 3 also shows the
209 distribution of *S. Typhimurium* phage types among the animal species. While comparing the phage
210 types and the animal species, falcons (n=12) showed the highest number of different phage types and
211 RDNC strains (n=14). In falcons, the primarily isolated phage types were DT104 (n=12) and PTU302

212 (n=6); in pigeons DT099 (n=10) and DT002 (n=5); in camels DT193 (n=8) and in horses DT099
213 (n=5). From 1996-1999, *S. Typhimurium* phage type DT104 was frequently isolated but last found in
214 2001 and 2003. In the year 2000, PTU302 was the most common serovar. In the following years the
215 phage types DT193 and DT099 were most regularly detected.

216 Distribution of the *S. Enteritidis* phage types is shown in Table 4. A total of 13 different phage
217 types were detected among 36 *S. Enteritidis* isolates. The most frequently isolated types were 6a/3a
218 (n=7), 4/6 (n=6) and 33/17 (n=4). In falcons, six different *S. Enteritidis* phage types were detected.
219 The phage type 6a/3a (n=7) was only isolated in falcons between 1997 and 1999.

220 The periodical rate of MDR *Salmonella* increased gradually until the period 2005-2007 (29%) and
221 has since declined. Furthermore, the periodical rate of resistant *Salmonella* peaked in the period 1999-
222 2001 (20%) and declined in the periods thereafter. In contrast, the annual rate of susceptible strains
223 decreased until its dip 1999-2001 (56%) and afterwards rose until the end of the study period.

224 Among the 1052 isolates tested for antimicrobial susceptibility (Table 5), 16 % were resistant
225 against one and two antimicrobial drug classes and 21 % were MDR. Table 5 also shows the resistance
226 observed among *Salmonella* isolates from the different animal species. The highest rate of susceptible
227 *Salmonella* strains was detected in reptiles (87%), followed by bovine (85%), antelopes (84%) and
228 camels (77%). 30 % of all isolates from quails were resistant to one or two antimicrobial classes, 23 %
229 from falcons, 23 % from stone curlews and 22 % from pigeons. The highest rate of MDR *Salmonella*
230 strains was observed with poultry (61%), followed by quails (41%), stone curlews (35%), bustards
231 (33%) and cheetahs (31%).

232 Temporal changes in the percentage of resistance to 10 antimicrobial drugs were observed (Figure
233 2). Overall, the resistance rates to AMP, CIP, CMP, COX, GEN, KAN, NAL, and STR have been
234 declining noticeably between the last two periods of the study. In contrast the resistance rate towards
235 OTE remained stable and towards SXT increased. The periodical resistance rates of AMP, and GEN
236 rose gradually until they peaked 2005-2007. Another important point to mention is that the resistant
237 rates to COX (4%) and CIP (13%) increased drastically in the period 2005-2007.

238 Table 6 presents antimicrobial resistance phenotypes. Among the total 1052 investigated
239 *Salmonella* strains, 23 % were resistant to OTE, STR 22 %, 18 % NAL, and 15 % to AMP. In contrast,
240 the lowest resistances were observed against COX (2%), CIP (5%), GEN (5%), and SXT (6%) and no
241 resistance against CTM, CTX and CAZ. When analysed by animal species, resistance to NAL was
242 primarily observed in isolates from poultry (52%), stone curlew (38%) and quails (37%), and
243 resistance to CIP in isolates from quails (15%), bustards (10%) and horses (11%). *Salmonella* strains
244 from horses showed the highest resistance rate to GEN (13%), whereas camel and bustard isolates to
245 KAN (both 13%). STR resistance was most common in *Salmonella* from bustards (32%). The highest
246 resistance rate to SXT was observed in isolates from camels (10%) and horses (10%).

247 As shown in Table 7, those isolates being most often MDR were *S. Infantis* (83%), *S. Albany*
248 (79%) and *S. Kentucky* (77%). 93 % of all *S. Virchow* strains and 90 % from both *S. Kentucky* and *S.*
249 *Typhimurium* DT 104 showed resistance to at least one and more drugs. On the contrary, 100 % of *S.*
250 *Hindmarsh*, *S. Frintrop*, *S. Muenster* and *S. Cerro* isolates were pan-susceptible to all tested
251 antimicrobials.

252 Resistant *S. Kentucky* strains were observed during the study (Figure 3). Before 2004 no resistant
253 strain was observed, however from 2005 to 2009, between 7 and 25 *S. Kentucky* strains were detected
254 annually. The occurrence of resistant strains peaked in 2007 due to the outbreak in one equine
255 hospital. Overall 61 % of all *S. Kentucky* isolates (n=25) showed resistance to CIP. The first CIP
256 resistant *S. Kentucky* was detected 2004 in a falcon and in a cheetah. MDR and CIP resistant *S.*
257 *Kentucky* were isolated from different animal species including wallabies, camels, cheetahs, falcons,
258 bustards, quails, rabbits, canines, antelopes, marmosets, and horses (data not shown). Furthermore, in
259 2007, an outbreak with five diseased horses was due to CIP resistant *S. Kentucky*. The *S. Kentucky*
260 outbreak occurred in Equine Hospital through a diseased horse from which only the third faecal
261 sample was positive for *S. Kentucky*. By then the pathogen had infected 4 other horses in the vicinity
262 of the first one.

263 In addition, in a reproduction center for houbara bustards, an MDR CIP resistant *S. Kentucky*
264 outbreak occurred with high mortality and morbidity among chicks, which was the result of CIP
265 resistant *S. Kentucky* positive mealworms of houbara bustard chick feed.

266

267 **Discussion**

268 As there is no coordinated *Salmonella* surveillance of humans or animals in the UAE, this study
269 provides important information on the epidemiology of this pathogen. It also reveals trends in the
270 prevalence of *Salmonella* serovars, phage types, and antibiotic resistance of strains collected from
271 different animal species over 14 years.

272 In this study, 176 samples from different wild and in zoos kept reptiles were examined and 36 %
273 were *Salmonella* positive (Table 1). This finding is in agreement with other studies from different
274 countries. In Bulgaria 83 % of 493 examined faecal samples from wild terrestrial turtles were
275 *Salmonella* positive between 1959 and 1961 (Dimow 1966). Furthermore, in a recent Spanish study,
276 16 terrestrial turtles have been examined and all were *Salmonella* positive (Hidalgo-Vila et al. 2007).
277 *Salmonellae* were also isolated from 56 % out of 17 samples from wild living reptiles in Germany and
278 Austria (Geue and Löschner 2002). Briones et al. (2004) reported a prevalence of 42 % in faecal
279 samples from 94 different wild living reptiles in Spain. In Trinidad, 14 % of 173 samples from healthy
280 and diseased reptiles of a zoo were *Salmonella* positive (Gopee et al. 2000). These findings indicate
281 that reptiles have a high *Salmonella* prevalence, and they therefore could be an important *Salmonella*
282 reservoir for both animals and humans.

283 Despite the fact, that 104 different *Salmonella* serovars were detected among a total 1052 isolates,
284 it was found that *S. Typhimurium* was responsible for most of the infections (25%; Table 2). This
285 finding is in agreement with other studies from various countries (Basu et al. 1965; Nabbut and Jamal;
286 1970; Molla et al. 2002; Oolya et al. 2007; Institute of Medical and Veterinary Science 2008; Friedrich
287 et al. 2010; Kidamemariam et al. 2010). The reason for this could be the broad host spectrum of
288 domestic and wild animals, which act as reservoir for new *Salmonella* infections. Furthermore, a

289 second factor could be virulence genes facilitating the spread. This hypothesis is supported by a
290 previous study, which showed a higher enteropathogenicity in the bovine ileal loop model associated
291 with presence of *sopE1* gene, leading to the emergence of an epidemic cattle-associated *S.*
292 Typhimurium strain (Bossi et al. 2003; Zhang et al. 2002). In addition, Saitoh et al. (2005) discovered
293 in the genome of the global endemical *S. Typhimurium* DT104 strain phage transferred *artAB* genes,
294 encoding a putative ADP-ribosyltransferase toxin in *S. Typhimurium* DT104. This virulence
295 mechanism, as well as, a genomic encoded pentaresistance against AMP, CMP, STR, SMZ and OTE
296 is believed to be the reason for the worldwide spread of *S. Typhimurium* DT104 (World Health
297 Organization 2005)

298 As falconry is a famous tradition in the UAE, falcons are very valuable for their owners.
299 *Salmonella* were isolated from diseased and healthy falcons and it is believed that salmonellosis in
300 falcons, concurrent with other infections could be fatal (Wernery et al. 1998). In this study, the
301 incidence of *S. Typhimurium* in falcons was 31 % (53/166). This finding is in agreement with previous
302 studies of healthy or diseased captive falcons in the UAE under the same conditions. Gierse (2001)
303 found *S. Typhimurium* in 38 % of a total 34 examined *Salmonella* strains. Moreover, in another study,
304 57 % of 21 examined strains were *S. Typhimurium* positive (Wernery et al. 1998). These and our
305 results indicate that *S. Typhimurium* is the most important serovar in falcons in the UAE. In our study,
306 we showed the same *S. Typhimurium* phage types both in falcons and their prey (pigeons, quails,
307 bustards and stone curlews; Table 3). This discovery indicates that the prey, especially, pigeons and
308 quails, are the most important infection source for falcons. This hypothesis is supported by a previous
309 study, which showed *S. Typhimurium* present in pigeons, quails, and bustards (Gierse 2001).

310 Camels are a *Salmonella* reservoir and therefore food of camel origin could be a potential hazard
311 for public health (Wernery and Kaaden 2002). In this study, *S. Frintrop* and *S. Hindmarsh* were the
312 most common serovars in camels with 28 % and 21 % of all isolates (n=232), respectively.
313 Furthermore, when compared to the total *Salmonella* incidence in all animals, 90 % and 87 %, respectively
314 of all *S. Hindmarsh* (n=72) and *S. Frintrop* (n=55) were detected with camels (Table 2). In
315 a previous study between 1987 and 1991, Wernery (1992) found *S. Saintpaul* (37%), *S. Frintrop*

316 (17%), and *S. Hindmarsh* (8%) were the most frequent of 187 *Salmonella* isolates from camels, under
317 the same conditions as in this study. Moore et al. (2002) examined faecal samples from 67 diarrheic
318 and healthy camel calves. In 10 samples, they detected *Salmonella* and all were *S. Hindmarsh*. The
319 previous studies and our results indicate that *S. Frintrop* and *S. Hindmarsh* are the most important
320 serovars and host adapted to camels.

321 MDR *Salmonellae* are of worldwide interest because they reduce the therapy options in human and
322 veterinary medicine (Threlfall et al. 2003). Our data show that MDR *Salmonella* were most common
323 in poultry (61%), quails (41%), stone curlews (35%) and bustards (33%; Table 5). These findings
324 indicate that the management system of poultry, quails, stone curlews and bustards promotes the
325 spread of resistant pathogens. Our speculation is in agreement with McEwen and Fedorka-Cray (2002)
326 who found that large numbers of animals in small stables enhance the spread of resistant bacteria.

327 Previous findings in the UAE have demonstrated that *Salmonella* isolated from captive houbara
328 bustards were resistant against amoxicillin and OTC, but showed no resistance against CMP, GEN and
329 the fluoroquinolone, enrofloxacin (Bailey et al. 1998). In our study however, we detected *Salmonella*
330 in bustards being resistant against all tested antimicrobial classes (Table 6). This finding indicates that
331 the development of antibiotic resistance could be facilitated due to the use of antimicrobial agents in
332 veterinary medicine. This view is supported by Bailey et al. (1998) who reported that enrofloxacin,
333 OTC, AMP, and GEN are used with captive bred houbara bustards. Moreover, a review by Rabsch et
334 al. (2001) reported that the use of antimicrobial agents in farm animals was the reason for the
335 development of antibiotic resistances. Since 18 % of all diagnostic samples from bustards were
336 *Salmonella* positive (Table 1), and therapy options in bustards are highly reduced, strict control
337 measures should be implicated. The *Salmonella* prevalence could be reduced from over 65 % to fewer
338 than 5 % in broiler flocks between 1989 and 2001 and from over 7 % to fewer than 2 % in layer hen
339 flocks in the period in Denmark from 1998 to 2001 using control programs (Wegener et al. 2003).

340 Fluoroquinolones (e.g., ciprofloxacin) and cephalosporins (e.g., cefoxitin) are the drugs of choice
341 for invasive salmonellosis in humans (World Health Organization 2005). Resistance to the quinolone
342 NAL, correlates with decreased susceptibility to CIP and possible fluoroquinolone treatment failure

343 (CDC 2010). In present study, 18 % of all *Salmonella* isolates showed resistance against NAL, 5 %
344 against CIP, and 2 % against COX (Table 6). In contrast, Zhao et al. (2007), who examined the
345 antibiotic resistance of 380 *Salmonella* strains from diseased domestic animals between 2002 and
346 2003 in the USA, detected only 4 % resistance against NAL and no resistance against CIP.
347 Furthermore, in the UAE between 2003 and 2005, Rotimi et al. (2008) reported that 0.8 % of non
348 typhoid *Salmonella* isolated from 122 hospitalized humans were resistant against CIP. Our data show
349 that NAL and CIP resistance is quite high in animals in the UAE. This could be due to the use of NAL
350 and CIP in veterinary medicine, which causes selection pressure on bacteria. This explanation is in
351 agreement with previous studies showing that quinolone resistance due to point mutations leads to
352 amino acid change in the *gyrA* gene (Hakanen et al. 2006; Piddock et al. 1993). However, quinolone
353 resistance maybe also caused by decreased permeability or the presence of efflux pump systems
354 without a mutation in the *gyrA* gene (Cebrian et al. 2005; Hakanen et al. 2006). These resistance
355 mechanisms provide a selection advantage for *Salmonella* under the use of quinolones in both
356 veterinary and human medicine.

357 In our study, we detected an occurrence of *S. Kentucky* between 2004 and 2009 (Figure 3). This
358 increase was primarily associated with the emergence of CIP resistant *S. Kentucky* strains which
359 infected 51 animals. Such *S. Kentucky* have been first isolated in 2002 in French travelers with
360 gastroenteritis returning from northeast and eastern Africa, and the number of these strains increased
361 in the following years (Weill et al. 2006; Le Hello et al. 2011). Recent experiences have demonstrated
362 that the endemic *S. Kentucky* strain had spread in different African and Middle Eastern countries and
363 was isolated from chicken and turkey in Africa (Le Hello et al. 2011). We found CIP resistant *S.*
364 *Kentucky* in different animal species including poultry, wallabies, camels, cheetahs, falcons, bustards,
365 quails, rabbits, canines, antelopes, marmosets, and rheas. This result and the CIP resistant *S. Kentucky*
366 outbreaks among horses and houbaras in the UAE, with high morbidity and mortality, suggest that
367 MDR and CIP resistant *S. Kentucky* strains are spreading among the animal population in the UAE.
368 Additionally, recent reports about *S. Typhimurium* DT104 showed the potential for national and
369 international spread of MDR *Salmonella* (Helms et al. 2005). For that reason, measures to monitor and

370 limit the spread of CIP resistant *S. Kentucky* should be implemented to protect animal and human
371 health.

372 In conclusion, this data analysis gives an important insight into the epidemiology of *Salmonella*
373 and their antibiotic resistance for animals in the Middle East. Furthermore, the high antibiotic
374 resistances, especially against important antibiotics for human like fluoroquinolones and
375 cephalosporins, implicate the necessity to establish a coordinated surveillance, monitoring, and control
376 program for *Salmonella* in this area. Thus, the prevalence of *Salmonella* in livestock could be reduced
377 and the development of resistance against antimicrobials better controlled.

378

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382

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384

385 **References**

- 386 Anderson, E., Ward, L., Saxe, M. and de Sa, J., 1977. Bacteriophage-typing designations of
387 *Salmonella typhimurium*, Journal of Hygiene, 78, 297-300
- 388 Bailey, T., Launay, F. and Sullivan, T., 2000a. Health Issues of the International Trade of Falcons and
389 Bustards in the Middle East: the Need for Regional Monitoring and Regulation?. In: Potapov,
390 S., Banzragch, S., Fox, N. and N. Barton (eds), Proceedings of the II MEFRG international
391 conference on Saker Falcon and Houbara Bustard, Ulaanbaatar, Mongolia, 2000, (Ministry of
392 Nature and Environment, Ulaanbaatar), 185-195
- 393 Bailey, T., Silvanose, C.D., Naldo, J., Combreau, O., Launay, F., Wernery, U., Kinne, J., Gough, R.
394 and Manvell, R., 2000b. Health considerations of the rehabilitation of illegally traded houbara
395 bustards *Chlamydotis undulata macqueenii* in the Middle East, Oryx, 34, 325-334
- 396 Bailey, T.A., Silvanose, C., Wernery, U., Samour, J.H. and Naldo, J., 1998. Antimicrobial resistance
397 and minimum inhibitory concentrations of bacteria isolated from bustards in the United Arab
398 Emirates, Avian diseases, 42, 690-697
- 399 Basu, S., Dewan, M. and Suri, J., 1975. Prevalence of *Salmonella* serotypes in India: a 16-year study,
400 Bulletin of the World Health Organization, 52, 331-336
- 401 Bossi, L., Fuentes, J.A., Mora, G. and Figueroa-Bossi, N., 2003. Prophage contribution to bacterial
402 population dynamics, Journal of Bacteriology, 185, 6467-6471
- 403 Briones, V., Tellez, S., Goyache, J., Ballesteros, C., del Pilar Lanzarot, M., Dominguez, L. and
404 Fernandez-Garayzabal, J.F., 2004. *Salmonella* diversity associated with wild reptiles and
405 amphibians in Spain, Environmental Microbiology, 6, 868-871
- 406 Casin, I., Breuil, J., Darchis, J.P., Guelpa, C. and Collatz, E., 2003. Fluoroquinolone resistance linked
407 to GyrA, GyrB, and ParC mutations in *Salmonella enterica typhimurium* isolates in humans,
408 Emerging Infectious Diseases, 9, 1455-1457

409 Centers for Disease Control and Prevention, 2010. National Antimicrobial Resistance Monitoring
410 System for Enteric Bacteria (NARMS): Human Isolates Final Report, 2008, (
411 U.S. Department of Health and Human Services, Atlanta, Georgia)

412 Cebrian, L., Rodriguez, J.C., Escribano, I. and Royo, G., 2005. Characterization of *Salmonella* spp.
413 mutants with reduced fluoroquinolone susceptibility: importance of efflux pump mechanisms,
414 Chemotherapy, 51, 40-43

415 Chiu, C.H., Wu, T.L., Su, L.H., Chu, C., Chia, J.H., Kuo, A.J., Chien, M.S. and Lin, T.Y., 2002. The
416 emergence in Taiwan of fluoroquinolone resistance in *Salmonella enterica* serotype
417 choleraesuis, New England Journal of Medicine, 346, 413-419

418 Clinical and Laboratory Standards Institute, 2010. Performance Standards for Antimicrobial
419 Susceptibility Testing, Twentieth Informational Supplement M 100-S20. (Wayne, PA,
420 USA)

421 D'Aoust, J.Y., 1994. *Salmonella* and the international food trade, International Journal of Food
422 Microbiology, 24, 11-31

423 Deutsches Institut für Normung, 2004. Empfindlichkeitsprüfung von mikrobiellen
424 Krankheitserregern gegen Chemotherapeutika. In: Deutsches Institut für Normung
425 e.V. (ed), Medizinische Mikrobiologie und Immunologie - Diagnostische Verfahren,
426 (Beuth Verlag, Berlin), pp. 245-430

427 Dimow, I., 1966. Die Verbreitung der fäkalen *Salmonella*-und Arizona-Dauerausscheidung bei den
428 freilebenden Schildkröten *Testudo graeca* und *Testudo hermanni*, Medical Microbiology and
429 Immunology, 152, 198-203

430 European Food Safety Authority, 2009. The Community Summary Report on Trends and Sources of
431 Zoonoses and Zoonotic Agent in the European Union in 2007, The EFSA Journal (2009), 30

432 Farmer, J.J., 3rd, Davis, B.R., Hickman-Brenner, F.W., McWhorter, A., Huntley-Carter, G.P., Asbury,
433 M.A., Riddle, C., Wathen-Grady, H.G., Elias, C., Fanning, G.R., et al., 1985. Biochemical
434 identification of new species and biogroups of Enterobacteriaceae isolated from clinical
435 specimens. Journal of Clinical Microbiology, 21, 46-76

436 Friedrich, A., Dorn, C., Schroeter, A., Szabo, I., Jaber, M., Berendonk, G., Brom, M., Ledwolorz, J.
437 and Helmuth, R., 2010. Bericht des Nationalen Referenzlabors zur Durchführung von
438 Analysen und Tests auf Zoonosen (Salmonellen) zum Vorkommen von Salmonellen in
439 Nutztieren, Lebens- und Futtermitteln über den Zeitraum der letzten 5 Jahre in Deutschland
440 (2004-2008), Berliner und Münchener Tierärztliche Wochenschrift, 123, 265-277

441 Geue, L. and Löschner, U., 2002. *Salmonella enterica* in reptiles of German and Austrian origin,
442 Veterinary microbiology, 84, 79-91

443 Gierse, S., 2001. Die wichtigsten Infektionskrankheiten bei Falken (Falconidae) und die Bedeutung
444 der Beutevögel als Überträger, (Dissertation med. vet., Ludwig-Maximilians-Universität
445 München)

446 Gopee, N.V., Adesiyun, A.A. and Caesar, K., 2000. Retrospective and longitudinal study of
447 salmonellosis in captive wildlife in Trinidad, Journal of Wildlife Diseases, 36, 284-293

448 Grimont, A.D., Weill, F.-X., 2007. Antigenic formulae of the *salmonella* serovars, (WHO
449 Collaborating Centre for Reference and Research on *Salmonella*, Paris)

450 Guibourdenche, M., Roggentin, P., Mikoleit, M., Fields, P.I., Bockemuhl, J., Grimont, P.A. and Weill,
451 F.X., 2010. Supplement 2003-2007 (No. 47) to the White-Kauffmann-Le Minor scheme,
452 Research in Microbiology, 161, 26-29

453 Hakanen, A.J., Kotilainen, P., Pitkanen, S., Huikko, S., Siitonen, A. and Huovinen, P., 2006.
454 Reduction in fluoroquinolone susceptibility among non-typhoidal strains of *Salmonella*
455 *enterica* isolated from Finnish patients, Journal of Antimicrobial Chemotherapy, 57, 569-572

456 Helms, M., Ethelberg, S. and Molbak, K., 2005. International *Salmonella* Typhimurium DT104
457 infections, 1992-2001, Emerging Infectious Diseases, 11, 859-867

458 Hidalgo-Vila, J., Díaz-Paniagua, C., de Frutos-Escobar, C., Jiménez-Martínez, C. and Pérez-Santigosa,
459 N., 2007. *Salmonella* in free living terrestrial and aquatic turtles, Veterinary microbiology,
460 119, 311-315

461 Institute of Medical and Veterinary Science, 2008. Australian *Salmonella* Reference Centre Annual
462 Report 2008, (Five Star Press, Australia)

463 Käsbohrer, A., Alt, K., Schroeter, A., Dorn, C., Tenhagen, B.A., 2009. *Salmonella*-
464 Monitoringprogramme. In: M. Hartung and A. Käsbohrer (eds), Erreger von Zoonosen
465 in Deutschland im Jahr 2011, (Bundesinstitut für Risikobewertung-Hausdruckerei,
466 Dahlem), 32-36

467 Institute of Medical and Veterinary Science, 2009. Australian *Salmonella* Reference Centre Annual
468 Report 2009 (Five Star Press, Australia), 10

469 Khakhria, R., Woodward, D., Johnson, W., Poppe, C., 1997. *Salmonella* isolated from humans,
470 animals and other sources in Canada, 1983–92. *Epidemiology and Infection* 119, 15-23

471 Kidanemariam, A., Engelbrecht, M. and Picard, J., 2010. Retrospective study on the incidence of
472 *Salmonella* isolations in animals in South Africa, 1996 to 2006, *Journal of the South African*
473 *Veterinary Association*, 81, 37-44

474 Kligler, I.J., 1917. A simple medium for the differentiation of members of the typhoid-paratyphoid
475 group. *Journal of Public Health* 7, 1042-1044

476 Kühn, H., Falta, R., Rische, H., 1973. Lysotypie, In: Rische, H. (ed.), *Lysotypie und andere*
477 *epidemiologische Laboratoriumsmethoden*. Jena, 1973, (VEB Gustav Fischer Verlag, Jena),
478 106-143.

479 Lászlo, V.G., Csorian, E.S. and Pászti, J., 1985. Phage types and epidemiological significance of
480 *Salmonella enteritidis* strains in Hungary between 1976 and 1983, *Acta Microbiologica et*
481 *Immunologica Hungarica Acta*, 32, 321-340

482 Le Hello, Hendriksen, R.S., Doublet, B., Fisher, I., Nielsen, E.M., Whichard, J.M., Bouchrif, B.,
483 Fashae, K., Granier, S.A., Jourdan-Da Silva N., Cloeckert A., Threlfall, E.J., Angulo, F.J.,
484 Aarestrup, F.M., Wain, J., Weill, F.X., 2011. International spread of an epidemic population
485 of *Salmonella enterica* serotype Kentucky ST198 resistant to ciprofloxacin. *Journal Infectious*
486 *Diseases*, 204, 675-684

487 McEwen, S.A. and Fedorka-Cray, P.J., 2002. Antimicrobial use and resistance in animals, *Clinical*
488 *Infectious Diseases*, 34, 93-106

489 Molla, B., Alemayehu, D. and Salah, W., 2003. Sources and distribution of *Salmonella* serotypes
490 isolated from food animals, slaughterhouse personnel and retail meat products in Ethiopia:
491 1997-2002, *Ethiopian Journal of Health Development*, 17, 63

492 Moore, J.E., McCalmont, M., Xu, J., Nation, G., Tinson, A.H., Crothers, L. and Harron, D.W., 2002.
493 Prevalence of faecal pathogens in calves of racing camels (*Camelus dromedarius*) in the
494 United Arab Emirates, *Tropical Animal Health and Production*, 34, 283-287

495 Nabbut, N.H. and Jamal, H.M., 1970. Distribution and epidemiological significance of *Salmonella*
496 serotypes of domestic animals in Lebanon, *Bulletin of the World Health Organization*, 42,
497 171-174

498 Oloya, J., Theis, M., Doetkott, D., Dyer, N., Gibbs, P. and Khaita, M.L., 2007. Evaluation of
499 *Salmonella* occurrence in domestic animals and humans in North Dakota (2000-2005),
500 *Foodborne Pathogens and Disease*, 4, 551-563

501 Olsen, S.J., DeBess, E.E., McGivern, T.E., Marano, N., Eby, T., Mauvais, S., Balan, V.K., Zirnstein,
502 G., Cieslak, P.R. and Angulo, F.J., 2001. A nosocomial outbreak of fluoroquinolone-resistant
503 *salmonella* infection, *New England Journal of Medicine*, 344, 1572-1579

504 Piddock, L.J., Griggs, D.J., Hall, M.C. and Jin, Y.F., 1993. Ciprofloxacin resistance in clinical isolates
505 of *Salmonella typhimurium* obtained from two patients, *Antimicrobial Agents and*
506 *Chemotherapy*, 37, 662-666

507 Rabsch, W., Prager, R., Braun, P. and Methner U., 2007. *Salmonella* in Poultry flocks and Humans- *S.*
508 *enterica* subspecies *enterica* serovar Enteritidis in the history, *Berliner und Münchner*
509 *Tierärztliche Wochenschrift*, 120, 328-333

510 Rabsch, W., Tschäpe, H. and Bäumlner, A.J., 2001. Non-typhoidal salmonellosis: emerging problems,
511 *Microbes and Infection*, 3, 237-247

512 Rolle, M. and Mayr, A., 2007, *Medizinische Mikrobiologie, Infektions- und Seuchenlehre*, (Enke
513 Verlag, Stuttgart), 437

514 Rotimi, V.O., Jamal, W., Pal, T., Sonnevend, A., Dimitrov, T.S. and Albert, M.J., 2008. Emergence of
515 multidrug-resistant *Salmonella* spp. and isolates with reduced susceptibility to ciprofloxacin in
516 Kuwait and the United Arab Emirates, *Diagnostic Microbiology and Infectious Disease*, 60,
517 71-77

- 518 Saitoh, M., Tanaka, K., Nishimori, K., Makino, S., Kanno, T., Ishihara, R., Hatama, S., Kitano, R.,
519 Kishima, M., Sameshima, T., Akiba, M., Nakazawa, M., Yokomizo, Y. and Uchida, I., 2005.
520 The artAB genes encode a putative ADP-ribosyltransferase toxin homologue associated with
521 *Salmonella enterica* serovar Typhimurium DT104, *Microbiology*, 151, 3089-3096
- 522 Threlfall, E.J., Fisher, I.S., Berghold, C., Gerner-Smidt, P., Tschape, H., Cormican, M., Luzzi, I.,
523 Schnieder, F., Wannet, W., Machado, J. and Edwards, G., 2003. Antimicrobial drug resistance
524 in isolates of *Salmonella enterica* from cases of salmonellosis in humans in Europe in 2000:
525 results of international multi-centre surveillance, *Euro Surveillance*, 8, 41-45
- 526 Van Duijkeren, E., Wannet, W., Heck, M., van Pelt, W., Sloet van Oldruitenborgh-Oosterbaan, M.,
527 Smit, J. and Houwers, D., 2002. Sero types, phage types and antibiotic susceptibilities of
528 *Salmonella* strains isolated from horses in The Netherlands from 1993 to 2000, *Veterinary*
529 *microbiology*, 86, 203-212
- 530 Ward, L., de Sa, J. and Rowe, B., 1987. A phage-typing scheme for *Salmonella enteritidis*,
531 *Epidemiology and Infection*, 99, 291-294
- 532 Wegener, H.C., Hald, T., Lo Fo, Wong, D., Madsen, M., Korsgaard, H., Bager, F., Gerner-Smidt, P.
533 and Molbak, K., 2003. *Salmonella* control programs in Denmark, *Emerging Infectious*
534 *Diseases*, 9, 774-780
- 535 Weill, F.X., Bertrand, S., Guesnier, F., Baucheron, S., Cloeckaert, A. and Grimont, P.A., 2006.
536 Ciprofloxacin-resistant *Salmonella* Kentucky in travelers, *Emerging Infectious Diseases*, 12,
537 1611-1612
- 538 Wernery, U., 1992. The prevalence of *Salmonella* infections in camels (*Camelus dromedarius*) in the
539 United Arab Emirates, *British Veterinary Journal*, 148, 445-450
- 540 Wernery, U. and Kaaden, O.R., 2002, *Infectious Diseases in Camelids*, (Blackwell Science, Berlin
541 Vienna)
- 542 Wernery, U. and Makarem, E.H., 1996. Comparative study on *salmonella* serovars isolated from
543 humans and camels in the United Arab Emirates, *Camel Newsletter*, 12, 55-59
- 544 Wernery, U. and Wernery, R., 2004. Tierhaltung und veterinärmedizinische Aspekte in den
545 Vereinigten Arabischen Emiraten, *Tierärztliche Umschau*, 59, 534-538
- 546 Wernery, U., Wernery, R., Zachariah, R. and Kinne, J., 1998. Salmonellosis in relation to
547 chlamydiosis and pox and *Salmonella* infections in captive falcons in the United Arab
548 Emirates, *Zentralblatt für Veterinärmedizin. Reihe B*, 45, 577-583
- 549 World Health Organization, 2005. Drug-resistant *Salmonella*, In: World Health Organization (ed), fact
550 sheet No 193
- 551 Williams, B., 1975. Environmental considerations in salmonellosis. *The Veterinary Record* 96, 318
- 552 Zhang, S., Santos, R.L., Tsois, R.M., Miold, S., Hardt, W.D., Adams, L.G. and Baumler, A.J., 2002.
553 Phage mediated horizontal transfer of the sopE1 gene increases enteropathogenicity of
554 *Salmonella enterica* serotype Typhimurium for calves, *FEMS Microbiology Letters*, 217, 243-
555 247
- 556 Zhao, S., McDermott, P., White, D., Qaiyumi, S., Friedman, S., Abbott, J., Glenn, A., Ayers, S., Post,
557 K. and Fales, W., 2007. Characterization of multidrug resistant *Salmonella* recovered from
558 diseased animals, *Veterinary microbiology*, 123, 122-132

560
561 **Legends to the figures**

562
563 Fig. 1 Occurrence of the top four serovars per year

564
565 Fig. 2 Resistance rate of different antimicrobial drugs

566
567 AMP: ampicillin; COX: cefoxitin; CMP: chloramphenicol; CIP: ciprofloxacin; GEN: gentamicin;
568 KAN: kanamycin; NAL: nalidixic acid; STR: streptomycin; OTE: tetracyclines; SXT;
569 trimethoprim+sulfamethoxazole

570
571 Fig. 3 Annual number of *S. Kentucky* isolates and the proportion of isolates resistant to Ciprofloxacin
572 (2000 – 2009)

Table 1 Distribution of diagnostic samples, *Salmonella* positive samples and percent positive by animal origin (1996-2009)

Animal species	Diagnostic samples (n)	<i>Salmonella</i> positive (n)	Prevalence (%)
Camel	3907	320	8
Falcon	3296	199	6
Poultry	2434	42	2
Horse	2042	73	4
Antelope	1646	115	7
Bustard	1265	225	18
Pigeon	865	222	26
Sheep/Goat	633	19	3
Quail	426	66	15
Rhea/Ostrich	364	108	30
Stone curlew	348	42	12
Cheetah	209	39	19
Bovine	85	20	24
Reptile	176	63	36
Other animals*	3175	375	12
Total	20871	1928**	9

* other animals see supplement Table 1

** typed only 1052 see Table 2

Table 2 Top 20 serovars from different animal species (1996-2009)

Serovar	Animal origin (no. of isolates)														Total (n=1052)
	Camel (n= 232)	Falcon (n= 166)	Bustard (n= 101)	Antelope (n= 66)	Horse (n= 63)	Pigeon (n= 51)	Ostrich/Rhea (n= 44)	Cheetah (n= 39)	Reptile** (n= 38)	Quail (n= 27)	Stone curlew (n= 26)	Bovine (n= 20)	Poultry (n= 18)	Other animals* (n= 160)	
S. Typhimurium	27	53	14	6	11	40	23	7	3	12	4	3	6	49	258
S. Kentucky	8	7	19	3	10	-	7	7	-	3	3	1	1	13	82
S. Frintrop	65	1	2	4	-	-	-	-	-	-	-	-	-	1	73
S. Hindmarsh	48	-	1	3	2	-	-	-	-	-	-	-	-	1	55
S. Enteritidis	1	13	5	2	-	-	-	2	1	-	-	1	1	10	36
S. Infantis	3	3	4	-	2	1	-	2	1	-	1	-	6	6	29
S. Newport	3	2	4	1	1	-	2	1	2	1	2	-	1	5	25
S. Agona	6	6	-	1	3	-	-	2	-	-	-	1	1	3	23
S. Anatum	2	-	-	2	7	1	2	1	-	-	-	1	-	5	21
S. Meleagridis	5	1	-	4	1	-	1	-	-	-	1	5	1	2	21
S. Amsterdam	5	2	4	1	2	1	1	1	-	1	-	1	-	2	21
S. Muenster	4	2	-	3	2	1	2	-	-	1	1	1	-	1	18
S. Reading	3	2	4	5	-	-	-	-	-	-	-	-	-	2	16
S. Albany	-	3	6	-	1	-	-	-	-	-	5	-	-	-	15
S. Adelaide	-	1	2	-	-	-	-	1	-	-	5	-	-	5	14
S. Virchow	2	6	1	1	-	1	-	2	1	-	-	-	-	-	14
S. Bovismorbificans	7	5	-	-	-	-	-	-	1	-	-	-	-	-	13
S. Muenchen	4	1	1	-	-	-	-	3	-	-	-	-	-	4	13
S. Cerro	1	1	1	4	-	-	1	-	-	-	-	2	-	-	10
S. Hadar	2	5	1	-	-	-	-	-	-	2	-	-	-	-	10
Other serovars*	36	52	32	26	21	6	5	10	29	7	4	4	1	52	285

* other animals and other serovars see suppl. Table 1

** serovar see suppl. Table 1

Table 3 Distribution of *S. Typhimurium* phage types by animal origin (1996-2009)

Phage type	n	Animal origin (no. of isolates)
DT104	29	falcon (12), quail (6), bustard (2), cat (2), poultry (2), ostrich/rhea (2), antelope (1), lion (1), horse (1)
DT193	28	camel (8), falcon (4), pigeon (4), poultry (3), antelope (1), bustard (1), hare (1), partridge (1), quail (1), sable (1), sand grouse (1), silver pheasant (1) stone curlew (1)
DT099	27	pigeon (10), horse (5), bustard (3), falcon (2), cheetah (1), saw-scaled viper (1), goat (1), ostrich/rhea (1), sand grouse (1), tiger (1), wild turkey (1)
PTU302	18	falcon (6), ostrich/rhea (3), pigeon (3), quail (2), flamingo (1), francolin (1), philby (1), starling (1)
DT185	10	falcon (4), parrot (4), camel (1) , cheetah (1)
DT120	8	bovine (3), camel (1), canine (1), caprine (1), cheetah (1), antelope (1)
DT001	7	camel (1), caracal (1), cheetah (1), gull (1), horse (1), squid (1), turtle (1)
DT002	7	pigeon (5), bustard (1), deer (1)
DT126	5	bustard (1), falcon (1), duck egg (1), stone curlew (1), pheasant egg (1)
DT003	4	pigeon (3), owl (1)
DT009	3	falcon (1), pigeon (1), pheasant (1)
DT089	3	falcon (2), stone curlew (1)
DT186	3	camel (1), horse (1), parrot (1)
DT 107	1	camel (1)
DT010	2	falcon (1), sheep (1)
DT160	2	falcon (2)
DT177	2	bustard (1), llama (1)
DT192	2	quail (1), ostrich/rhea (1)
DT013	1	horse (1)
DT036	1	falcon (1)
DT040	1	ostrich/rhea (1)
DT041	1	bustard (1)
DT066	1	cheetah (1)
DT080	1	storck (1)
U277	1	camel (1)
RDNC*	70	falcon (14), ostrich/rhea (15), pigeon (13), camel (4), bustard (4), antelope (3), cheetah (2), horse (2), dog (1), parrot (1), poultry (2), crane (1), finch (1), fox (1), sand grouse (1), scarlet ibis (1), secretary bird (1), wild turkey (1)
ut**	20	camel (9), falcon (4), quail (2), cat (1), crane (1), patridge (1), pigeon (1), hare (1)

* RDNC = React with phages but does not conform with definite or provisional types

**ut = untypable, no reaction with phages

Table 4 Distribution of *S. Enteritidis* phage types by animal origin (1996-2009)

Phage type	n	Animal origin (no. of isolates)	Year of isolation (no. Isolates)
6a/3a*	7	falcon (7)	1997 (2), 1998 (2), 1999 (3)
4/6	7	bustard (1), camel (1), antelope (1), cheetah (1), mamoset (1), fox (1), sand cat (1)	1997 (1), 2000 (1), 2004 (2), 2005 (1), 2007 (1), 2008 (1)
33/17	4	parrot (4)	2007 (1), 2008 (3)
14b/n.c.**	3	falcon (2), bustard (1)	1997 (1), 2004 (1), 2005 (1)
1/1	3	bustard (2), lizzard (1)	2001 (3)
6/6	2	falcon (1), cat (1)	1999 (1), 2003 (1)
7/n.c.	2	falcon (1), bustard (1)	2000 (1)
n.c./3a	2	falcon (1), antelope (1)	2008 (1)
6a/n.c.	2	falcon (1), bovine (1)	2003 (1), 2006 (1)
8/7	1	canine (1)	2006 (1)
13a/7	1	chicken (1)	2003 (1)
42/n.c.	1	parrot (1)	2007 (1)
15/n.c.	1	cheetah (1)	2008 (1)

* typing scheme after Ward / Lalko and Laszlo

**n.c. = non characteristic

Table 5 Resistance among *Salmonella* from different animal species (1996-2009)

Animal species (no. of isolates)	% of resistant isolates (no. of antimicrobial drug classes)		
	Susceptible (0)	Resistant (1-2)	Multidrug-resistant (≥ 3)
Camels (n= 232)	77	6	17
Falcons (n= 166)	55	23	22
Bustard (n= 101)	50	17	33
Antelope (n= 66)	84	7	9
Horse (n= 63)	63	17	19
Pigeon (n= 51)	69	22	10
Ostrich/Rhea (n= 44)	73	5	23
Cheetah (n= 39)	49	21	31
Reptile (n= 38)	87	8	5
Quail (n= 27)	30	30	41
Stone curlew (n= 26)	42	23	35
Bovine (n= 20)	85	10	5
Poultry (n= 18)	28	11	61
Other animals (n= 160)	52	24	24
Total (n= 1052)	63	16	21

Table 6 Antimicrobial resistance phenotypes of *Salmonella* from animals (1996-2009)

Antimicrobial agent	Resistant breakpoint (µg/ml)	% of resistance														Total (n= 1052)
		Camel (n= 232)	Falcon (n= 166)	Bustard (n= 101)	Antelope (n=66)	Horse (n= 63)	Pigeon (n= 51)	Ostrich/ Nandu (n= 44)	Cheetah (n= 39)	Reptile (n= 38)	Quail (n= 27)	Stone curlew (n= 26)	Bovine (n= 21)	Poultry (n= 18)	Other animals (n= 160)	
AMP	≥16	13	19	20	5	16	4	9	28	-	30	8	10	29	20	15
CTM	≥8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CTX	≥16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CAZ	≥32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
COX*	≥32	-	-	4	-	5	2	-	-	-	-	4	-	-	-	2
CMP	≥16	6	6	8	3	6	8	9	10	3	22	4	-	52	13	8
CIP	≥4	3	2	10	5	11	-	2	8	-	15	8	5	5	7	5
GEN	≥8	3	4	4	3	13	0	5	10	0	11	8	-	-	6	5
KAN	≥32	13	8	13	8	8	6	11	8	0	11	8	5	10	12	9
NAL	≥32	10	22	31	8	18	10	18	26	5	37	38	10	52	24	18
STR	≥32	16	25	32	9	19	24	14	28	16	33	31	10	52	26	22
OTE	≥8	17	22	25	9	19	18	20	33	8	37	50	-	71	32	23
SXT	≥32	10	2	5	3	10	4	-	10	3	4	-	0	19	6	6

AMP: ampicillin , CAZ: ceftazidim CTM: cefotiam, CTX: cefotaxime, COX: ceftioxin, CMP: chloramphenicol, CIP: ciprofloxacin,

GEN: gentamicin, KAN: kanamycin, NAL: nalidixic acid, STR: streptomycin,

OTE: oxytetracylin, SXT: trimethoprim+sulfamethoxazole

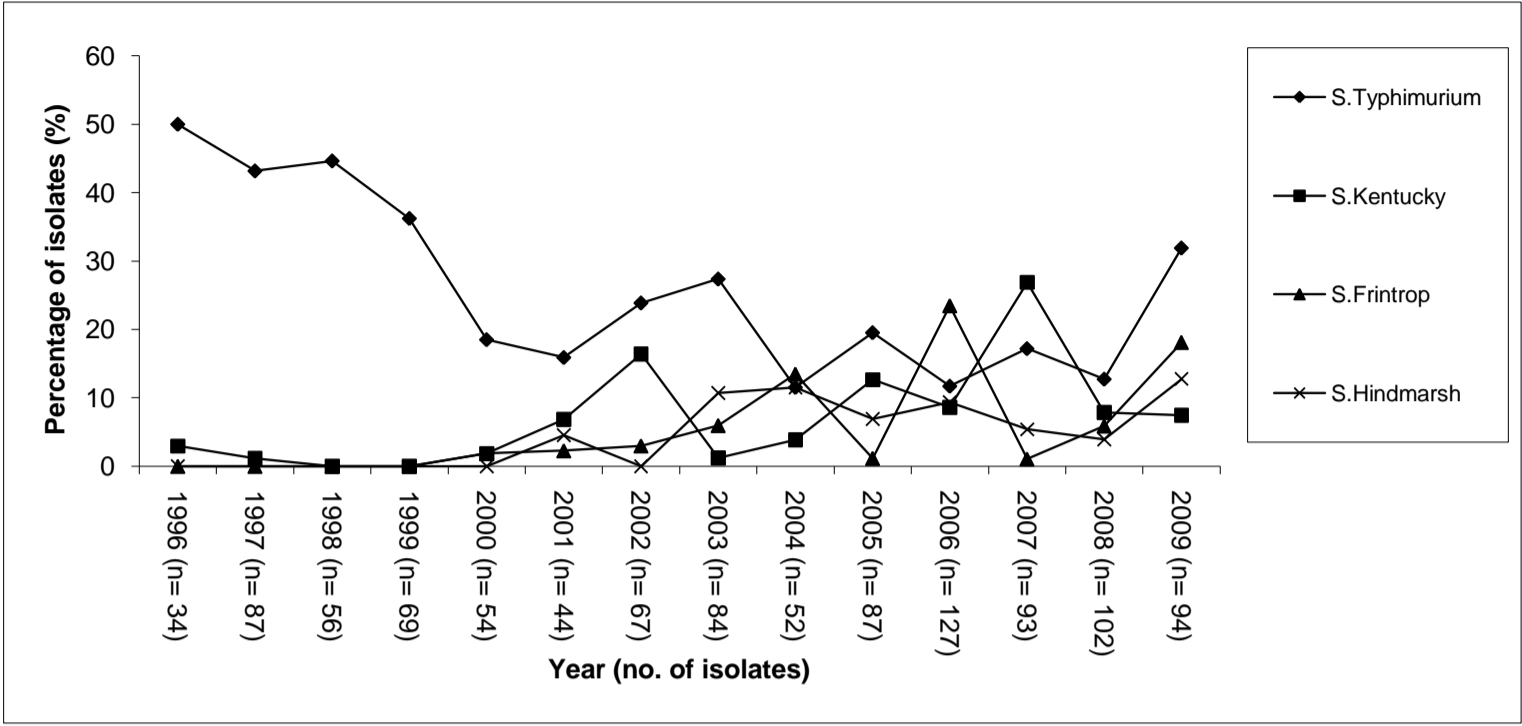
* COX resistance was only found in *S. Infantis*

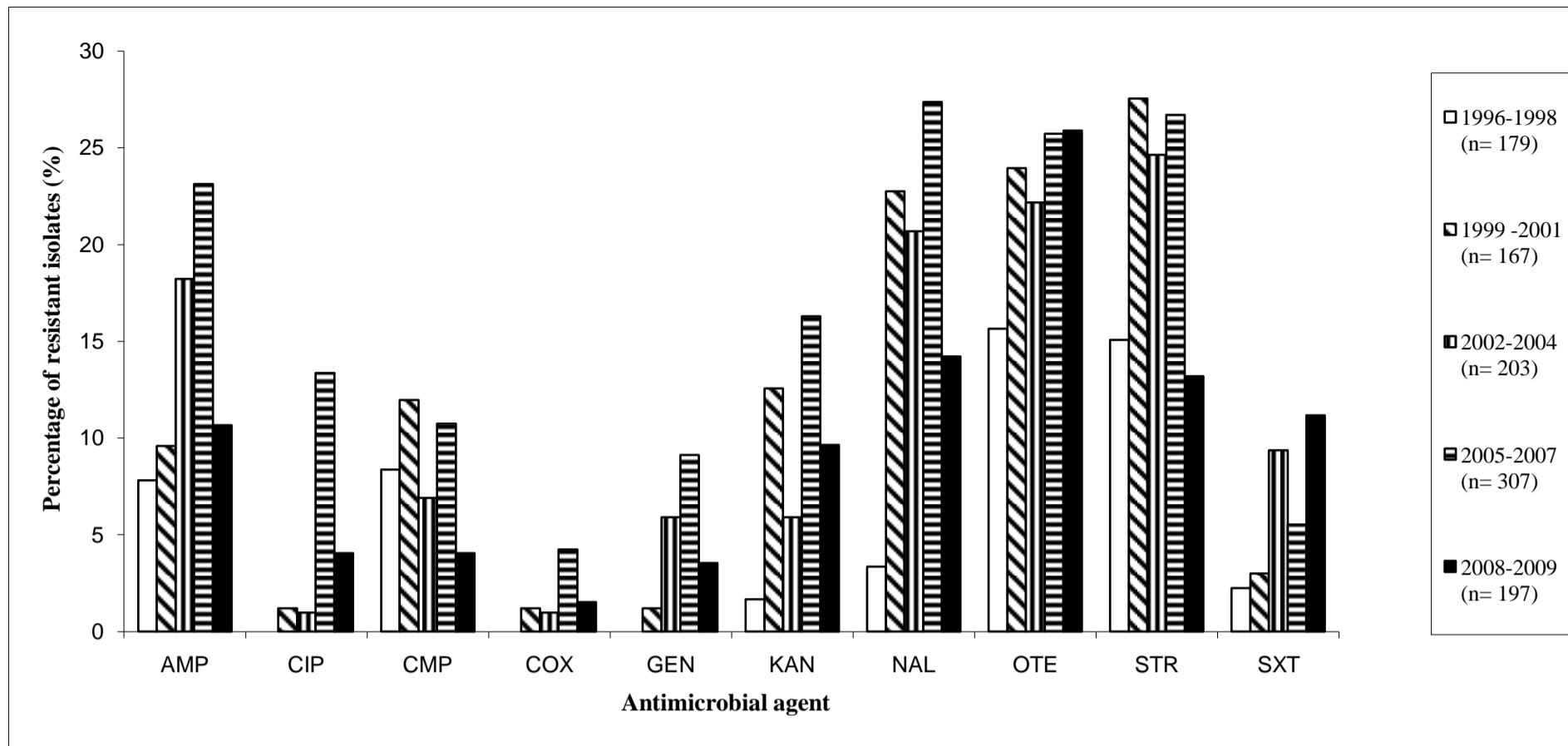
Table 7 Resistance among *Salmonella* serovars obtained from animals (1996-2009)

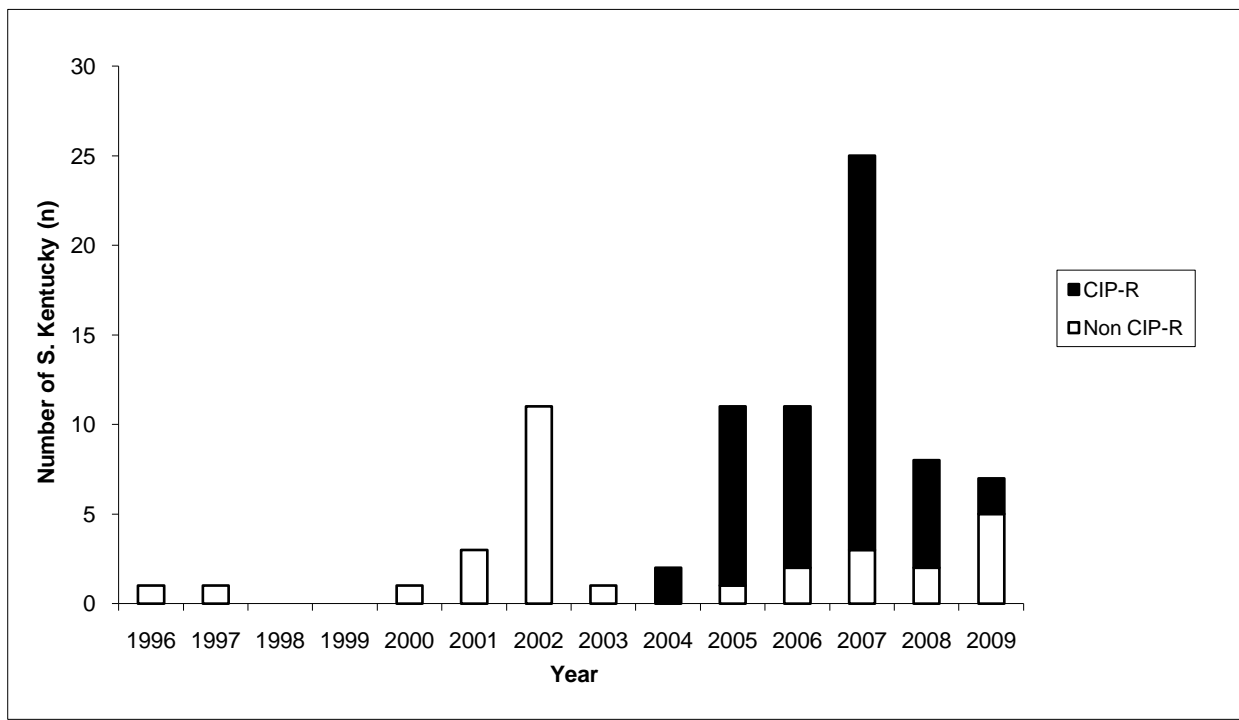
Serovars (no. of isolates)	% of isolates (no. antimicrobial agent classes)		
	Susceptible	Resistant	Multidrug-resistant
	(0)	(1-2)	(≥3)
<i>S. Typhimurium</i> (258)**	49	28	23
DT 104 (29)	10	38	52
DT 193 (28)	85	15	0
DT 99 (27)	33	26	41
other DT (174)*	52	29	18
<i>S. Kentucky</i> (82)	13	10	77
<i>S. Frintrop</i> (72)	100	0	0
<i>S. Hindmarsh</i> (55)	100	0	0
<i>S. Enteritidis</i> (38)	69	25	6
<i>S. Infantis</i> (29)	10	7	83
<i>S. Newport</i> (25)	68	8	24
<i>S. Agona</i> (23)	52	26	22
<i>S. Anatum</i> (22)	67	19	14
<i>S. Meleagridis</i> (21)	86	10	5
<i>S. Amsterdam</i> (21)	76	19	5
<i>S. Muenster</i> (18)	100	0	0
<i>S. Reading</i> (16)	94	6	0
<i>S. Albany</i> (15)	21	0	79
<i>S. Adelaide</i> (14)	21	7	71
<i>S. Virchow</i> (14)	7	93	0
<i>S. Bovismorbificans</i> (13)	92	8	0
<i>S. Muenchen</i> (13)	85	15	0
<i>S. Hadar</i> (10)	30	40	30
<i>S. Cerro</i> (10)	100	0	0
Other Serovars (286)	75	12	13

* other phagetypes see Table 3

** includes all phage types







Suppl. Table 1: Distribution of *Salmonella* serovars from other animals including other serovars from camels, falcons, bustards and horses*

birds	n	Serovar (no. of isolates)
Falcon (other serovars)	52	<i>S. Poona</i> (5), <i>S. Tennessee</i> (4), <i>S. Schwarzengrund</i> (3), <i>S. Worthington</i> (3), <i>S. Chailey</i> (2), <i>S. Kiambu</i> (2), <i>S. Mbandaka</i> (2), <i>S. Altona</i> (1), <i>S. Blockley</i> (1), <i>S. Bredeney</i> (1), <i>S. Haifa</i> (1), <i>S. Stanley</i> (1), <i>S. Sundsvall</i> (1), <i>S. London</i> (1), <i>S. Montevideo</i> (1), <i>S. Indiana</i> (1), <i>Salmonella</i> subsp. II 1,40:-:z39 (1), <i>Salmonella</i> subsp. IIIa 48:z4,z24:- (1), <i>Salmonella</i> subsp. I serological rough (20)
Bustard (other serovars)	32	<i>S. Weltevreden</i> (3), <i>S. Orion</i> (3), <i>S. Alachua</i> (2), <i>S. Eastbourne</i> (2), <i>S. Havana</i> (2), <i>S. Johannesburg</i> (2), <i>S. Mbandaka</i> (2), <i>Salmonella</i> subsp. II 9:l,w:e,n,x (2), <i>S. Altona</i> (1), <i>S. Chicago</i> (1), <i>S. Gaminara</i> (1), <i>S. Ituri</i> (1), <i>S. Kottbus</i> (1), <i>S. London</i> (1), <i>S. Pomona</i> (1), <i>S. Richmond</i> (1), <i>S. Stanley</i> (1), <i>S. Sundsvall</i> (1), <i>S. Vitkin</i> (1), <i>Salmonella</i> subsp. I serological rough (3)
Parrot	14	<i>S. Typhimurium</i> (7), <i>S. Enteritidis</i> (5), <i>S. Blockley</i> (1), <i>S. Meleagridis</i> (1)
Pheasant	9	<i>S. Adelaide</i> (4), <i>S. Typhimurium</i> (2), <i>S. Lexington</i> (1), <i>S. Newport</i> (1), <i>S. Typhimurium</i> (egg) (1)
Quail	7	<i>S. Ruiru</i> (2), <i>S. Blockley</i> (1), <i>S. Kiambu</i> (1), <i>Salmonella</i> subsp. I serological rough (3)
Pigeon (other serovars)	6	<i>S. Blockley</i> (2), <i>S. Brandenburg</i> (1), <i>S. Bredeney</i> (1), <i>S. Livingstone</i> (1), <i>S. Oranienburg</i> (1)
Ostrich/Rhea (other)	5	<i>S. Kiambu</i> (1), <i>S. Manhattan</i> (1), <i>S. Ruiru</i> (1), <i>S. Sundsvall</i> (1), <i>S. Tarshyne</i> (1)
Duck	5	<i>S. Anatum</i> (2), <i>S. Infantis</i> (1), <i>S. Typhimurium</i> (egg) (1), <i>Salmonella</i> subsp. I 4,5:z10:- (1)
Partridge	5	<i>S. Typhimurium</i> (4), <i>S. Infantis</i> (1)
Eagle Owl	5	<i>S. Stanley</i> (2), <i>S. Newport</i> (1), <i>S. Typhimurium</i> (1), <i>S. Vitkin</i> (1)
Stone curlew (other)	4	<i>S. Brandenburg</i> (2), <i>S. Johannesburg</i> (1), <i>S. Orion</i> (1)
Sand Grouse	4	<i>S. Typhimurium</i> (3), <i>S. Amsterdam</i> (1)
Scarlet ibis	3	<i>Salmonella</i> subsp. II 13,23:z:1,5 (2), <i>S. Typhimurium</i> (1)
Crane	2	<i>S. Typhimurium</i> (2)
Flamingo	2	<i>S. Typhimurium</i> (1), <i>S. Meleagridis</i> (1)
Secretary bird	2	<i>S. Altona</i> (1), <i>S. Typhimurium</i> (1)
Wild turkey	2	<i>S. Typhimurium</i> (2)
Afrikan Stork	1	<i>S. Typhimurium</i> (1)
Barn owl	1	<i>S. Stanley</i> (1)
Buderiou	1	<i>S. Matopeni</i> (1)
Cockatoo	1	<i>S. Poona</i> (1)
Egret	1	<i>S. Kentucky</i> (1)
Finch	1	<i>S. Typhimurium</i> (1)
Francolin	1	<i>S. Typhimurium</i> (1)
Ground Hornbill	1	<i>S. Onderstepoort</i> (1)
Guinea fowl	1	<i>S. Weltevreden</i> (1)
Gull	1	<i>S. Typhimurium</i> (1)
Poultry (other serovars)	1	<i>S. Liverpool</i> (feed) (1)
Starling	1	<i>S. Typhimurium</i> (1)
Yellow billed stork	1	<i>S. Saintpaul</i> (1)
mammals	n	Serovar (no. of isolates)
Camel (other serovars)	36	<i>S. Nchanga</i> (7), <i>S. Altona</i> (3), <i>S. Bahrenfeld</i> (2), <i>S. Gaminara</i> (2), <i>S. Saintpaul</i> (2), <i>S. Stanley</i> (2), <i>S. Give</i> (1), <i>S. Blockley</i> (1), <i>S. Schwarzengrund</i> (1), <i>S. Bredeney</i> (1), <i>S. Chester</i> (1), <i>S. Manhattan</i> (1), <i>S. Djibouti</i> (1), <i>S. Panama</i> (1), <i>S. Vejle</i> (1), <i>Salmonella</i> subsp. I serological rough (9)
Antelope (other serovars)	26	<i>S. Oranienburg</i> (5), <i>S. Hindmarsh</i> (3), <i>S. Give</i> (2), <i>S. Johannesburg</i> (2), <i>S. Kedougou</i> (2), <i>Salmonella</i> subsp. I serological rough (2), <i>S. Aberdeen</i> (1), <i>S. Bahrenfeld</i> (1), <i>S. Brandenburg</i> (1), <i>S. Chester</i> (1), <i>S. Haifa</i> (1), <i>S. Hull</i> (1), <i>S. Kottbus</i> (1), <i>S. Magwa</i> (1), <i>S. Mbandaka</i> (1), <i>S. Saintpaul</i> (1), <i>S. Tarshyne</i> (1), <i>Salmonella</i> subsp. II 13,213:z:1,5 (1), <i>Salmonella</i> subsp. IIIb 61:r:z53 (1)
Horse (other serovars)	21	<i>S. Give</i> (6), <i>S. Hvitvingfoss</i> (2), <i>S. Poona</i> (2), <i>S. Weltevreden</i> (2), <i>S. Brandenburg</i> (1), <i>S. Haifa</i> (1), <i>S. Havana</i> (1), <i>S. Huettwilen</i> (1), <i>S. Kiambu</i> (1), <i>S. Montevideo</i> (1), <i>S. Ruiru</i> (1), <i>S. Sheffield</i> (1), <i>Salmonella</i> subsp. I serological rough (1)
Canine	13	<i>S. Kentucky</i> (3), <i>S. Typhimurium</i> (2), <i>S. Agona</i> (1), <i>S. Enteritidis</i> (1), <i>S. Heidelberg</i> (1), <i>S. Hindmarsh</i> (1), <i>S. Kedougou</i> (1), <i>S. Newport</i> (1), <i>S. Stanley</i> (1), <i>Salmonella</i> subsp. IIIb 65:z10:e,nx,z15 (1)
Sheep/Goat	11	<i>S. Typhimurium</i> (3), <i>S. Altona</i> (2), <i>S. Anatum</i> (1), <i>S. Blockley</i> (1), <i>S. Colindale</i> (1), <i>S. Elomrane</i> (1), <i>S. Muenchen</i> (1), <i>S. Reading</i> (1),

Cheetah (other serovars)	10	<i>S. Kiambu</i> (2), <i>S. Weltevreden</i> (2), <i>S. Altona</i> (1), <i>S. Braenderup</i> (1), <i>S. Dublin</i> (1), <i>S. Haifa</i> (1), <i>S. Huettwilen</i> (1), <i>S. Ruiru</i> (1)
Lion	6	<i>S. Agona</i> (1), <i>S. Anatum</i> (1), <i>S. Frintrop</i> (1), <i>S. Havana</i> (1), <i>S. Newport</i> (1), <i>S. Typhimurium</i> (1)
Tiger	6	<i>S. Infantis</i> (1), <i>S. Kedougou</i> (1), <i>S. Kiambu</i> (1), <i>S. Kottbus</i> (1), <i>S. Ruiru</i> (1), <i>S. Typhimurium</i> (1)
Cat	5	<i>S. Typhimurium</i> (3), <i>S. Enteritidis</i> (1), <i>S. Miami</i> (1)
Mammoset	5	<i>S. Kentucky</i> (2), <i>S. Adelaide</i> (1), <i>S. Enteritidis</i> (1), <i>S. Heidelberg</i> (1)
Bovine (other serovars)	4	<i>S. Dublin</i> (1), <i>S. Elomrane</i> (1), <i>S. Grumpensis</i> (1), <i>Salmonella</i> subsp. I serological rough (1)
Giraffe	4	<i>S. Ibaragi</i> (1), <i>S. Urbana</i> (1), <i>S. Oranienburg</i> (1), <i>S. Muenchen</i> (1)
Hare	4	<i>S. Typhimurium</i> (2), <i>S. Blockley</i> (1), <i>S. Muenchen</i> (1)
Leopard	4	<i>S. Infantis</i> (2), <i>S. Anatum</i> (1), <i>S. Senftenberg</i> (1)
Jaguar	3	<i>S. Havana</i> (1), <i>S. Kedougou</i> (1), <i>S. Kentucky</i> (1)
Wallaby	2	<i>S. Kentucky</i> (1), <i>S. Muenster</i> (1)
Caracal	2	<i>S. Tarshyne</i> (1), <i>S. Typhimurium</i> (1)
Dear	2	<i>S. Amsterdam</i> (1), <i>S. Typhimurium</i> (1), <i>S. Poona</i> (1)
Fox	2	<i>S. Typhimurium</i> (1), <i>S. Enteritidis</i> (1), <i>S. Kentucky</i> (1)
Llama	2	<i>S. Newport</i> (1), <i>S. Typhimurium</i> (1)
Arabian Leopard	1	<i>S. Chester</i> (1)
Arabian Toad	1	<i>S. Uganda</i> (1)
Arabian Wolf	1	<i>S. Reading</i> (1)
Badger	1	<i>S. Muenchen</i> (1)
Black Leopard	1	<i>S. Havana</i> (1)
Chimpanzee	1	<i>S. Oakland</i> (1)
Gerbels	1	<i>S. Kiambu</i> (1)
Grey Mongoose	1	<i>S. Havana</i> (1)
Hyena	1	<i>S. Kentucky</i> (1)
Mouse	1	<i>S. Infantis</i> (1)
Ocelot	1	<i>S. Ruiru</i> (1)
Rabbit	1	<i>S. Kentucky</i> (1)
Sable	1	<i>S. London</i> (1)
Sand cat	1	<i>S. Enteritidis</i> (1)
Serval	1	<i>S. Miami</i> (1)
Sugar Glider	1	<i>Salmonella</i> subsp. IIIb 50:r:z (1)
Zebra	1	<i>S. Agona</i> (1)
reptiles (all species)	n	Serovar (no. of isolates)
Turtle	9	<i>S. Bovismorbificans</i> (1), <i>S. Gaminara</i> (1), <i>S. Havana</i> (1), <i>S. Johannesburg</i> (1), <i>S. Kottbus</i> (1), <i>S. Newport</i> (1), <i>S. Pomona</i> (1), <i>S. Salford</i> (1), <i>S. Typhimurium</i> (1)
Snake	8	<i>Salmonella</i> subsp. IIIa 41:z4z23:- (2), <i>S. Haifa</i> (1), <i>S. Newport</i> (1), <i>S. Virchow</i> (1), <i>Salmonella</i> subsp. IIIa 44:z4,z24 (1), <i>Salmonella</i> subspez. IIIa serological rough (1), <i>Salmonella</i> subspez. IV serological rough (1)
Green Turtle	5	<i>S. Chailey</i> (2), <i>S. Ruiru</i> (1), <i>Salmonella</i> subsp. IIIb 60:r:z35 (1), <i>Salmonella</i> subsp. IIIb 65:z10:e,n,x,z15 (1)
Lizzard	3	<i>Salmonella</i> subsp. IV serological rough (1), <i>Salmonella</i> subsp. IV 48:l,v:1,5,7 (1), <i>Salmonella</i> subsp. I serological rough (1)
Tegu lizzard	1	<i>S. Cubana</i> (1)
Chameleon	1	<i>Salmonella</i> subsp. IV 44:z4,z32:- (1)
Crocodile	1	<i>S. Chailey</i> (1)
Dragon	1	<i>S. Heidelberg</i> (1)
Saw-scaled viper	1	<i>S. Typhimurium</i> (1)
Giant skink	1	<i>Salmonella</i> subsp. IV 44:z4,z23:- (1)
Hawksbill turtle	3	<i>S. Typhimurium</i> (1), <i>S. Weltevreden</i> , <i>Salmonella</i> subsp. I serological rough (1)
Komodo Dragon	1	<i>S. Infantis</i> (1)
Phyton	1	<i>Salmonella</i> subsp. IIIb 48:l,v:1,5,7 (1)
Sand Snake	1	<i>Salmonella</i> subsp. IIIb 48:k:z53 (1)
Spiny tailed lizzard	1	<i>S. Enteritidis</i> (1)
other species	n	Serovar (no. of isolates)
Meal worm	2	<i>S. Kentucky</i> (2)
squid	1	<i>S. Typhimurium</i> (1)

* additionally to Table 2