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*Title Page

Contamination of pig carcass with *Salmonella enterica* serovar Typhimurium monophasic variant 1,4 [5], 12: i:- originates mainly in live animals

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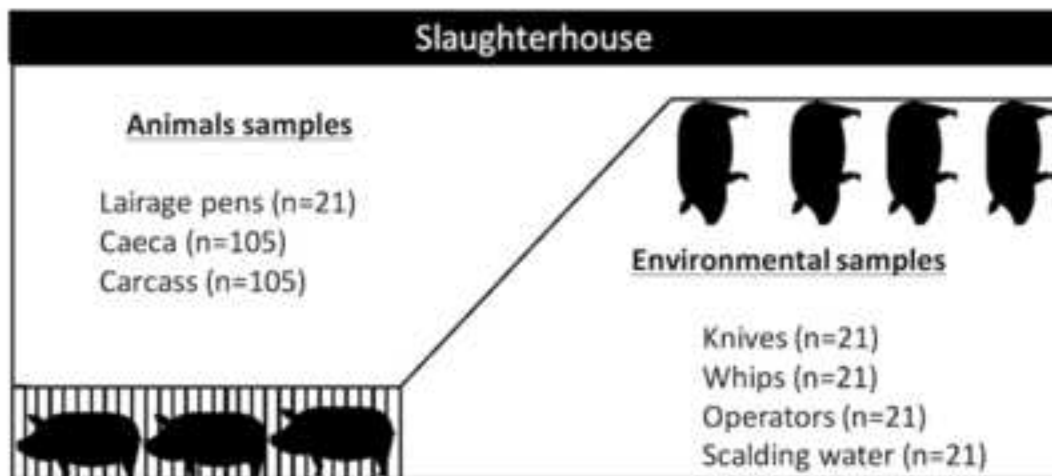
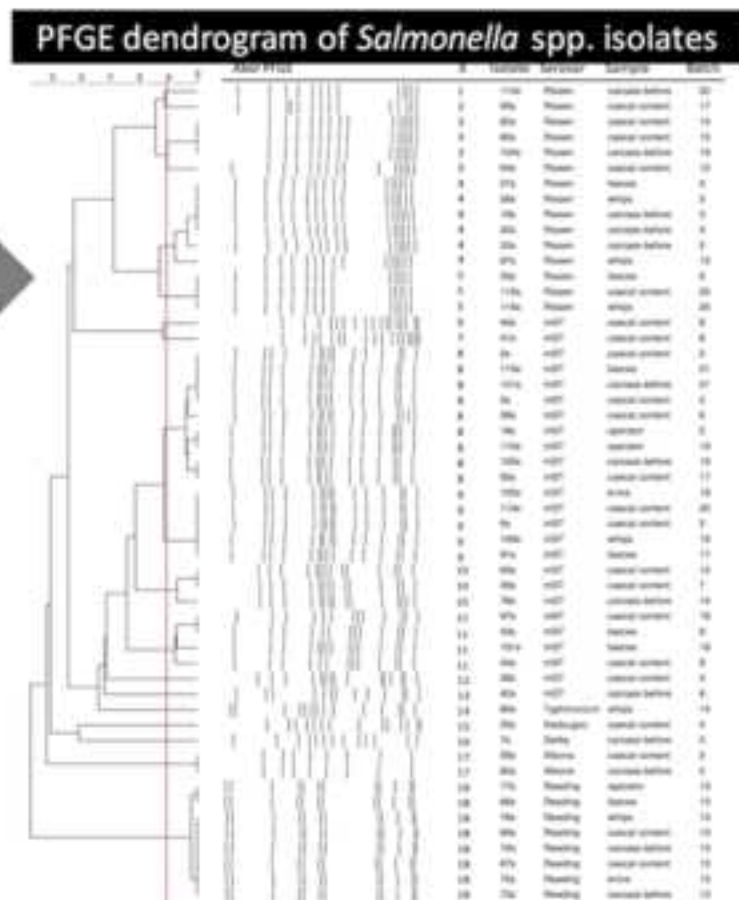
***Graphical Abstract**



Sample type	n	*Salmonella* (%)	
		All serovars	Typhimurium monophasic variant
Faeces	21	52.4 ± 10.9^{a}	45.4 ± 15.0^{abc}
Caeca	105	46.7 ± 4.9^{a}	53.1 ± 7.2^{b}
Carcass	105	32.4 ± 4.6^{b}	38.2 ± 8.2^{abc}
Whips	21	38.1 ± 10.6^{ab}	12.5 ± 10.9^{c}
Operator	21	14.3 ± 7.6^{b}	66.7 ± 36.5^{a}
Knives	21	9.5 ± 6.4^{b}	50.0 ± 27.0^{abc}

a,b,c superscript: Data in the same column with uncommon letters are different ($P < 0.05$)



***Highlights (for review : 3 to 5 bullet points (maximum 85 characters including spaces per bullet point)**

Highlights

Pork meat is considered one of the major sources of Salmonella food infection in humans and distribution of virulent serotypes such as monophasic variants of S. Typhimurium have emerged as a public health threat.

A high proportion of pigs were infected Salmonella spp. being the monophasic variant the most prevalent.

Necessity of a mandatory European programme to control the bacteria during pork production.

*Manuscript (double-spaced and continuously LINE and PAGE numbered)-for final publication
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2 **monophasic variant 1,4 [5], 12: i:- originates mainly in live animals**
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24
25

26 **Abstract**

27 Pork is considered, after eggs, the major source of infection in humans in the EU, with Salmonella
28 Typhimurium, including monophasic strains. Widespread distribution of virulent serotypes such as
29 monophasic variants of *S.* Typhimurium (mST, 1,4,[5],12:i- and 1,4,12:i-) have emerged as a public
30 health threat. mST constitutes a high proportion of the multi-drug-resistant isolates and has been
31 increasing in pigs since 2010. Despite the current situation, within the EU there is no mandatory
32 programme for the control of Salmonella at pork production level. In this context, the aim of this
33 study was to investigate the relationship between Salmonella strains isolated from animals at the
34 slaughterhouse and those isolated from carcass before chilling. During the study, a total of 21 pig
35 herds were intensively sampled during processing at the slaughterhouse. ERIC-PCR was
36 performed among isolates recovered at the different steps in the slaughterhouse to assess the
37 genetic relationship. Then, PFGE was done to study the pulsotypes among the different
38 *Salmonella* serovars isolated. The results showed a high level of *Salmonella* pork batch
39 contamination upon arrival at the slaughterhouse (71.4%) and at the end of the slaughtering
40 process (66.7%), with mST the main serovar isolated from both origins (53.1% and 38.2%,
41 respectively). The slaughter environment poses a potential risk for carcass contamination and it is
42 considered an important source of *Salmonella* spp. Similarly, this study shows that 14.3% of the
43 strains isolated from carcasses have the same XbaI-PFGE profile as those previously recovered in
44 the slaughterhouse environment, but not in the live animals from that same batch. Moreover, this
45 study demonstrates a strong association between the *Salmonella* status of the batch on arrival at
46 the slaughterhouse and pork carcass contamination. These results highlight the importance of
47 *Salmonella* control during pork production despite the lack of a mandatory European programme to
48 control the bacteria.

49

50 Keywords: Pork, mST, PFGE, ERIC-PCR, Slaughterhouse

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1. Introduction

According to the 2018 EFSA summary report on zoonoses, zoonotic agents and food-borne outbreaks, *Salmonella* was responsible for 24.4% (91,662) of food-borne outbreaks in the European Union (EU) (EFSA, 2018). It is estimated that 4.5% of outbreaks are associated with pig meat and products thereof (EFSA, 2016). Pork is considered, after eggs, the major source of infection in humans in the EU, with *S*. Typhimurium, including monophasic strains (*S*. 1,4,[5],12:i- and *S*. 1,4,12:i-) being frequently implicated (Andres and Davies, 2015; Davies et al., 2016). Nonetheless, no outbreak data have been reported by Spain, as the notification of non-typhoidal salmonellosis in humans is voluntary (EFSA, 2016). This is striking, as Spain is the second largest swine producer in the EU and fourth worldwide (Marquer et al., 2014). In fact, Spain is among the countries with the highest *Salmonella* prevalence, 36.2% at slaughterhouse, with 31.3% prevalence of monophasic strains of *S*. Typhimurium (EFSA, 2016). Widespread distribution of virulent serotypes such as monophasic variants of *S*. Typhimurium (1,4,[5],12:i- and 1,4,12:i-) have emerged as a public health threat, as it is the third most frequently isolated serovar from human cases of salmonellosis in Europe, representing 8.3% of confirmed human cases in 2015 (EFSA, 2016). Monophasic *S*. Typhimurium constitutes a high proportion of the multi-drug-resistant isolates and has been increasing in pigs since 2010 (EFSA, 2016). Despite the current situation, there is no mandatory programme within the EU for the control of *Salmonella* at pork production level. In fact, each member state has to consider whether interventions should be set at farm and/or slaughterhouse level (De Busser et al., 2013).

The control of *Salmonella* carriage and shedding in swine remains a challenge (Davies et al., 2016). The risk of *Salmonella* contamination is known to increase across the production chain, at farm level and transport from the farm to the slaughterhouse, reaching its maximum at the slaughterhouse and in subsequent processing (Arguello et al.,2013a,b; Duggan et al., 2010; Visscher et al., 2011;). At the moment, the slaughterhouse remains the most appropriate stage of the food chain for evaluation of the carriage of *Salmonella* and other zoonotic agents by farm animals, particularly in swine (Bonardi et al., 2013). When animals and the carcass are processed,

83 contamination of pig carcass can result from the skin or intestinal contents from the pig itself, but
84 also due to cross-contamination from other carcasses or surfaces at the slaughterhouse
85 (Botteldoorn et al., 2003). *Salmonella* serovars present on pig carcass can be different from those
86 detected in the same batches from the farm (Bonardi et al., 2017). However, many studies have
87 shown that good hygienic practices at slaughter are more effective in reducing the prevalence of
88 *Salmonella* than on-farm interventions (Baptista et al., 2010a). Despite all the efforts made during
89 the last 20 years in the control of *Salmonella* in pig production (Andres and Davies, 2015), our
90 driving hypothesis was that the vast majority of *Salmonella* serovars present on pig carcass ready
91 for commercialisation have their origin in the same batches on the farm, so that *Salmonella* enters
92 the slaughterhouse mainly along with the live animals. Thus, a longitudinal study was conducted to
93 investigate the possible relationship between *Salmonella* strains isolated from animals at the
94 slaughterhouse and those isolated from carcass before chilling.
95
96 **2. Material and methods**
97
98 All the procedures used in this study were performed in accordance with Directive
99 2010/63/EU EEC for animal experiments.
100
101 2.1 Study design
102 This study was conducted from September 2015 to September 2016 in 8 slaughterhouses
103 from the Valencian Region, Eastern Spain. The processing plants selected slaughters 90% of the
104 pork production in the Valencia Region (MAGRAMA, 2016). Samples were collected during 21
105 sampling visits from 21 batches of pigs. The batch definition used was a group of pigs coming from
106 a single farm in a given day. All farms were finishing farms, with minimum nine-month old pigs at
107 an average live weight of 160 kg.
108
109 2.2 Sample collection
110 At each sampling visit, pooled faecal material was collected from lairage pens at the

111 slaughterhouse. Faeces samples (≥500 g) were taken aseptically into a sterile jar from five
112 different points distributed all over the pen. Pens were washed and disinfected between batches;
113 the faeces collected were thus linked to an individual batch. Overall, 21 batches were studied.
114 From each batch, five animals were randomly selected and followed along the processing line.
115 Then, the caecum from each individual animal was aseptically collected and placed into a sterile
116 bag. Caeca were incised with a sterile scalpel blade and approximately 50 mL of the contents were
117 placed in a 500 mL sterile jar. Finally, carcass swabs from individual animals were collected at the
118 end of the processing line by swabbing a 100 cm^2 area at each of the four sampling sites (ham,
119 belly, rump and jowl) rubbing the sterile swab (bioMerieux, Madrid, Spain) 10 times vertically and
120 horizontally (Mannion et al., 2012).
121 At the same time, immediately after each individual was processed, environmental swabs of the
122 slaughtering staff were collected from three sites (knives, whips and operators) by vigorous
123 swabbing of the surface, using sterile wet swabs (bioMerieux, Madrid, Spain). Moreover, 1 L of
124 scalding water was collected directly into a sterile jar.
125
126 2.3 *Salmonella* isolation
127 Samples were collected directly into sterile sample jars and analysed according to ISO
128 6579:2002 (Annex D). Firstly, samples were pre-enriched in 1:10 vol/vol Buffered Peptone Water
129 2.5% (BPW, Scharlau®, Barcelona, Spain) and then incubated at 37±1 ºC for 18±2 h. The pre-
130 enriched samples were transferred onto Semi-Solid Modified Rappaport Vassiliadis (MSRV,
131 Difco®, Valencia, Spain) agar plates and incubated at 41.5±1 ºC for 24-48 h. Plates showing the
132 typical haze around the inoculation spot on the MSRV plates were subcultured onto Xylose–
133 Lysine–Deoxycholate (XLD, Liofilchem®, Valencia, Spain) and ASAP (Chromogenic *Salmonella*
134 spp. agar plate, bioMerieux, Madrid, Spain) and incubated at 37±1 ºC for 24-48 h. After incubation,
135 five presumptive *Salmonella* colonies were streaked onto nutrient agar plates (Scharlab®,
136 Barcelona, Spain) and incubated at 37±1 ºC for 24±3 h. Then, a biochemical test (API-20®,
137 bioMerieux, Madrid, Spain) was performed to confirm *Salmonella* spp. Confirmed *Salmonella*
138 strains were serotyped in accordance with the Kauffman–White–Le–Minor technique (Grimont and

139 Weill, 2007) at the Laboratori Agroalimentari (Cabrils, Spain) of the Departament
140 d'Agricultura,Ramaderia, Pesca i Alimentació.
141
142 2.4 Molecular typing of *Salmonella* isolates
143 Two different subtyping methods were carried out for genotyping *Salmonella* isolates. All
144 isolates were first genotyped by enterobacterial repetitive intergenic consensus (ERIC)-PCR, as
145 previously described (Moré et al., 2017). Representative isolates from the different *Salmonella*
146 ERIC-PCR patterns identified per sample were further analysed by pulsed-field gel electrophoresis
147 (PFGE).
148 PFGE was performed according to the PulseNet standardised protocol "Standard
149 Operating Procedure for PulseNet PFGE of *Escherichia coli* O157:H7, *Escherichia coli* non-O157
150 (STEC), *Salmonella* serotypes, *Shigella sonnei* and *Shigella flexneri*"
151 (www.pulsenetinternational.org). Restriction endonuclease digestion was carried out using XbaI
152 (Roche Applied Science, Indianapolis, IN, USA).
153 ERIC and PFGE band patterns were analysed using Fingerprinting II software, v3.0 (Bio-
154 Rad, Hercules, CA, USA). Similarity matrices were calculated with the Dice coefficient and cluster
155 analysis was performed by the unweighted-pair group method with arithmetic mean (UPGMA).
156 The isolates with a minimum level of similarity of 90% were considered genetically similar or
157 identical.
158
159 2.5 Statistical analysis
160 A generalised linear model (GLM), which assumed a binomial distribution for *Salmonella*
161 presence, was fitted to the data to determine whether there was an association between sample
162 type collected (faeces, caeca, carcass, whips, operator and knives) and *Salmonella* status of the
163 batch. A batch was considered infected upon arrival at the slaughterhouse, if at least one of the
164 five samples collected from caeca was positive. A batch was considered positive at the end of the
165 processing, if at least one of the five samples collected from the carcasses was positive. For this
166 analysis, the error was designated as having a binomial distribution, and the probit link function

167 was used. Binomial data for each sample were assigned a one if they had *Salmonella* or a zero if
168 they did not. A P-value of less than 0.05 was considered to indicate a statistically significant
169 difference. Data are presented as least squares means ± standard error of the least squares
170 means. All statistical analyses were carried out using a commercially available software program
171 (SPSS 21.0; SPSS Inc., Chicago, IL).
172
173 **3. Results**
174
175 During this study, a total of 315 samples were collected from different points of the
176 slaughterhouse (Fig. 1). Samples were collected from the lairage pens (faeces, n=21), scalding
177 water (n=21), whip surfaces (n=21), operators (n=21), working knives (n=21), caecal content
178 (n=105) and carcasses after processing (n=105).
179 According to the different batches sampled (n=21), 71.4% (n=15) arrived at the
180 slaughterhouse colonised by *Salmonella* spp. (caecal content) and 66.7% (14/21) of carcasses
181 were also contaminated with *Salmonella* spp. at the end of processing.
182 The frequency of *Salmonella* contamination throughout the different slaughter steps according to
183 the samples collected is summarised in Table 1. From all samples collected at the slaughterhouse,
184 34.0% (107/315) were positive for *Salmonella* spp. The higher prevalence was found in faeces
185 from lairage pens and caecal content (52.4±10.9% and 46.7±4.9%, respectively), followed by
186 whips (38.1±10.6%), carcass (32.4±4.6%), operator (14.3±7.6%) and knives (9.5±6.4%). None of
187 water samples collected were positives to *Salmonella* spp.
188 *Salmonella* Typhimurium monophasic variant (mST) was the serovar more frequently
189 isolated in that kind of samples, most frequently being contaminated with *Salmonella* (faeces and
190 caeca), (45.4±15.0% and 53.1±7.2%, respectively) (Table 1). Carcass samples showed
191 significantly reduced frequency of positives (32.4±4.6%, P=0.000), but a similar rate of mST
192 serovar (38.2±8.2%, P=0.523), compared with faeces and caecal samples. For environmental
193 samples, no significant differences were observed for operator and knife samples, which showed a
194 low proportion of positives (14.3±7.6%, P=0.523 and 9.5±6.4%, P=0.523, respectively). However,

195 a high percentage of mST was found in both samples (66.7±6.5% and 50.0±27.0%, respectively).
196 On the contrary, a relatively high proportion of *Salmonella*-positive samples was observed in whips
197 (38.1±10.6%), but mST frequency was lower (12.5±10.9%).
198
199 The frequency of *Salmonella* serovar isolated during the slaughter processing is summarised in
200 Table 2. As reported above, from 107 isolates recovered, the most prevalent *Salmonella* serovar
201 isolated during the slaughter processing was mST (44.9%), followed by serovars Rissen (21.5%),
202 Reading (11.2%), Albona (4.7%), Derby (1.9%), Kedougou and Typhimurium (0.9%). From all
203 strains isolated, 14.0% (15/107) could not be revived and, consequently, were not serotyped; the
204 results were expressed as *Salmonella* spp. The results obtained from different serovars related to
205 the sample collected are represented in Table 2.
206 To assess the genetic relationship among isolates recovered at the different steps of the
207 slaughterhouse, 107 isolates were typed by ERIC-PCR. Next, 57 different ERIC-PCR profiles were
208 further analysed by PGFE. The PFGE analysis showed a total of 18 different PFGE pulsotypes
209 among the different serovars (Fig. 2). No PFGE pattern could be obtained from six isolates. mST
210 and *S.* Rissen, the two most abundant serovars, also showed the highest genetic diversity, with 8
211 and 5 different pulsotypes, respectively (Fig. 2). In contrast, Reading, the third most frequent
212 serovar, showed a low diversity, with all isolates grouped in a single cluster with the same
213 pulsotype. The remaining serovars (Albona, Derby, Kedougou, Typhimurium) were represented by
214 one or two pulsotypes, each including only one or two isolates.
215 Isolates of carcass origin were distributed among 9 different pulsotypes, 3 for S. Rissen
216 isolates, 3 for mST, 1 for each of the serovars Albona, Derby and Reading. Isolates of faeces were
217 allocated in 5 different pulsotypes associated with three serovars: mST with 3 pulsotypes, Rissen
218 with 2 and Reading with 1.
219 Ten pulsotypes (X3, X4, X5, X8, X9, X10, X11, X16, X17, X18) included isolates of faeces,
220 caecal content and/or carcass (Fig. 2). Notably, some of them (X4-batch 3, X8-batch 21, X17-
221 batch 2, X18-batch 13) showed carcass strains to have the same XbaI-PFGE pattern as their own
222 animal batch upon arrival at the slaughterhouse (faeces or caecal content isolates). Also, the same

strain (pulsotype) was isolated from carcasses and slaughterhouse environment (knives, whips and operator) during processing (same batch), represented by pulsotypes X4, X8, X18 (batches 3, 19, 13, respectively). Similarly, the same pulsotype was found among caecal isolates and the slaughterhouse environment (whips, operator) from the same batch (X5-batch 20, X8-batch 2, X18-batch13). Finally, the same pulsotype was found in carcass isolates and the slaughterhouse environment, but different from their own animal batch. On the contrary, several PFGE patterns obtained from caecal content and animal faeces isolates show several strains not to be disseminated during the carcass processing, as they were not found in carcasses or in environmental samples.

4. Discussion

This study demonstrated a high level of *Salmonella* pork batch contamination upon arrival at the slaughterhouse (71.4%) and at the end of the slaughtering process (66.7%), mST being the main serovar isolated from both sources (53.1% and 38.2%, respectively). The high level of *Salmonella* spp. detected can be explained by the lack of a *Salmonella* control programme in pork in Spain (Arguello et al., 2012). Moreover, the results obtained correlate with the previously reported high prevalence of *Salmonella* infection in Spanish pig farms (EFSA, 2018). Pork is considered the second source of *Salmonella* human infection in the EU, with *S.* Typhimurium, including monophasic variants (1,4,[5],12:i- and 1,4,12:i-), being frequently implicated (EFSA, 2018). Notably, mST strains were the most frequent in this study. Currently, monophasic variants of *S.* Typhimurium (1,4,[5],12:i- and 1,4,12:i) have emerged as a public health threat, as it is the third most frequently isolated serovar from human cases of salmonellosis in Europe, representing 7.9% of confirmed food-borne outbreaks. It also constitutes a high proportion of the multi-drug-resistant isolates and has been increasing in pigs since 2010. The international dissemination of 1,4,[5],12:i:- mST in swine populations is likely to be related to the selective advantage offered by multi-drug-resistant strains associated with stable genetic elements, also carrying virulence

250 determinants within bacterial lineages that are well adapted to the porcine host and are prevalent
251 in human infections as a result of contaminated pig meat (EFSA, 2018).

252 The slaughter environment poses a potential risk for carcass contamination and is
253 considered an important source of *Salmonella* spp. by several authors (Arguello et al., 2012;
254 Gomes-Neves et al., 2012; Mannion et al., 2012; De Busser et al., 2013). Similarly, this study
255 shows that 14.3% of the strains isolated from carcasses have the same XbaI-PFGE profile as
256 those previously recovered in the slaughterhouse environment, but not in the live animals from
257 that same batch (caecal content or lairage pens faeces). This could be explained because
258 *Salmonella* could remain on contaminated equipment and be transferred to other carcasses that
259 are subsequently slaughtered. Moreover, *Salmonella* can also be spread by workers, as the
260 hands and tools of meat handlers can frequently be contaminated. However, cross-contamination
261 at slaughterhouse is easy to control with the implementation of proper measures of hygiene and
262 staff protocols that reduce the impact of the slaughterhouse environment on carcass
263 contamination. According to the current legislation, these control measures should be registered in
264 the Slaughterhouse Hazard Analysis and Critical Control Points (HACCP) (Hernández et al.,
265 2012).

266 On the other hand, this study shows that there is a strong association between the *Salmonella*
267 status of the batch upon arrival at the slaughterhouse and pork carcass contamination, as
268 previously reported (Baptista et al., 2010b; Andres and Davies, 2015). In fact, the same strains
269 were isolated from carcasses and from their corresponding animal batch upon their arrival at the
270 slaughterhouse, with a high frequency. Thus, control measures applied in pre-harvest stage
271 (mainly at farm level) would reduce the burden on subsequent steps of the production chain,
272 consequently leading to less-contaminated pork carcasses (Andres and Davies, 2015).
273 *Salmonella* status of the batch at farm can vary depending on several factors, such as feeding
274 practices, including the degree to which the feed is ground, and the pH and type of feed, the
275 management procedures, such as continuous or all-in/all-out production systems, different types
276 of herds (farrow-to-finish herds or fattening herds), size of the herds and the level of hygiene and
277 general health status of the pigs (Bonardi, 2017). However, despite all the investments made at

278 farm level over the last 20 years to control *Salmonella* spp. in pig production, no reduction of the
279 on-farm *Salmonella* prevalence has been shown (EFSA, 2016). This is mainly because, within the
280 EU, there is no mandatory programme for the control of *Salmonella* at primary swine production
281 level, as indicated above. For this reason, more studies are needed to develop measures for
282 *Salmonella* control at farm level.

283 Moreover, the importance of transport and the stay in the lairage pens must be studied in
284 depth, as these stages play a double role. In one way, some authors demonstrate the animal
285 transport to the processing plant or long stays in lairage pens increases *Salmonella* prevalence in
286 faeces (Bonardi, 2017). This fact could be explained because a stressful situation could induce
287 the carrier batch to shed *Salmonella* at higher rates due to a disturbance in intestinal functions
288 that may increase the spread of intestinal bacteria in livestock (Mulder, 1995; Marin and Lainez,
289 2009). Thus, the assessment of *Salmonella* status of the pig batch at the slaughterhouse could be
290 the best option to detect the bacteria and to avoid underestimating the prevalence obtained when
291 samples are collected at farm level (EFSA, 2008; Arguello et al., 2012; EFSA 2016).

292

293 Moreover, some authors highlight that transport to the slaughterhouse in contaminated
294 trucks or long stays in lairage contaminated pens are of great concern, as *Salmonella* may be
295 introduced into a *Salmonella*-free batch (Hurd et al., 2002; Bonardi, 2017). Although it is difficult to
296 avoid animal stress in pig production during transport and lairage stay, the role of contaminated
297 trucks and lairage pens can easily be controlled. This can be achieved with proper cleansing and
298 disinfection of the truck and the pens between batches, according to the current standard
299 implemented in European slaughterhouses (HAAPC), as reported above. The controls set out by
300 slaughterhouses that took part in this study certified that the cleaning and disinfection of the trucks
301 and lairage pens were accurate and sufficient to remove the bacteria between different batches.

302 It has been argued that biosecurity plays a very important role in avoiding the introduction of
303 *Salmonella* and other pathogens and also in limiting its spread once it has entered the production
304 chain (Andres and Davies, 2015). However, there is no universal biosecurity protocol that all farms
305 can put into place to minimise the risk of disease introduction. Each farm is unique in terms of

306 location, facilities, management, host susceptibility and other influential factors (Andres and
307 Davies, 2015). Therefore, biosecurity should be a continuous process which assesses the risks,
308 implements protocols according to needs and costs, evaluates the effectiveness and modifies the
309 procedures as critical areas of risk change (Amass, 2005ab). To this end, it is important to follow
310 the example applied in *Salmonella* control in poultry, which has obtained excellent results at
311 primary production stage, and subsequently in poultry meat. It is important to emphasise that,
312 unlike poultry production, which is much more homogeneous and integrated in few companies, the
313 swine production system is not generally integrated and each farm has its own particularities,
314 making it more difficult to apply proper and standardised biosecurity plans to control the bacteria.
315
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317
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323
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465 **Figure Legends**

466

467 **Fig 1.** Samples taken during the study.

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469 **Fig 2.** PFGE dendrogram of KpnI profiles of *Salmonella* spp. isolates. The similarity matrices were
470 calculated using the Dice coefficient and UPGMA clustering method. Profiles with a similarity ≥
471 90% were considered same pulsotype. X: pulsotypes.

472

Table 1
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Table 1.
Salmonella spp. isolated according to the sample type collected and the relationship with monophasic *Salmonella* Typhimurium, the most prevalent serovar isolated. Data are presented as least squares means ± standard error of the least squares means.

Sample type		n	All *Salmonella* serovars (%)	mST (%)
Animal samples	**Faeces**	21	52.4±10.9[a]	45.4±15.0[abc]
	Caeca	105	46.7±4.9[a]	53.1±7.2[b]
	Carcass	105	32.4±4.6[b]	38.2±8.2[abc]
Environmental samples	**Whips**	21	38.1±10.6[ab]	12.5±10.9[c]
	Operator	21	14.3±7.6[b]	66.7±6.5[a]
	Knives	21	9.5±6.4[b]	50.0±27.0[abc]

n: total samples collected, mST: *Salmonella* Typhimurium monophasic variant. [a,b,c] superscript: Data in the same column with uncommon letters are different (P <0.05).

Table 2
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Table 2.

Percentage of each *Salmonella* serovar isolated by sample type (excluding mST).

***Salmonella* serovars**	**n**	**Total (%)**	**Sample type (%)**					
			Animal samples			**Environmental samples**		
			Faeces	**Caeca**	**Carcass**	**Whips**	**Operator**	**Knives**
Rissen	23	21.5	8.7	39.1	39.1	13.0	-	-
Reading	12	11.2	8.3	41.7	25.0	8.3	8.3	8.3
Albona	5	4.7	-	40	60	-	-	-
Derby	2	1.9	-	-	100	-	-	-
Kedougou	1	0.9	-	100	-	-	-	-
Typhimurium	1	0.9	-	-	-	100	-	-
NA	15	14.0	20.0	40.0	26.7	13.3	-	-

n= number of isolates from each serovar. NA: isolates not serotyped.

Figure 1

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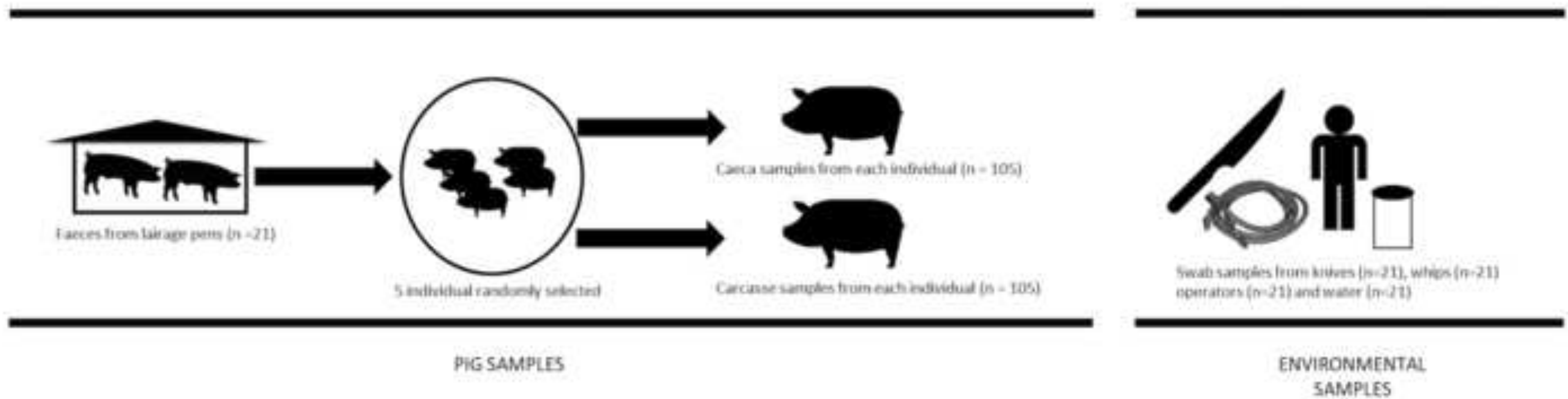

Figure 2
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