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1 **A farm transmission model for Salmonella in pigs, applicable to EU**

2 **Members States**

3

## Abstract

The burden of Salmonella entering pig slaughterhouses across the European Union (EU) is considered a primary food safety concern. In order to assist EU Member States with the development of National Control Plans, we have developed a farm transmission model applicable to all Member States. It is an individual-based stochastic Susceptible-Infected model, that takes into account four different sources of infection of pigs (sows, feed, external contaminants such as rodents and new stock) and various management practices linked to Salmonella transmission/protection (housing, flooring, feed, All-In-All-Out production). A novel development within the model is the assessment of dynamic shedding rates.

**1 The results of the model, parameterized for two case study Member States (one high and one low prevalence) suggest that breeding herd prevalence is a strong indicator of slaughter pig prevalence. Until a Member States' breeding herd prevalence is brought below 10% then the sow will be the dominant source of infection to pigs raised for meat production; below this level of breeding herd prevalence, feed becomes the dominant force of infection. INTRODUCTION**

Salmonella infection and transmission in pigs has been widely described in the literature<sup>(1-4)</sup>. Several serotypes commonly isolated from pigs in Europe (for example Typhimurium and Enteritidis) are of significance to human health<sup>(5, 6)</sup>. Hence, the burden of Salmonella entering pig slaughterhouses across the European Union (EU) is considered a primary food safety concern. Therefore, through EU legislation, the intention of the European Commission was to set targets for each Member State (MS) to reduce the prevalence of Salmonella infection in pigs at slaughter (although the EU has recently decided to achieve reductions through stricter process hygiene controls instead – see Commission Regulation No 217/2014). The targets were to be based on scientific evidence, including information gathered through two baseline surveys of Salmonella prevalence in slaughter and breeding pigs<sup>(5, 7)</sup>, a European Food Safety Authority (EFSA) Scientific Opinion<sup>(8)</sup>, a Quantitative Microbiological Risk Assessment (QMRA)<sup>(9)</sup> and finally cost-benefit analyses for Salmonella control in slaughter and breeding pigs<sup>(10, 11)</sup>. The

34 primary aim of the overall QMRA was to assess the effectiveness of on-farm and abattoir interventions in  
35 reducing Salmonella levels in pigs and/or humans, dependent on MS production systems and current  
36 prevalence of infection in breeding (sow) and finishing units. The QMRA modelled the full farm-to-  
37 consumption pathway, split into a number of modules: Farm, Transport & Lairage, Slaughter &  
38 Processing, Preparation & Consumption and Dose-Response <sup>(9)</sup>. In this paper we discuss in detail the  
39 farm model, which describes the transmission of Salmonella within pig herds, and which can be used to  
40 investigate interventions that may reduce prevalence in pigs at slaughter.

41 The main aim of the farm model was to i) better understand and describe the introduction and dynamics  
42 of Salmonella infection, and how these are affected by the various management practices across the EU,  
43 and ii) to assess the differences in the effect of practical on-farm interventions between EU MSs. The aim  
44 of identifying the MS-dependent effectiveness of interventions is key and the results of on-farm  
45 interventions, and how these affect MS-level slaughter pig prevalence and subsequently human incidence  
46 of Salmonella infection, are described in an accompanying paper <sup>(12)</sup>. In this paper we focus on  
47 describing the dynamics of infection, and what are the main sources and drivers of infection in different  
48 MSs.

49  
50 Infectious disease transmission models have been developed for a variety of animal diseases, including  
51 Salmonella in pigs <sup>(13-16)</sup>. Typically the latter models have become more detailed over time and in the  
52 case of a recent study the traditional use of “general” transmission parameters was replaced by  
53 specifically modelling the environmental transfer of Salmonella via the faecal-oral route <sup>(14)</sup>. A  
54 transmission parameter is essentially a “black-box”, which describes the force of infection resulting from  
55 Salmonella being present in the environment. An estimate of the parameter thus encompasses many  
56 different factors, including the resistance of the pig to infection, the level of contamination in the  
57 environment and the frequency of contact with that contaminated environment, without explicitly

58 describing their individual contribution. However, in order to investigate interventions (such as cleaning  
59 and disinfection, vaccination etc...) it is necessary to differentiate between those factors that  
60 increase/reduce the level of contamination in the environment and those factors that affect the resistance  
61 of the pig to infection. In addition, in order to ensure that any model is relevant across EU MSs then the  
62 varying management practices across the EU must be considered. We therefore consider differences in  
63 environmental transfer caused by management factors (for example flooring or whether pigs are produced  
64 on an All-In-All-Out (AIAO) basis). The farm model was designed to be generic and can be  
65 parameterised (given relevant and available data) to represent any EU MS. Within the wider QMRA,  
66 four case study MSs were chosen <sup>(9)</sup>; in this paper the results from two of these case study MSs are  
67 described (one “low-prevalence” MS and one “high-prevalence” MS, as defined by lymph node  
68 prevalence as taken from the baseline EFSA slaughter pig survey <sup>(5)</sup>).

## 69 **2 METHODS**

70

### 71 **2.1 Overview of farm transmission model**

72

73 The farm model is an individual-based stochastic Susceptible-Infected-Susceptible (SIS) model, adapted  
74 to take account of i) multiple changing populations, rather than a single closed population, and ii)  
75 intermittent shedding of Salmonella. The model is implemented using Monte-Carlo simulation, where  
76 each iteration represents production from one farm over a 500 day period, incorporating farrowing,  
77 weaning, and grower and finisher production. Over this 500-day cycle of production batches of pigs are  
78 sent to slaughter each week. Two outputs are generated for each batch of pigs sent to slaughter (the  
79 inputs to the Transport & Lairage module): the prevalence of lymph-node infection and a distribution for  
80 the concentration of Salmonella shed within the faeces of infected pigs. Lymph-node infection is the  
81 metric of interest as this is the sample type used in the EFSA slaughter pig baseline survey <sup>(7)</sup>; hence we

82 wish to be able to validate the model results against this robust EU-wide survey, as well as providing  
83 relevant predictive model results for the reduction in a MS's slaughter-age pig prevalence in light of an  
84 intervention program.

85

86 For each iteration there are a large number of spatial and temporal events that can occur at random,  
87 including the seeding of infection into the farm, the response to exposure (in terms of whether or not  
88 infection occurs) and subsequently the shedding rate. All farms are set to be Salmonella-negative at the  
89 start of an iteration (day 1). There are four assumed sources of infection: sows, feed, wildlife and the  
90 introduction of new infected stock. Following initial infection of the herd, which can occur at any time,  
91 transmission is described by an individual-based environmental infection model, which tracks i) the  
92 shedding and inactivation/movement of Salmonella in the environment and ii) the dose-response of pigs  
93 exposed to environmental contamination.

94

95 The baseline model was run for 1000 iterations (representing 1000 farms). Management factors (for  
96 example flooring, feed type used) were used to define farm types, for which more description is given  
97 later. Farm types were allocated proportionally to the 1000 farms to represent the national structure of the  
98 pig herd within a particular MS. Hence, it was assumed that summing the predicted number of lymph-  
99 node positive pigs over all batches/farms and dividing by the total number of pigs within the batches  
100 provided an estimate for the prevalence of lymph-node positive pigs being sent to slaughter (i.e. leaving  
101 the farm gate) for a particular MS.

102

103 For clarity we define a distinct difference between the use of the terms "sow" and "pig". Pigs are  
104 explicitly defined as those animals which are raised only for slaughter and progress through all the rearing

105 stages of farrowing, weaning, growing and finishing. Sows are explicitly those animals producing the  
106 pigs raised for slaughter (as opposed to breeding sows in multiplier or nucleus herds).

## 108 2.2 Management of farms

109  
110 Large variability in breeding (sow) and slaughter pig prevalence across EU MSs is apparent from two  
111 baseline surveys carried out in 2006-8 <sup>(7, 5)</sup>. While some of this variability can be assumed to originate  
112 from topography and climate, the majority will result from the types of production systems used by  
113 farmers. Management systems and practices for which there was sufficient evidence to show a direct  
114 effect on transmission of Salmonella were included. Individual farms within the model are assigned a  
115 farm type based on these relevant characteristics. The options modelled are described in Table I.

116  
117 INSERT TABLE I HERE.

118  
119 It was assumed that all slaughter pigs will go through four main stages of rearing: farrowing, weaning,  
120 growing and finishing (fattening) and will be moved into specialist accommodation for each stage of  
121 rearing (pigs can be transported between farms at the end of weaning if a two-site system is used). Pigs  
122 will spend  $sa$  days in the farrowing house before being weaned, then  $wa$  days in the weaning  
123 accommodation, and then  $ga$  and  $fa$  days in the grower and finishing stages respectively, before being  
124 sent to slaughter on a weekly basis at days  $t = (1, 8, 15, \dots, 498)$ . There are  $n_{pig}$  pigs in pen  $j$ ,  $n_{pen}$  pens in  
125 room  $l$ , and  $n_{room}$  rooms in a building. At the beginning of the model ( $t=1$ ) each pen/room/building is  
126 populated with pigs (except for one farrowing building, which is left empty for cleaning and disinfection  
127 for one week). Assuming most large systems will raise pigs using some form of weekly/fortnightly

128 batching, the model system described in Figure 1 is used. We also assume Figure 1 is applicable to all  
129 MSs (small adjustments to the parameter estimates are possible to reflect a MS more accurately). The  
130 system is flexible, and differences between rearing stage, inside/outside and AIAO/continuous production  
131 are captured via parameter estimation.

132

133 INSERT FIGURE 1 HERE.

134

135 For computational efficiency it was also assumed that pig movement is regimented and efficient, such  
136 that the pens containing the individual batch of pigs sent to slaughter at times  $t$  are filled immediately  
137 with the group of pigs within the growing house that have reached finishing weight and that group is  
138 replaced by the batch of pigs reaching the required growing weight etc... For slaughter pigs that are  
139 finished on a grower-finisher farm, it is assumed that they were reared on a breeder-weaner farm and  
140 transported to the grower-finisher farm. Transport has been highlighted as a risk factor for Salmonella  
141 transmission between pigs<sup>(17)</sup>, hence transport is included if this farm type is selected. Transport between  
142 farms is assumed to be almost identical to transport between the finishing house and abattoir, hence the  
143 model we use here is largely based on the Transport & Lairage model<sup>(18)</sup>, except it is assumed only one  
144 cohort (batch) is transported at a time.

145

## 146 **2.3 Transmission model**

147

### 148 **2.3.1 Shedding and removal of faeces**

149



150 Salmonella is primarily transmitted via the faecal-oral route <sup>(19, 20)</sup> and the probability of infection is  
 151 dependent on the dose ingested <sup>(21)</sup>. In order to examine a range of specific interventions (for example  
 152 vaccination, changing feed type, cleaning) the amount of Salmonella ingested by a pig and the subsequent  
 153 dose-response relationship must be considered. The methods used in previous models <sup>(13, 14)</sup> were  
 154 expanded; in particular shedding and the subsequent movement/ingestion of faecal material. For the rest  
 155 of this section a general parameter definition is used for all stages of production (farrowing, weaning  
 156 etc...) unless explicitly stated.

157

158 The total amount of faecal material in pen  $j$  of room  $l$  at time  $t$  is defined as  $F(j,t)$ . The amount of faecal  
 159 material shed by an animal,  $k$ , during any one timestep (one day) is defined as  $f(k, j, t) \sim N(\mu_f, \sigma_f^2)$  for  
 160 pigs. Similarly,  $f_{sow}(j, t) \sim N(\mu_s, \sigma_s^2)$  for sows. It is assumed that fresh faeces (i.e. those shed on day  $t$ )  
 161 will be more viscous than older faeces and will hence be more amenable to fall through slatted flooring.  
 162 The proportions of faecal material shed on day  $t$  in pen  $j$  of house  $l$  and removed that day via slatted  
 163 flooring and cross-contamination to an adjacent pen are given by  $\beta_{F,day}(j,t)$  and  $\beta_{xc}(j,t)$  respectively.  
 164 Regarding faecal material shed prior to day  $t$ , that is faecal material present on day  $t-1$ , the proportions  
 165 removed via slatted flooring and cross-contamination are  $\beta_{F,old}(j,t)$ . The amount of faecal material  
 166 present in pen  $j$  of house  $l$  at the end of day  $t$  is calculated using equations (1) – (4) as follows:

167

168 The total amount of faecal material shed by pigs on day  $t$  is

169

$$170 \quad F_{pig}(j, t) = \sum_{k=1}^{n_{pig}} f(k, j, t). \quad (1)$$

171 except in the farrowing building where  $F_{pig}(j, t) = \sum_{k=1}^{n_{pig}} f(k, j, t) + f_{sow}(j, t)$

172 The amount of faecal material shed on day  $t$  removed from pen  $j$  is given by

173 
$$F_{day}(j,t) = F_{pig}(j,t) \cdot (1 - \beta_{F,day}(j,t) - \beta_{xc}(j,t)). \quad (2)$$

174 The amount of faecal material shed before day  $t$  and removed via slatted flooring on day  $t$  is given by

175 
$$F_{old}(j,t) = F(j,t-1) \cdot \beta_{F,old}(j,t). \quad (3)$$

176

177 The amount of faecal material shed before day  $t$  and cross-contaminated to either pen  $j-1$  or  $j+1$  on day  $t$

178 is given by

179 
$$F_{xc}(j,t) = F(j,t-1) \cdot \beta_{xc}(j,t) \quad (4)$$

180 Finally,

181 
$$F(j,t) = \begin{cases} F(j,t-1) + F_{day}(j,t) - F_{old}(j,t) - F_{xc}(j,t) / 2 + F_{xc}(j+1,t) / 2 & \text{if } j=1 \\ F(j,t-1) + F_{day}(j,t) - F_{old}(j,t) - F_{xc}(j,t) + F_{xc}(j-1,t) / 2 + F_{xc}(j+1,t) / 2 & \text{if } j = \{2, \dots, n_{pen} - 1\} \\ F(j,t-1) + F_{day}(j,t) - F_{old}(j,t) - F_{xc}(j,t) / 2 + F_{xc}(j-1,t) / 2 & \text{if } j = n_{pen} \end{cases}$$

182 
$$(5)$$

183

184 The set of pens depopulated through each production stage are assumed to be cleaned out before new pigs

185 are moved in. We assume cleaning out of faecal material at this depopulation time is efficient, therefore

186  $F(j,t) = 0$ , for all rooms which are depopulated/re-populated at times  $\mathbf{t}$ . In contrast, it is assumed that

187 Salmonella removal will not be 100% efficient (as Salmonella may be released from the faecal material

188 and reside in biofilms or hard-to-clean areas such as feeder tube nipples).

189

### 190 2.3.2 Introduction of Salmonella into pig herd

191

192 It was assumed that a pig will be in any one of two states at time  $t$ ; Susceptible or Lymph-node positive

193 (specifically infection in the ileo-caecal lymph node). The concentration of Salmonella shed by Lymph-

194 node positive pigs is dependent on whether the pig was infected by a “low” ( $<10^6$  CFUs) or “high” ( $\geq 10^6$   
195 CFUs) dose (which is described in more detail in Section 1.4).

196  
197 Lymph-node positive status was used to determine infection as it is an ideal characteristic at the point of  
198 slaughter for which to validate the model (given the ileo-caecal lymph node was the primary sample type  
199 for the EFSA baseline slaughter pig survey <sup>(5)</sup>). However, being lymph-node positive does not necessarily  
200 mean that the pig will be actively excreting Salmonella. Rather, it is an indication of the fact that the pig  
201 still has a Salmonella infection and can *potentially* shed Salmonella. Therefore, it is important to note  
202 that at some timepoints no shedding of Salmonella may occur, even if a pig is lymph-node positive (i.e.  
203 “intermittent shedding”). As no data were available, it was assumed that pigs immediately return to the  
204 “Susceptible” state following recovery from being lymph-node positive. Recovery from the “Lymph-  
205 node positive” state takes  $t_{LN}$  days.

206  
207 The sources of infection were based on the opinion of EFSA (2006), which are: other infected pigs  
208 (sows/new stock/mixing of cohorts), feed and wildlife <sup>(8)</sup>. The herd prevalence for Salmonella infection  
209 in breeding sows,  $p_{herd}$ , was estimated for each MS within the EU from the EFSA breeding survey <sup>(7)</sup>. At  
210 the start of each iteration, infection status of the breeding herd (infected/not infected) is randomly  
211 assigned according to the value of  $p_{herd}$ . The within-herd prevalence of Salmonella shedding on breeding  
212 herds,  $p_w$ , will vary between farms, as well as MSs. The number of sows shedding Salmonella within a  
213 batch cohort,  $l$ , is binomially distributed according to  $p_w$  and the number of sows within the cohort,  $n_{sow}$ ,  
214 that is  $I_{sow}(j,t) \sim \text{Binomial}(n_{sow}, p_w)$ . As each group of piglets reach weaning age the group of sows is  
215 replaced with another group of sows reaching parturition, after a week of the pen being empty for  
216 cleaning and disinfection (C&D). The number of infected sows in the new group is recalculated using the  
217 same process as above.

218

219 Each sow will produce  $f_{sow}(j,t)$  faeces per day. If the sow is currently shedding it will excrete Salmonella  
220 into the environment at a rate  $c_s(j,t)$  (CFUs per gram of faeces). Therefore over a daily period a sow will  
221 shed  $\lambda(j,t)=f_{sow}(j,t)*c_s(j,t)$  salmonellas. Note that sows are treated as a “static” source of infection within  
222 the model: they are not infected by either of the other sources considered, or by the shedding of their  
223 neighbours. Each sow remains in the same infection state for the duration of farrowing.

224

225 For simplicity, it was assumed that feed can be broken down into two major types: wet ( $w$ ) and dry ( $d$ ).  
226 Pigs will consume  $g$  grams of feed per day and it was assumed that a pig is exposed to a new batch of  
227 feed every 4 days. We define the prevalence of feed batch contamination as  $p_{feed}$ . The concentration of  
228 Salmonella within contaminated feed is denoted as  $c_f(k,j,t)$  per gram feed (equal to zero if feed batch is  
229 Salmonella-negative). The number of Salmonella ingested per day by a pig, through consumption of  
230 contaminated feed is given by  $\lambda_f(k,j,t) = g \cdot c_f(k, j, t)$ .

231

232 There are little data to quantify the frequency and magnitude (and the associated variability over time and  
233 between farms) of any external contamination of the farm. However, there are some data on wildlife  
234 incursions onto farms and the amount of Salmonella rodents or birds might contaminate the environment  
235 with via defecation <sup>(22, 23)</sup>. While recognising other external sources of infection exist, it was decided to  
236 incorporate only wildlife (specifically rodents and birds) as a source of infection.

237

238 A study into the transmission of Salmonella between wildlife and pigs suggests that wildlife within the  
239 vicinity of farms are more commonly infected with Salmonella if the pigs themselves are infected <sup>(23)</sup>.  
240 Therefore, it was assumed that the Salmonella status of the wildlife is equivalent to the status of the farm,

241 i.e. infected or not infected. Rodents and birds are then assumed to contribute  $\lambda_e(k,j,t)$  salmonellas to the  
242 exposure dose of each pig for each time step onwards from when infection occurs on a farm (assuming, in  
243 the absence of any other data, each pig will ingest roughly 1g of rodent/bird faeces per day). Studies have  
244 shown that prevalence within rodents/birds on an infected pig farm ( $p_{wild}$ ) are fairly low, around 1-5%<sup>(22,</sup>  
245 <sup>23)</sup>. Therefore a Bernoulli random variable (with  $p=0.03$ ) was used to indicate whether a pig would ingest  
246 contaminated wildlife faeces such that pig ingestion of Salmonella through external contamination occurs  
247 relative to the prevalence of infection within the wildlife. The concentration of Salmonella within  
248 wildlife faeces appears to be similar to that within pigs<sup>(22)</sup>. Hence, in the absence of rigorous quantitative  
249 data, a lognormal distribution for  $\lambda_e(k,j,t)$  was assumed as this is a commonly used distribution to describe  
250 microbiological count data (see Table IV).

### 252 **2.3.3 Transmission of infection via the contaminated environment**

253  
254 Once infection of one or more pigs occurs, transmission between pigs is driven not only by the sources of  
255 infection but also by the shedding of contaminated faeces. Observational studies<sup>(3, 4, 24)</sup> show intermittent  
256 shedding by infected pigs at low levels (usually less than 100 CFU/g of faeces) and a fairly low incidence  
257 of infection (apart from the period immediately post-weaning, when there is typically a distinct increase  
258 in incidence/prevalence). A schematic diagram of this dynamic is shown in the transmission model  
259 framework for one pen (relevant to all pens, buildings and stages of production), given in Figure 2.

260  
261 INSERT FIGURE 2 HERE.

263 The amount of Salmonella shed into the pen environment each day by each pig ( $\gamma(j,t)$ ) or sow ( $\gamma_s(j,t)$ ) can  
 264 be given by

$$265 \quad \gamma(j,t) = \begin{cases} \sum_{k=1}^{n_{pig}} c_p(k,j,t) \cdot f(k,j,t) & \text{if wean, grow or finishing stage} \\ \sum_{k=1}^{n_{pig}} (c_p(k,j,t) \cdot f(k,j,t)) + c_s(j,t) \cdot f_{sow}(j,t) & \text{if farrowing stage} \end{cases}$$

266 where  $c_p(k,j,t)$  and  $c_s(j,t)$  are the concentrations of Salmonella per gram of faeces shed by a pig and sow  
 267 respectively ( $c_p(k,j,t)$  or  $c_s(j,t)$  is zero for susceptible pigs;  $c_p(k,j,t)$  and/or  $c_s(j,t)$  may also be zero for  
 268 infected pigs/sows that are intermittently shedding). Similar equations for the total number of  
 269 Salmonella in the pen environment, as for faecal material (Equations 1-4), can be defined. Therefore,

$$270 \quad E_{day}(j,t) = \gamma(j,t) \cdot (1 - \beta_{f,day}(j,t) - \beta_{xc}(j,t)),$$

$$271 \quad E_{old}(j,t) = E(j,t-1) \cdot \beta_{f,old}(j,t),$$

$$272 \quad E_{xc}(j,t) = E(j,t-1) \cdot \beta_{xc}(j,t),$$

273 where  $E_{old}$  and  $E_{xc}$  are the amounts of Salmonella present at day  $t-1$  and removed during day  $t$  via slatted  
 274 flooring and cross-contamination respectively. Therefore, the total amount of Salmonella in pen  $j$  at the  
 275 end of day  $t$ ,  $E(j,t)$  is given by

$$276 \quad E(j,t) = \begin{cases} (10^{\log(E(j,t-1)) - \delta \cdot t_c}) + E_{day} - E_{old}(j,t) - E_{xc}(j,t) / 2 + E_{xc}(j+1,t) / 2 & \text{if } j=1 \\ (10^{\log(E(j,t-1)) - \delta \cdot t_c}) + E_{day} - E_{old}(j,t) - E_{xc}(j,t) + E_{xc}(j-1,t) / 2 + E_{xc}(j+1,t) / 2 & \text{if } j = \{2, \dots, n_{pen} - 1\} \\ (10^{\log(E(j,t-1)) - \delta \cdot t_c}) + E_{day} - E_{old}(j,t) - E_{xc}(j,t) / 2 + E_{xc}(j-1,t) / 2 & \text{if } j = n_{pen} \end{cases} \quad (7)$$

280 where  $\delta$  is the decay rate of Salmonella (in logs) per day,  $t_C$  is the time between depopulation and  
281 repopulation (7 days for farrowing, zero days for other stages).

282

283 We assume there is imperfect removal of Salmonella during cleaning and/or disinfection. Therefore, for  
284 rooms depopulated/repopulated at times  $\mathbf{t}$ ,  $E(j,t) = E(j,t) \cdot \beta_C$ , where  $\beta_C \sim \text{Beta}(\alpha_{\beta_C}, \beta_{\beta_C})$  and is the  
285 fraction of Salmonella remaining in the pen environment after cleaning.

286

287 For simplicity it was assumed that Salmonella is homogeneously mixed within all faecal material in the  
288 pen. Therefore the average concentration of Salmonella within a gram of contaminated faecal material,  $c$ ,  
289 is given by

290

$$291 \quad c(j,t) = \frac{E(j,t)}{F(j,t)}.$$

292

### 293 **2.3.4 Infection of pigs**

294

295 It was assumed that all (Salmonella-negative and positive) pigs ingest some faecal material each day.

296 Therefore, each pig will ingest  $\lambda_i(k,j,t)$  organisms through faecal ingestion, where

297

$$298 \quad \lambda_i(k, j, t) = \mu \cdot c(j, t)$$

299 where  $\mu$  is a random variable describing the mass of faeces ingested by a pig. The total number of

300 Salmonella ingested by each pig on day  $t$ ,  $\lambda(k,j,t)$  can therefore be given as

301

302

$$\lambda(k, j, t) = \lambda_i(k, j, t) + \lambda_f(k, j, t) + \lambda_e(k, j, t). \quad (8)$$

303

304

From experimental data <sup>(21)</sup>, the probability of a pig becoming infected through ingesting  $\lambda(k, j, t)$

305

organisms,  $p_{inf}(k, j, t)$ , was shown to follow a beta-binomial dose-response relationship. Hence, at the

306

individual pig level

307

308

$$p_{inf}(k, j, t) = 1 - \left(1 - \text{Beta}(\alpha_{DR}, \beta_{DR})\right)^{\lambda(k, j, t)}. \quad (9)$$

309

310

where  $\alpha_{DR}$  and  $\beta_{DR}$  are the shape and scale parameters of the Beta-Binomial dose response model, and are

311

dependent on feed type. The number of newly infected pigs in pen  $j$ ,  $e(j, t)$ , can therefore be defined as

312

$$e(j, t) \sim B(S(j, t), p_{inf}(k, j, t)).$$

313

314

Each of the newly infected pigs are assigned a duration for being lymph-node positive,  $t_{LN}$ . Hence, at

315

time  $t_{inf} + t_{LN}$  (time of infection + duration of infection) a pig will return to the ‘‘Susceptible’’ status (if it

316

has not been transported to slaughter first). We define  $w(j, t)$  to be the sum of infected pigs in pen  $j$  of

317

room  $l$ , that have reached the end of their infection period at time  $t$ . Therefore, the number of susceptible

318

( $S(j, t)$ ) and infected ( $I(j, t)$ ) pigs within a pen at the end of day  $t$  is calculated as follows:

319

320

$$\begin{aligned} I(j, t) &= I(j, t-1) + e(j, t) - w(j, t) \\ S(j, t) &= n_{pig} - I(j, t) \end{aligned},$$



321 where at  $t = 1$   $S(j,t) = n_{pig}$  and  $I(j,t) = 0$ . The prevalence of infection within each pen at time  $t$ ,  $p(j,t)$  is  
322  $I(j,t)/n_{pig}$ .

323

324 The output of the model is the prevalence of infection (defined as lymph-node positive) within batches of  
325 pigs placed on transport to slaughter. Transport to slaughter occurs weekly, i.e. one finishing room (4  
326 pens) from one of the finishing buildings is emptied on each of the movement timesteps  $\mathbf{t}$  discussed  
327 above. The first five batches of pigs sent to slaughter are not included in the results in order to allow  
328 sufficient introduction and transmission of infection to occur through the originally Salmonella-free pig  
329 population.

330

331 Therefore, the prevalence of lymph-node positive pigs at slaughter within a batch of pigs sent to slaughter  
332 at times  $\mathbf{t}$ ,  $p_i(\mathbf{t})$ , is given by

333

334 
$$p_i(\mathbf{t}) = \frac{\sum_{j=1}^4 I(j, \mathbf{t})}{4 * n_{pig}} . \quad (8)$$

#### 335 2.4 Parameter estimation

336

337 There are little or no data to reflect the variation of Salmonella introduction/transmission across EU MSs  
338 caused by some of the management factors in terms, and hence for simplicity these parameters were  
339 assumed to be equal across all case study MSs (see Table II). The weightings for apportioning farm types  
340 were taken from data collected from the EFSA baseline survey for breeding pigs <sup>(7)</sup>. For farms which the

341 EFSA baseline survey data did not cover (i.e. farms with no breeding herd) other relevant sources were  
342 used (Table III).

343

344 INSERT TABLE II & III HERE.

345

346 All other parameter estimates are detailed in Table IV. The breeding herd prevalence of each case study  
347 MS was taken from the EFSA breeding pig survey and assumed to be directly equivalent to  $p_{herd}$ . In the  
348 absence of data for all case study MSs, it was assumed that, as a worse case scenario, the within-herd  
349 prevalence was equal to the MS2 estimate. The prevalence of Salmonella contamination has been  
350 identified to be between 1-10% for samples from feed types commonly used for pigs <sup>(25)</sup>. However, there  
351 are many issues with sampling of feed for determining prevalence <sup>(6)</sup>. Of concern is the extremely small  
352 sample mass (relative to the tonnage produced), meaning that it is highly likely that positive batches are  
353 missed if contamination is heterogeneous. Therefore, a conservative estimate of  $p_{feed} = 10\%$  was used for  
354 both case study MSs.

355

356 Assuming that pigs excrete intermittently during the whole time period of infection (as defined by  
357 presence of Salmonella in lymph-node), survival analysis methods were used to estimate the duration of  
358 both lymph-node positivity and excretion <sup>(26, 3)</sup>. The resulting shedding profile is highly variable between  
359 individual pigs. A recent longitudinal study of outdoor pigs <sup>(3)</sup> enumerated Salmonella at the individual  
360 pig level for six weeks (six weekly samples). Two cohorts of pigs (one high and one low dose group)  
361 were seeded with experimentally infected pigs on outdoor paddocks, before these cohorts were removed  
362 and two new cohorts placed on the vacated paddocks. There were significantly greater concentrations  
363 shed by the high dose group (between 0-10<sup>6</sup> CFU/g) than by the low dose group (0-100 CFU/g). Pigs in

364 the second experiment cohorts were then infected quasi-naturally from the contaminated faecal material  
365 shed by the first cohorts. Once a pig has been infected then the magnitude of shedding is randomly  
366 assigned from 0 – 6 log CFU/g faeces, according to the dose with which the pig was infected. For every  
367 proceeding week after initial infection that a pig remains within the Lymph-node positive state then the  
368 magnitude of shedding is determined based on the previous week’s magnitude. On each day an infected  
369 pig may shed up to  $x$  log CFU/g faeces, therefore  $c_p(k, j, l, t) \sim U(10^{x-2}, 10^x)$  if  $x > 0$ , else  $c_p(k, j, t) = 0$ .  
370 Correlation matrices have been generated from the dataset describing the magnitude of shedding (either 0,  
371 2, 4, 6 log CFU/g faeces) from infected pigs in the second, quasi-naturally infected, cohort, one matrix for  
372 each dose group (“low”, 1-10<sup>6</sup> CFU, or “high”, >10<sup>6</sup> CFU). Hence these correlation matrices give the  
373 probability of a pig shedding  $x$  log CFU/g faeces one week, given it had shed  $y$  log CFU/g faeces the  
374 previous week.

375

376 In order to derive the dose response parameters,  $\alpha_{DR}$  and  $\beta_{DR}$ , a Beta-Poisson model was fitted to  
377 experimental dose-response data for pigs fed on dry feed (from ileo-caecal lymph-nodes)<sup>(21)</sup>. The  $\alpha_{DR}$   
378 and  $\beta_{DR}$  parameters from the Beta-Poisson model are also equivalent to the  $\alpha_{DR}$  and  $\beta_{DR}$  parameters of the  
379 Beta-Binomial model. Pigs on wet feed will have a greater resistance to infection, due to the lowering of  
380 pH within the gut making it a more hostile environment for Salmonella<sup>(27)</sup>. The wet feed parameters  
381 were estimated by anchoring the relative change in prevalence between dry and wet-feed farms produced  
382 by the model to the relative change in prevalence observed within a German risk factor study using data  
383 collected through the EFSA baseline survey for slaughter pigs<sup>(28)</sup>.

384

## 385 **2.5 Sensitivity analysis and model interrogation**

386

387 An Analysis of variance (ANOVA) method was used for sensitivity analysis <sup>(29)</sup>. The inputs (or  
388 “factors”) were grouped by quartiles and the resultant F-value from ANOVA gives the confidence that a  
389 given factor has an effect on the output mean, i.e. the prevalence of infection within a batch of pigs sent to  
390 slaughter ( $p_i(\underline{t})$ ). Many of the distributions used within the model are sampled many times during one  
391 iteration of the model. In order to use the ANOVA method then the mean of the random variable samples  
392 drawn from each distribution of one iteration is used to describe the variability between batches. For  
393 example the relationship between  $p_i(\underline{t})$  and the amount of Salmonella ingested via external contamination,  
394  $\lambda_e(k,j,t)$ , is determined by investigating how the value of  $p_i(\underline{t})$  is influenced by the mean value of all the  
395 individual values of  $\lambda_e(k,j,t)$  drawn from the distribution described in Table III for the relevant pigs ( $k$ ),  
396 pens ( $j$ ) and building ( $l$ ).

397

398 The relative contribution of each source of infection (sow, feed, external contamination) was investigated  
399 by setting, in turn, the contribution of each source to zero. Analysis of individual iterations was used to  
400 investigate complex dynamics, such as comparing the distribution of doses ingested against the  
401 contamination of the pig environment. Finally, the output was stratified by management factors (for  
402 example feed type, flooring type) and by farm type to elucidate any potentially significant differences  
403 between farm types.

404

## 405 **3 RESULTS**

### 406 **3.1 Baseline results**

407

408 The average within-batch prevalence of lymph-node positive pigs at slaughter age was estimated to be  
409 0.007 (5th percentile 0, 95th percentile 0.031) for MS1, and 0.176 (0, 0.813) for MS2. The percentage of  
410 positive batches for MS1 and MS2 were estimated to be 0.380 and 0.629 respectively. The distribution of

411 within-batch prevalence (showing only positive batches) is shown in Figure 3. It is clear that most  
412 batches being sent to slaughter are either Salmonella-negative, or infected at a low prevalence. Batches  
413 with a high within-batch prevalence are rarely sent to the slaughterhouse, but it is these high-infection  
414 events that determine the magnitude of the estimated national MS prevalence.

415  
416 INSERT FIGURE 3 HERE  
417

### 418 3.2 Sensitivity analysis and model interrogation 419

420 The results of the sensitivity analysis are shown in Figure 4. For MS2 the average load of Salmonella  
421 shed by sows is dominant (to the point where the other parameters make little difference). However, for  
422 MS1 feed and external contamination parameters are relatively much more important than the load shed  
423 by the sows (although ultimately the variability associated with the within-batch prevalence is still largely  
424 driven by the average load shed by piglets and weaners within the batch). Further investigation (not  
425 shown) supports the results of the sensitivity analysis; if a sow/pig sheds Salmonella the relative  
426 contribution of the sow/pig to the dose ingested by susceptible pigs is typically much larger than that  
427 contributed by contaminated feed and/or contaminated wildlife faeces.

428  
429 INSERT FIGURE 4 HERE  
430

431 Figure 5 summarises the impact of each source of infection in determining the slaughter pig prevalence  
432 within the two case study MSs. Within MS2 reducing breeding herd prevalence to zero (i.e.  $p_{herd} = 0$ )  
433 removes the vast majority of infections at depopulation; conversely, removing feed or external  
434 contamination as sources does little to change the national pig prevalence. Again, this result suggests that

435 the sow is a major source of infection; only when sow infection is rare (as in MS1), does feed play an  
436 important role in determining slaughter pig prevalence.

437

438 INSERT FIGURE 5 HERE

439

440 Given the above results, further scenario analysis showed that national breeding herd prevalence was  
441 strongly correlated with slaughter pig prevalence (in fact, this was the only MS-dependent parameter that  
442 had any major bearing on MS slaughter pig prevalence). Caution must be taken when interpreting this  
443 result, especially as it is assumed that the strain of Salmonella infecting the sows is the one which infects  
444 the pigs all the way through to slaughter (longitudinal studies suggests a much more complex dynamic of  
445 competing strain colonisation <sup>(3, 4)</sup>). However, comparison of breeding and slaughter pig prevalence for  
446 each MS from the respective EFSA baseline surveys suggests that there is at least some correlation  
447 between slaughter and breeding pig prevalence at a MS level (correlation coefficient 0.457, see Figure 6)  
448 <sup>(7, 5)</sup>.

449

450 INSERT FIGURE 6 HERE.

451

452 The dynamics which produce the distributions of within-batch prevalence as shown in Figure 3 were also  
453 considered by analysing pen contamination rates and the subsequent Salmonella doses ingested by pigs.  
454 Comparison of the non-zero doses ingested by pigs on infected farms with the average dose-response  
455 curve for Salmonella infection is shown in Figure 7. Infection is, on average, only more likely to occur  
456 than not occur (i.e.  $p_{inf} > 0.5$ ) for a very small proportion of exposure events (those above  $10^6$  CFUs). This  
457 dynamic corresponds to the results of Figure 3, where the vast majority of batches sent to slaughter are  
458 infected at a very low prevalence level.

459

460 INSERT FIGURE 7 HERE.

461

462 A novel aspect of this model was the inclusion of a number of farm types, based on the characteristics of  
463 the four management factors (feed, flooring, production system, number of sites). Preliminary analysis  
464 showed that there were significant confounding factors with the management data (for example within  
465 MS2, dry feed was far more common on AIAO farms than on continuous production farms). Therefore,  
466 reliable insight can only be generated by observing the results stratified by farm type as a package of  
467 management factors (seeFigure 8). The significant result is that one management factor, the production  
468 system (AIAO versus continuous) dominates the risk by farm type. AIAO production reduces risk to  
469 approximately one third of that for continuous production. The impact of other management factors is  
470 negligible by comparison.

471

472 INSERT FIGURE 8 HERE

473

## 474 **4 DISCUSSION**

475

476

477 The objective of developing the farm model was to describe the dynamics of Salmonella transmission in  
478 pigs in sufficient detail to a) differentiate between the dynamics of infection at a MS level, b) investigate  
479 the sources of infection and the link, if any, between the breeding herd and infection at slaughter and c)  
480 investigate the effect of interventions in reducing slaughter-age prevalence of infection within and  
481 between MSs. Objective (c) is ultimately the primary aim of the model and is discussed in depth in an  
482 accompanying paper<sup>(12)</sup>, but the intention is that the mechanistic approach taken here allows investigation  
483 of the difference of effect of varying interventions across MSs. This is achieved by allowing the user to

484 parameterise the model for individual MSs; the inputs of the model will then directly determine the  
485 outcome of an intervention via the different interactions between model variables at different  
486 parameterisations. For example, an initial condition of the model is the breeding herd prevalence;  
487 differences in this input directly influence the effectiveness of different interventions, hence showing that  
488 feed interventions are not a priority for those MSs that have breeding herd prevalences greater than  
489 around 10%.

490

491 In order to meet the objectives of the model, the methodology of previous Salmonella in pig transmission  
492 models has been modified and advanced (including modelling of the pig environment in detail) <sup>(13, 15, 14)</sup>.  
493 Specifically, we model and parameterise the environmental contamination of pig pens in more explicit  
494 detail than previous models<sup>(14, 15)</sup>. We also explicitly include varying management practices (such as feed  
495 types and production systems) and the sources of pig infection, which has not been done before.  
496 Differentiating between farm types and sources of infection is fundamental in describing the variability  
497 between MSs and the current management factors/sources of infection included do mean that the results  
498 produced for each MS are very different, according to their particular parameter estimation. As a result of  
499 the increased level of modelling detail, the variability between individual pigs, farms and MSs has been  
500 captured to a degree not shown before. This is a much needed development, as variation in infection  
501 dynamics and management is crucial in determining the end result (i.e. Salmonella infection in slaughter-  
502 age pigs) both within and between MSs. The model also allows investigation of specific mechanisms that  
503 could be used to intervene and prevent Salmonella transmission in more detail than has been done before.

504

505 Exposure to Salmonella, and the response to Salmonella infection in pigs, is incredibly variable, as  
506 evidenced by a number of observational and longitudinal studies <sup>(3, 4, 30)</sup>. The model reflects this  
507 variability, hence contamination of the pen can vary between  $10$ - $10^9$  organisms over short time periods;



508 such large variation in contamination unsurprisingly leads to large variation in the amount of Salmonella  
509 ingested by a pig and subsequently the incidence of Salmonella infection. However, in the majority of  
510 situations contamination of the pig environment will result in exposure at a level insufficient to cause  
511 infection. It is only in rare cases, where a sow sheds a high level of Salmonella numbers (or rarer still  
512 when feed or the environment is contaminated at a very high level) that a high incidence of infection  
513 within a batch is predicted. Accordingly, the results of the model suggest that within-batch prevalence is  
514 relatively low. It is the relative contribution of highly-infected batches that determine whether a MS has a  
515 low or high slaughter pig prevalence.

516

517 Management factors applied to each MS are confounded, for example in MS2 dry feed is more likely to  
518 be fed on AIAO farms than continuous ones. Hence, analysis of management factors was only possible at  
519 a broader farm type level. This analysis (shown in **Figure 8**) clearly demonstrates that AIAO production is  
520 by far the most important risk factor of the management factors considered. Indeed, there were negligible  
521 differences between all other farm management factors (for example feed, flooring). It must be pointed  
522 out that the AIAO production system assumed in the model is a theoretical description unlikely to be  
523 achieved in reality on all but the strictest systems of AIAO production. Of note is that it was not cleaning  
524 and disinfection that makes AIAO farms less of a risk, but rather the strict segregation of pigs minimising  
525 the opportunity for spread of infection (indeed, cleaning and disinfection has little impact at all in  
526 reducing prevalence of infection in slaughter-age pigs<sup>(12)</sup>).

527

528 Piglets are able to become infected while still suckling from their mother, although the evidence is mixed  
529 for whether (sero-) positive sows confer maternal immunity to their progeny, hence meaning piglets are  
530 less likely to be infected at the point of weaning, or whether seropositive pigs are more likely to shed  
531 Salmonella and hence result in a higher likelihood of piglet infection<sup>(30, 24)</sup>. It is likely that there is a

532 delicate balance between the strength of immunity and the strength of the burden of infection, which  
533 sometimes results in immunity or infection dependent on the strength of each. Within these studies there  
534 is the indication that infection in piglets could be under-estimated because of a high likelihood of false  
535 negatives. Indeed, the studies referenced were relatively small given the number of animals followed –  
536 there is certainly the probability they simply didn't sample any highly-infected piglet groups because  
537 these are relatively rare. However, the broad consensus from these studies is that it is not until weaning  
538 (when piglets are faced with the double stresses of being weaned and mixed with other unfamiliar pigs)  
539 that a significant proportion of pigs may become infected with Salmonella. Comparing the model and  
540 these findings, the broad trends are certainly the same as observed in these studies. Infection in piglets is  
541 rare and usually at a low incidence rate. While stress/feed change during weaning is not explicitly  
542 modelled, pigs are mixed together. The larger amount of Salmonella shed by weaners relative to piglets,  
543 and the fact there are more pigs directly exposed to this Salmonella, means that the peak prevalence of  
544 infection is usually observed during the weaning period. There is generally a diminishing prevalence of  
545 infection at the point of slaughter. This agrees with current observational data <sup>(4, 31)</sup>.

546

547 While the model mathematically describes more variability than most equivalent models, not all factors  
548 that describe variability in Salmonella risk in individual slaughter pigs between farms or between MSs  
549 have been included. Indeed, the variability included is limited to the data available for quantitative  
550 modelling. For example, most management factors have been split into dichotomous options: wet/dry  
551 feed, solid/slatted flooring, AIAO/continuous production. However, in reality the options available for  
552 each factor are multiple and complex. The following potentially important factors have not been included  
553 in the farm model: further differentiation between feed types (for example pelleted versus non-pelleted),  
554 clustering of Salmonella in faeces, varying growth rate (such that pigs are held back in production), and  
555 transmission dynamics between sows. Further differentiation between feed types would have been

556 difficult to parameterise, but could potentially be important. However the difference in risk between  
557 wet/dry feed was assessed to be the largest of all potential feed type combinations, and this difference in  
558 risk was negligible when compared to the difference in risk between AIAO and continuous production.  
559 Clustering of Salmonella in faecal material has been modelled before <sup>(32)</sup>, but would also require a more  
560 complex model. The effect of clustering in faeces would be to vary (even more so) the daily exposure of  
561 pigs to Salmonella, where some pigs would ingest considerably more organisms, and some considerably  
562 less. Over the large number of pigs and timesteps it can be hypothesised that the effect of this clustering  
563 averages out, but this cannot be stated with certainty. In reality, a varying growth rate of individual pigs  
564 means pigs may need to be kept back behind their cohort before reaching the correct weight to be moved  
565 into a different stage of production or sent to slaughter. This has not been included because of the  
566 difficulty in including any variation in pig group size (computationally pig cohorts are represented as  
567 matrices, and matrix manipulation is only possible with identical or compatible matrices). Keeping  
568 certain pigs back and allowing more mixing between cohorts would almost certainly increase the spread  
569 of infection within the model, as the allowance for contact between cohorts in continuous production  
570 systems within the model is one of the greatest upward pressures on prevalence for the prevalence of  
571 infection in slaughter pigs.

572

573 Important data gaps highlighted by the model development were the (variation in) dose-response of pigs  
574 to infection, the movement of faecal material and the amount of Salmonella that might be present in the  
575 environment due to feed or other external sources of contamination (rodents, birds etc). However, for all  
576 information gathered for this model, the trend was that regardless of the type of data needed, it was  
577 unlikely that current observational, experimental, longitudinal or survey data would be sufficient to be  
578 confident that all the variability had been accurately captured (for example the amount of Salmonella shed  
579 by a sow is based on one study that shows high variation between pigs – but did they capture the entire

580 range of variation?). Given the importance of the breeding herd in seeding infection through the pig  
581 production chain, there is a distinct lack of quantitative information to model this crucial area. Better  
582 information on the duration of sow infection, the variance in the shedding rate when infected (and  
583 whether this is dependent on pregnancy) and the sources of sow infection would be needed before much  
584 more extensive modelling could be done in this area. Hence, as with all models, the results produced  
585 must be viewed in conjunction with the simplifying assumptions made, which were necessary both  
586 because of the need to reduce the complexity of a highly variable pig production system across the EU  
587 and the data gaps that result because of this complex system.

588

589 It is difficult to quantitatively validate the current farm transmission model, as quantitative data are  
590 scarce. However, qualitatively the farm transmission model appears to agree well with observed data,  
591 and replicates a number of important trends observed in the field (for example relationship between  
592 breeding herd prevalence and MS-level slaughter pig prevalence, peak and troughs in prevalence at  
593 weaning and finishing, extremely variable nature of infection, and the difference between AIAO and  
594 continuous production). The results of the combined Farm and Transport & Lairage models for slaughter  
595 pig lymph node prevalence in the two case study MSs compared well to the results of the EFSA slaughter  
596 pig baseline survey <sup>(5, 18)</sup>. In summary, given the need to balance potentially myriad risk factors against  
597 the need for a parsimonious model that uses reliable data, we are of the opinion that the model provides a  
598 useful summary of the variation that is sufficient to describe the relative importance of different risk  
599 factors between farms and MSs and provides a strong platform for investigating on-farm interventions.

600

601 Another validation approach is to compare our results with recent, similar models. Such a comparison  
602 identifies the progressive complexity required to model interventions by incorporating environmental  
603 contamination and considering the contact structure of pigs through commercial pig production systems

604 <sup>(33, 14, 34)</sup>. The result of these previous models is that “super-shedding” sows or pigs are key drivers of  
605 infection; as we have found, Berriman et al. <sup>(33)</sup> also note that cleaning and disinfection is essentially  
606 made redundant if there are super-shedding pigs entering the rooms after cleaning. Minimising contact of  
607 susceptible pigs with these super-shedding pigs is crucial if spread of infection is to be controlled, hence  
608 why AIAO production is the most important management factor in controlling Salmonella. In short, most  
609 recent models for Salmonella in pigs are in agreement that explicit consideration of the batch  
610 management system and the variability in shedding and/or environmental contamination is absolutely  
611 necessary for accurate representation of infection dynamics. The model presented here advances the  
612 methodology by including a data-based dose response model for pig infection, as well as incorporating  
613 several different farm management practices and three sources of Salmonella infection.

614

615 Analysis of the model pointed to one overwhelming conclusion: the level of infection within a MS’s  
616 breeding herd largely determines the slaughter pig prevalence for that MS. The analysis showed that if  
617 the sow is infected and shedding at high levels, then commonly (although not always) this will mean one  
618 or more piglets will become infected: when this occurs then the shedding of Salmonella by infected pigs,  
619 at the farrowing stage or later, dominates the risk (as once a slaughter pig is infected, the subsequent  
620 shedding of Salmonella more than outweighs the contribution of contamination within the environment  
621 provided by feed and/or the external environment). Such a phenomenon is also hypothesised as a major  
622 risk factor for cattle “super-shedding” VTEC O157 <sup>(35, 36)</sup>. However, in low prevalence MSs of which  
623 MS1 is typical, infection of the sow is relatively rare (such that it is unlikely that a “super-shedder” sow  
624 will occur in the 500 days of production modelled) and the proportion of initial infections of a piglet,  
625 weaner etc... via either feed or external contamination are relatively much higher. This result of breeding  
626 herd prevalence determining slaughter pig prevalence is supported by data from the EFSA Salmonella in  
627 pig surveys; breeding herd prevalence was correlated, at least to some degree, with slaughter pig

628 prevalence <sup>(7, 5)</sup>(although the low correlation coefficient may be the result of sampling bias/errors, it could  
629 also represent variation in MSs that our model has yet to capture). Incoming infected pigs are also  
630 considered to be a primary source of infection for weaning and finishing houses <sup>(8)</sup>. In summary, breeding  
631 herd prevalence is likely to be a strong predictor of national pig prevalence for many MSs and feed only  
632 becomes an important source of infection once contamination of the environment by sows or other  
633 slaughter pigs is reduced to low levels.

634

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764 **6 Tables**

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766 Table I: Description of management factors included within the farm model.

<b>Management factor</b>	<b>Description</b>
<i>One site or two-site farm</i>	Two types of farm are considered: farms rearing slaughter pigs from birth to slaughter weight (breeder-finisher) or farms rearing birth to approximately 8 weeks old and then transferring pigs to a specialist finisher site (breeder-weaner and finisher only). These two types are considered sufficient to capture differences in transmission that would occur through transport of pigs during production.
<i>All-in-all-out versus continuous production</i>	All-in-all-out (AIAO) production has been shown to be a protective factor for Salmonella infection <sup>(37, 38)</sup> . AIAO production as modelled is the theoretical ideal; batches of pigs are kept together in one room for each of the weaning, growing and finishing stages without any direct contact with any other batches all the way through rearing. All other systems are termed “continuous”.
<i>Indoor versus outdoor production</i>	Outdoor production has become more popular for large-scale production within the last couple of decades. According to data from the EFSA baseline survey for breeding pigs <sup>(7)</sup> large-scale outside production is still quite rare for pigs beyond the stage of weaning, and therefore only the farrowing stage is included as a possible outside production stage.
<i>Feed type</i>	Feed can be both a source of Salmonella infection in pigs and a factor in determining the level of transmission. As with management systems, feeding systems are variable between farms. Of particular importance is whether the feed is presented in a dry or wet form, or whether it is pelleted or non-pelleted <sup>(39, 30, 38)</sup> . Only the distinction between wet or dry feed is assumed because there is some information on the relative effect of wet/dry feed on the prevalence of Salmonella infection in pigs and good information on whether a farmer uses wet/dry feed from the EFSA baseline survey for breeding pigs <sup>(7)</sup> .
<i>Flooring type</i>	While the evidence for flooring type affecting Salmonella transmission is varied <sup>(37, 40)</sup> , logical thinking suggests that properly maintained slatted flooring may well have some effect as it will remove faeces/Salmonella from the pig environment. Again, there are many flooring types (partially slatted, bare concrete, straw-laden), but it is not possible with current data to differentiate between individual types of flooring, and hence only the distinction between slatted and solid flooring is considered.

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768 **Table II:** Estimates for farm management parameters.

Notation	Description	Stage*	Unit	Value (for large and small farms unless otherwise stated)	Comment/reference
$n_{pig}$	Number of pigs within a pen	Far W G Fin	-	11 40 40 40	Far - 1 sow, 10 piglets (41-43)
$n_{pen}$	Number of pens within a room/building	Far W G Fin	-	Large 16 Small 10 AIAO 4 Cont (Large 16 Small 10) AIAO 4 (Large 24 Small 10) AIAO 4 (Large 24 Small 10)	Assumed
$n_{room}$	Number of rooms within a building	Far W G Fin	-	1 Large 4 Small 1 Large 6 Small 1 Large 6 (2 buildings) Small 1 (1 building)	Assumed
$wa$	Age at weaning		Day	28	(41-43)
$ga$	Growing period		Day	Large 42 Small 28	(43)
$fa$	Finishing period		Days	Large 84 Small 63	(43)

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777 **Table III: Structure of case study MS pig populations reflected using the percentage of slaughtered head production that is reared through each farm type (raw data**  
 778 **provided from EFSA breeding pig survey <sup>(7)</sup> and a MS2 research project <sup>(31)</sup>.**

Farm type	Case study member state					
	MS1			MS2		
	Breeder-Finisher	Breeder-weaner	Finisher only <sup>+*</sup>	Breeder-Finisher	Breeder-weaner	Finisher only <sup>+*</sup>
I - A - So - D	0.00%	0.00%	0.00%	8.09%	4.94%	52.26%
I - A - So - W	3.30%	3.85%	3.30%	2.73%	0.21%	11.56%
I - A - SI - D	3.30%	5.13%	3.30%	20.50%	15.05%	18.59%
I - A - SI - W	20.88%	28.21%	20.88%	6.91%	0.63%	4.28%
I - C - So - D	0.00%	0.00%	0.00%	11.89%	3.86%	7.91%
I - C - So - W	10.99%	7.69%	10.99%	4.01%	0.16%	1.82%
I - C - SI - D	1.10%	3.85%	1.10%	30.12%	11.77%	2.93%
I - C - SI - W	45.05%	35.90%	60.43%	10.15%	0.49%	0.67%
O - A - So - D	0.00%	1.28%	0%	0.48%	8.37%	0%
O - A - So - W	1.10%	0.00%	0%	0.16%	0.35%	0%
O - A - SI - D	0.00%	0.00%	0%	1.22%	25.51%	0%
O - A - SI - W	5.49%	3.85%	0%	0.41%	1.06%	0%
O - C - So - D	0.00%	0.00%	0%	0.71%	6.55%	0%
O - C - So - W	4.40%	5.13%	0%	0.24%	0.27%	0%
O - C - SI - D	0.00%	0.00%	0%	1.79%	19.96%	0%
O - C - SI - W	4.40%	5.13%	0%	0.60%	0.83%	0%

779 Key: I – Inside, O- Outside, A – AIAO production, C – Continuous production, So – Solid floor, SI – Slatted floor, D – Dry feed, W – Wet feed

780 \* Breeding survey does not include finisher-only farms.

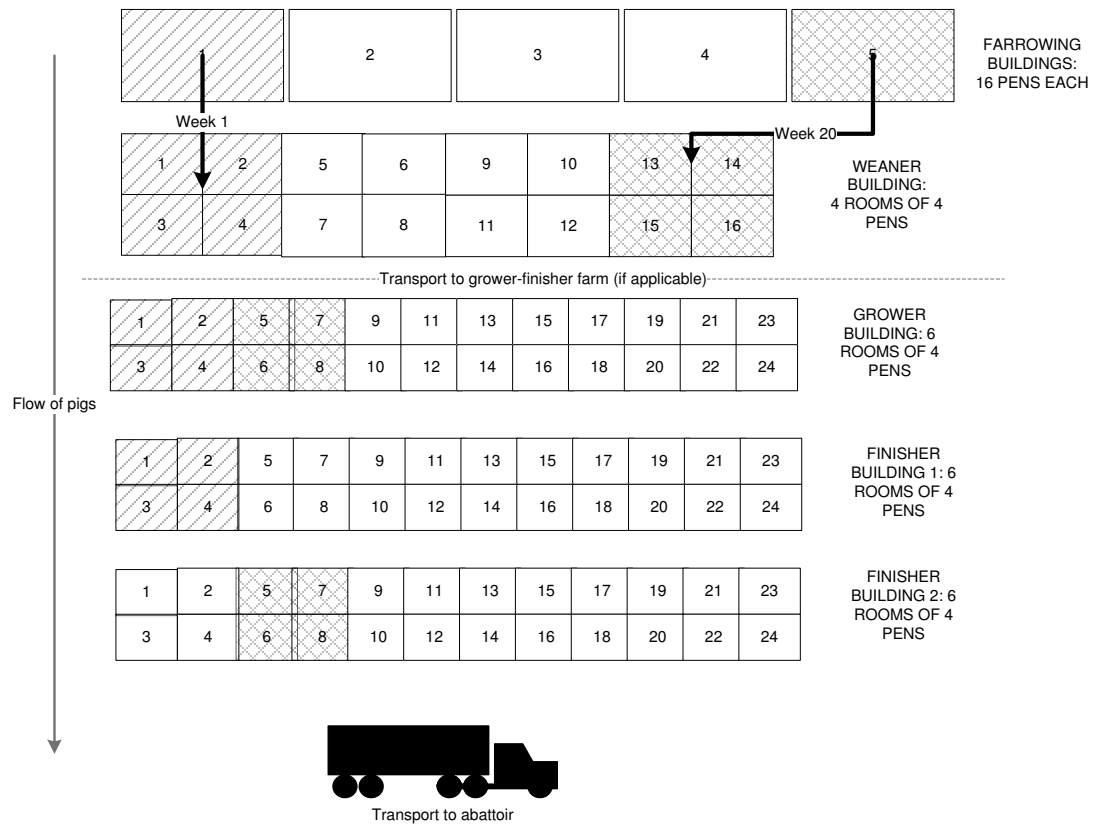
781 \* Breeding survey does not include finisher-only farms; it was assumed that finisher-only farms have same proportions as breeder-finisher farms.

782 + Given negligible production from outside sources, for simplicity we assume only piglets reared outside; therefore outside production for finisher-only farms set to 0% (remainder added to most common type)

**Table IV: Estimates for parameters relating to Salmonella infection.**

Notation	Description	Units	Value/Distribution	Source
<i>Source of infection</i>				
$p_{herd}$	National prevalence of Salmonella-positive breeding herds	-	MS1: 0.059 MS2: 0.44	<sup>(7)</sup>
$p_w$	Prevalence of infection within a breeding herd	-	MS1: 0.21 (MS2) MS2: 0.21	<sup>(7)</sup>
$p_{feed}$	Probability of feed lot contamination	-	0.10	Assumed from <sup>(25, 44)</sup>
$f_{sow}(j,t)$	Mass of faeces defecated by sow per day	g	N(3000,150)	<sup>(42)</sup> . S.D. assumed
$g$	Amount of feed consumed per day at stage H: Weaners ( $H=wean$ ), Growers ( $H=grow$ ), Finishers ( $H=fin$ )	g	Wean (~6 wks): 500 Grow (~12wks): 1620 Fin (~18wks): 3200	<sup>(45)</sup>
$c_s$	Concentration of Salmonella in contaminated sow faeces	CFU/g	LogNormal(2.36,4.39)	<sup>(31)</sup>
$c_f$	Concentration of Salmonella in contaminated pig feed	CFU/g	GPareto(0.001,0,1)	<sup>(46)</sup>
$\lambda_e$	Concentration of Salmonella in external environment	CFU/g	LogNormal(0.1,3)	<sup>(22)</sup>
<i>Transmission</i>				
$f$	Mass of faeces defecated by piglet per day Mass of faeces per day; weaner Mass of faeces per day; grower Mass of faeces per day; finisher	g	N(100,10) N(753,50) N(1194,50) N(2580,50)	<sup>(45)</sup> (assumed S.D.) <sup>(47)</sup> assumed S.D.
$c_p$	Concentration of Salmonella in contaminated pig faeces	CFU/g	0-10 <sup>6</sup> CFU/g (see text)	<sup>(3)</sup>
$\beta_{F,day}$	Removal coefficient for fresh faeces on slatted flooring	-	Beta(40,10)	Assumed
$\beta_{F,old}$	Removal coefficient for old faeces on slatted flooring	-	Beta(2,10)	Assumed
$\beta_C$	Cleaning coefficient for solid flooring Cleaning coefficient for slatted flooring	-	Beta(3,2) Beta(1,2)	Assumed
$\beta_{xc}$	Cross-contamination coefficient	-	Beta(1,10)	Assumed
$\delta$	Decay constant	day <sup>-1</sup>	0.04	<sup>(48, 49)</sup>
$\mu$	Mass of faeces ingested by piglets per day Mass of faeces ingested by weaners/growers/finishers per day	g	U(0,21) U(0,100)	<sup>(50, 51)</sup> Based on <sup>(52)</sup> and expert opinion
$\alpha_{DR}, \beta_{DR}$	Parameters of dose response model	-	Wet: $\alpha_{DR}$ , 0.1766; $\beta_{DR}$ 50235 Dry: $\alpha_{DR}$ , 0.1766; $\beta_{DR}$ 20235	<sup>(28, 21)</sup>
$t_{LN}$	Duration of intermittent shedding	days	Weibull(44.94,1.68)	<sup>(3)</sup>

786 **Figures**



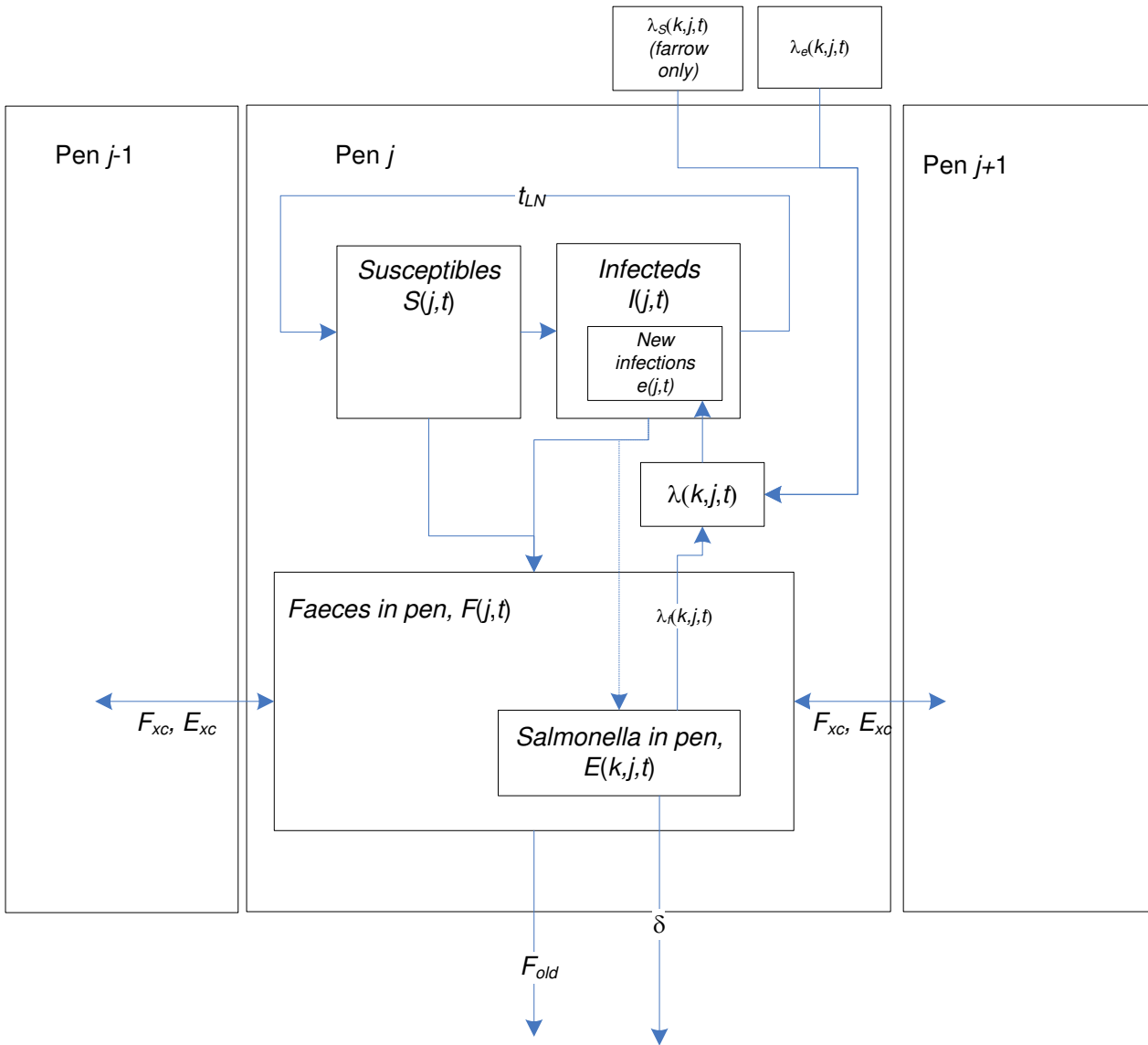
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788 **Figure 1:** Schematic of pig flow through generic large farm system as modelled. Pigs are reared through 4 distinct stages:  
 789 farrowing (4 weeks - upon which one batch of pigs from farrowing building is mixed into 1 room of 4 pens in weaner  
 790 building), weaning (4 weeks), growing (6 weeks) and finishing (12 weeks). Examples of flow are given by shaded  
 791 annotations: i) single-hatched; piglets are weaned and grouped into batch of 4 pens within one weaner room at the start of  
 792 Week 1, moved to growing accommodation on Week 5, finishing accommodation on Week 11 and slaughtered on Week 23; ii)  
 793 double-hatched; new group of sows moved into vacated farrowing building 5 on Week 16; piglets are weaned at start of Week  
 794 20 and pass through rooms in subsequent accommodation as they become empty at the time where movement occurs.

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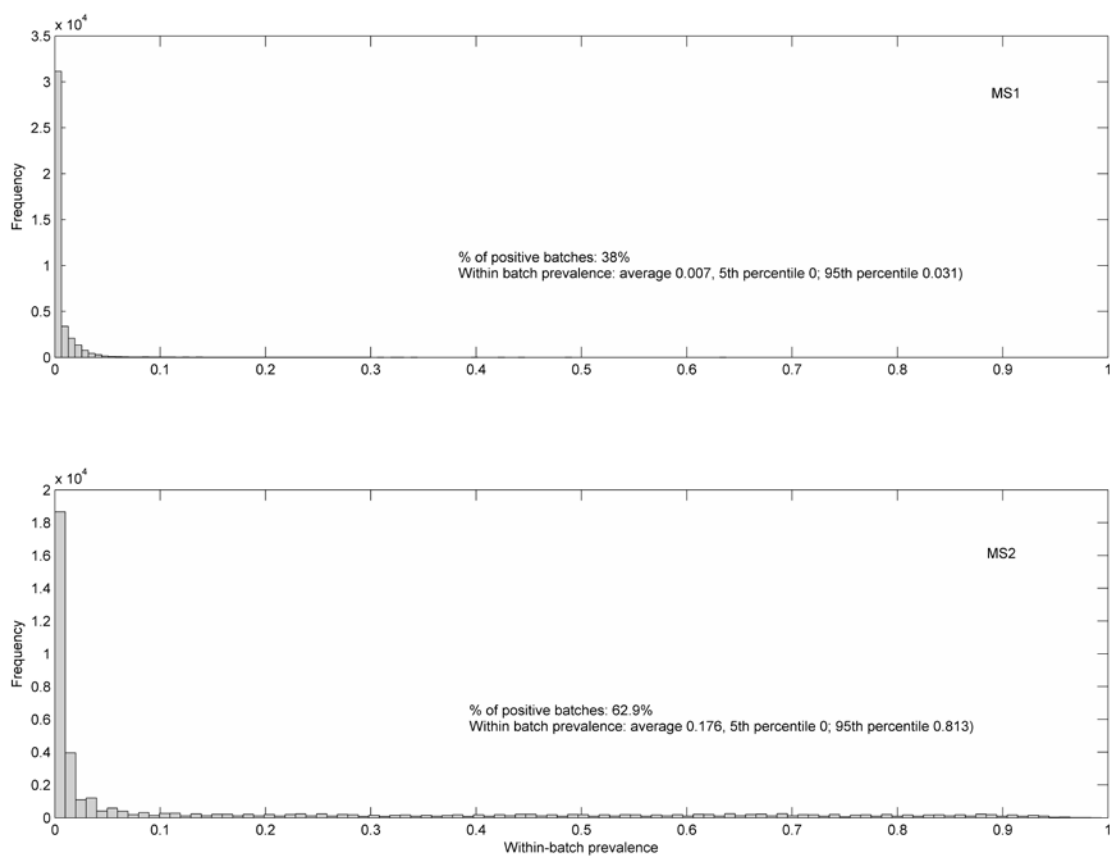
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**Figure 2:** Schematic diagram of transmission model. Only the interactions associated with pen(j) are shown. The total faecal material in the pen,  $F(j,t)$ , is added to each day by Susceptibles ( $S(j,t)$ ), Infecteds ( $I(j,t)$ ) and cross-contamination from other pens ( $F_{xc}$ ) while it is simultaneously reduced each day via cross-contamination ( $F_{xc}$ ) or removal,  $F_{old}$ . This faecal material contains  $E(j,t)$  salmonellas, which are added to each day from the infected group via shedding in their faeces and reduced each day as a result of decay,  $\delta$ , and cross-contamination  $E_{xc}$ . Pigs ingest  $\lambda_i$  organisms per day via the amount in the faeces,  $\lambda_f$  via feed and  $\lambda_e$  via the environment (and  $\lambda_s$ , organism from sow faeces if piglets during farrowing). This process results in  $e(j,t)$  new infections according to the dose ingested and the dose-response relationship applied.

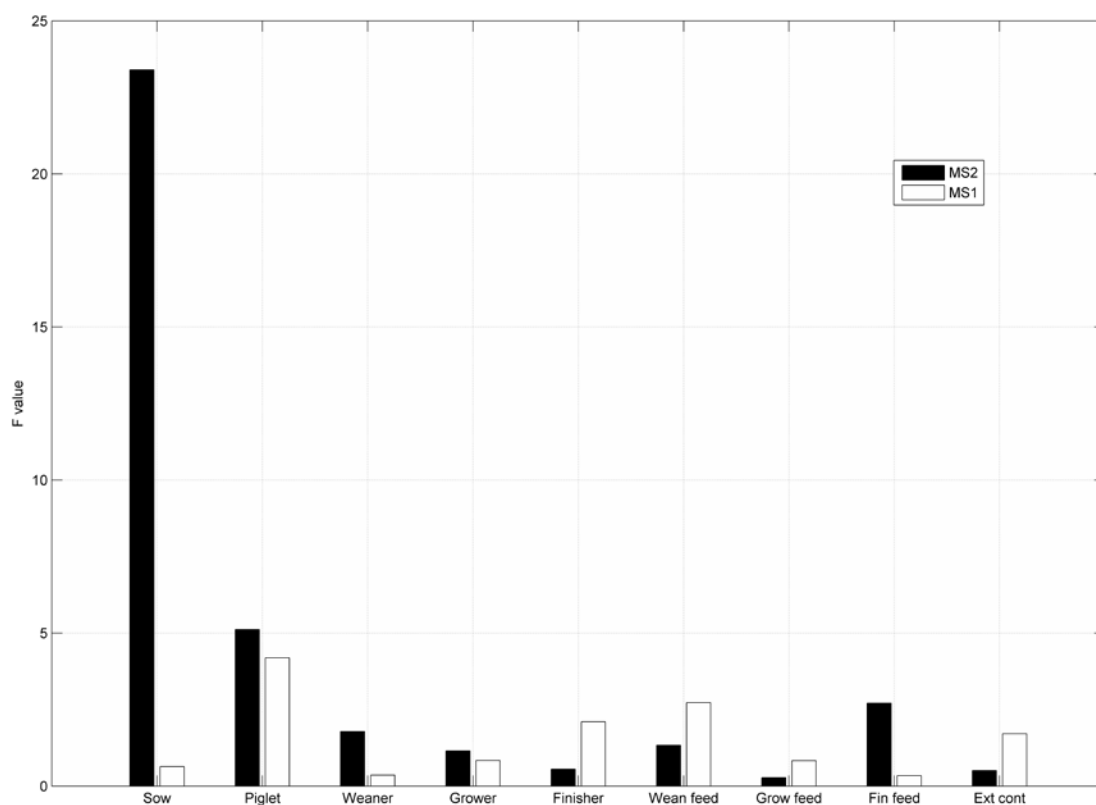
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**Figure 3:** Distribution of within-batch prevalence at the point of pigs being loaded onto slaughterhouse transport. The majority of batches are either Salmonella –negative or infected at a low prevalence.



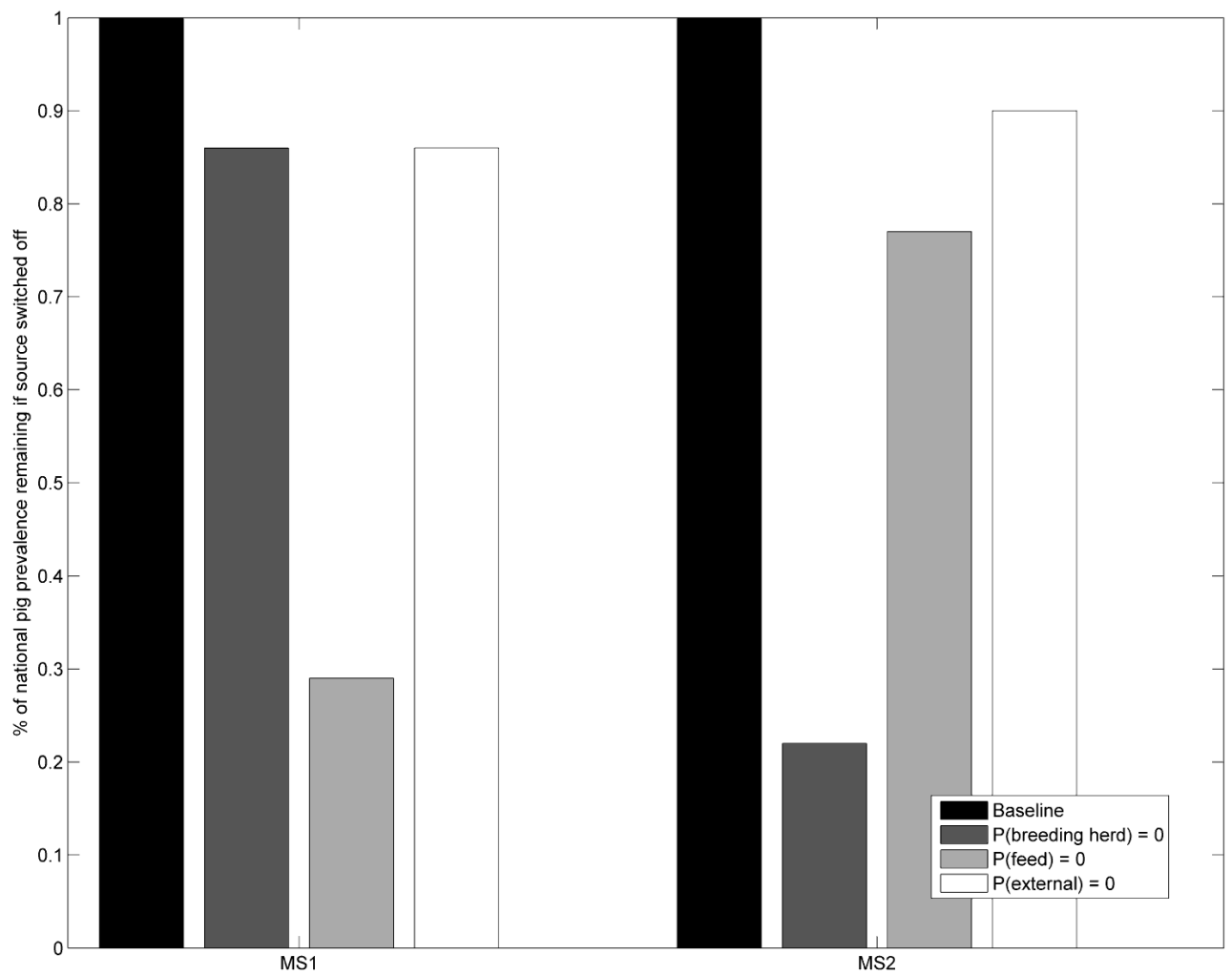


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816 **Figure 4:** Sensitivity analysis for MS2 (high prevalence) and MS1 (low prevalence). The response variable is the prevalence of  
 817 infection within a batch of pigs being sent to slaughter. Sow – average number of Salmonella shed by sows that gave birth to  
 818 pigs within batch, Piglet, Weaner, Grower, Finisher – average number of Salmonella shed by piglets, weaners, growers and  
 819 finisher pigs respectively, Wean feed, Grow feed, Fin feed – average number of Salmonella contaminating feed during  
 820 weaning, growing and finishing periods of the batch, Ext cont – average external contamination dose ingested by pigs during  
 821 rearing period of batch. For MSs with high breeding herd prevalence (MS2) the load shed by the sow is the most important  
 822 parameter in the model, as this provides an initial burden of infection for piglets. If the breeding herd prevalence is low (MS1)  
 823 then the amount of Salmonella in the feed becomes relatively more important (although the amount of Salmonella shed by  
 824 piglets is the factor with the largest F value).

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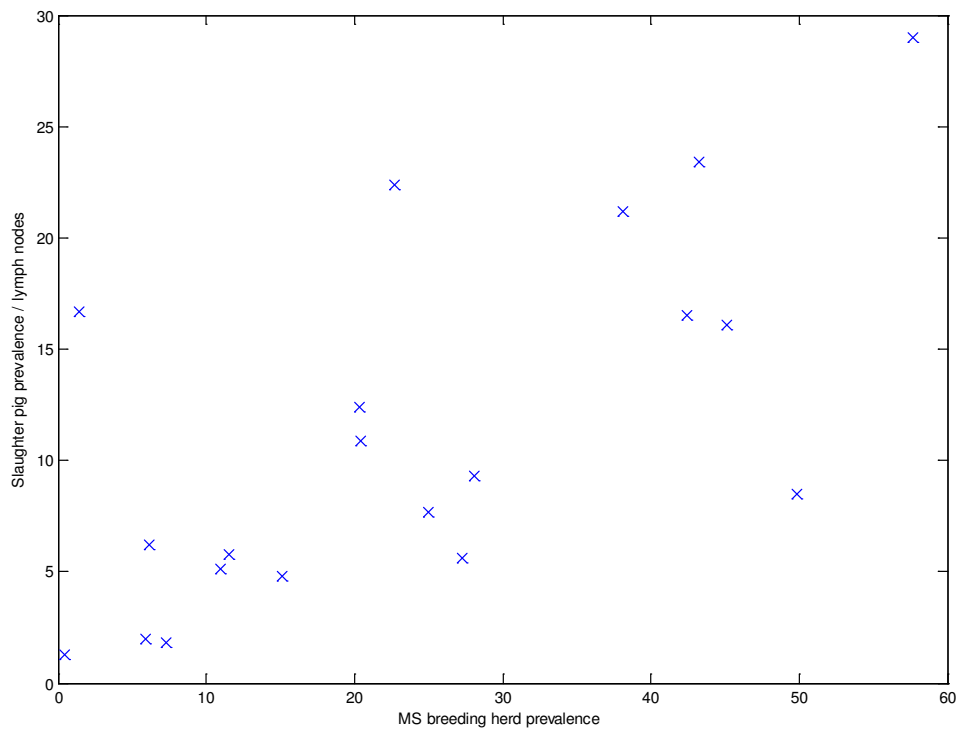
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828 **Figure 5: Relative impact on national pig prevalence for each MS if each source of infection is set to zero. Baseline (black),**  
 829 **breeding herds all negative (dark grey), feed all negative (light grey), no external contamination events (white).**

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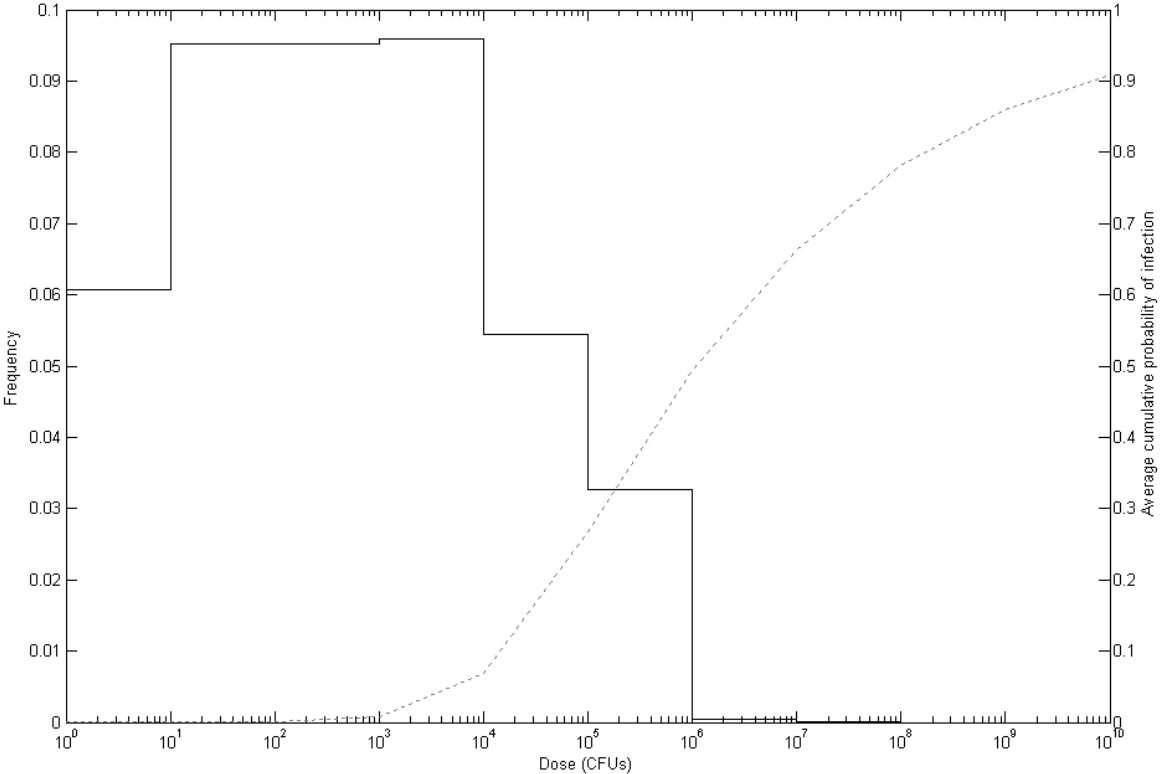


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834 **Figure 6:** Plot of breeding pig herd prevalence within EU MSs (x-axis) vs slaughter pig prevalence.

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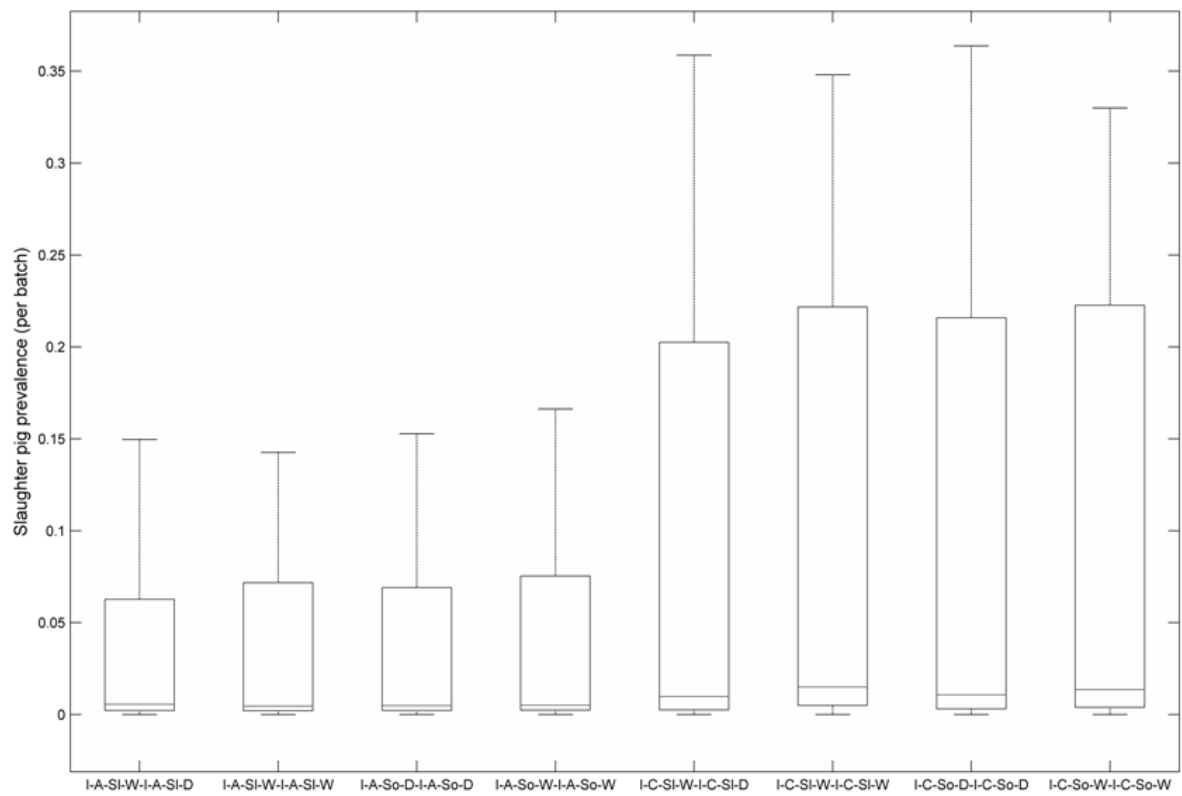


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841 **Figure 7:** Comparison of doses ingested by individual pigs (from all stages of production) (solid line – left hand y axes) against  
842 the average probability of infection (using only non-zero doses from the model) (dotted line – right hand y axes). The majority  
843 of doses ingested by pigs (from faeces, feed and external contamination) are unlikely to result in infection at the average  
844 probability of infection. Note different scales of two y axes.

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852 Figure 8: Stratification of output by farm type (for clarity only MS2 inside breeder-finisher herds shown, however results apply  
 853 to all types). Only significant management factor is production system; the average prevalence in AIAO farms is around one  
 854 third of that for continuous farms (~0.03 compared to ~0.1). Other management factors did not have any significant effect.  
 855 Key: I – Inside, A – AIAO production, C – Continuous production, So – Solid floor, SI – Slatted floor, D – Dry feed, W – Wet  
 856 feed

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