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Modelling *Salmonella* transmission among pigs from farm to slaughterhouse: Interplay between management variability and epidemiological uncertainty

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ABSTRACT

Salmonella carriage and cutaneous contamination of pigs at slaughter are a major risk for carcass contamination. They depend on *Salmonella* prevalence at farm, but also on transmission and skin soiling among pigs during their journey from farm to slaughterhouse. To better understand and potentially control what influences *Salmonella* transmission within a pig batch during this transport and lairage step, we proposed a compartmental, discrete-time and stochastic model. We calibrated the model using pork chain data from Brittany. We carried out a sensitivity analysis to evaluate the impact of the variability in management protocols and of the uncertainty in epidemiological parameters on three model outcomes: prevalence of infection, average cutaneous contamination and number of new infections at slaughter. Each outcome is mainly influenced by a single management factor: prevalence at slaughter mainly depends on the prevalence at farm, cutaneous contamination on the contamination of lairage pens and new infections on the total duration of transport and lairage. However, these results are strongly affected by the uncertainty in epidemiological parameters. Re-excretion of carriers due to stress does not have a major impact on the number of new infections.

1. Introduction

Human salmonellosis is the second most common foodborne zoonosis in the European Union (EU) and it is frequently attributed to the consumption of pork products (Hald et al., 2003; Pires and Hald, 2010). According to surveillance estimates by the European Food Safety Authority (EFSA), *Salmonella* is endemic in the pig population: around 10% of pigs at slaughter have infected lymph nodes and around 8% of the processed carcasses are contaminated (European Food Safety Authority, 2008). In order to reduce the incidence of human salmonellosis, EU states are required to monitor each stage of the pork supply chain and urged to adopt control strategies ensuring pig health and welfare, depending on their country-specific pig industry, herd statuses, slaughterhouse structures and compliance with hygienic measures (EFSA Panel on Biological Hazards (BIOHAZ), 2010).

Non-negligible transmission rates during pig transport and lairage were reported, both among animals belonging to the same herd and across herds (Hurd et al., 2001a, 2001b). Transmission occurs primarily *via* the faecal–oral route: a healthy pig gets infected after ingesting a large number of microorganisms. In turn, infected individuals intermittently excrete large numbers of the bacteria in their faeces, contaminating their local environment. Stress imposed by food withdrawal, transportation, or lairage can significantly increase the number of shedding pigs, as well as the amount of both excreted and ingested *Salmonella* (Scherer et al., 2008).

There is strong evidence showing that prevalence at slaughter depends on (i) the proportion of animals shedding at departure from farm (Boughton et al., 2007), (ii) the degree of environmental contamination and (iii) the duration of exposure to this contamination (Hurd et al., 2001a; Mannion et al., 2012). However, there is a wide diversity in the epidemiological status of pigs departing from farms (European Food Safety Authority, 2008), in the transport conditions and in the exposure to environmental contamination (Rostagno et al., 2003), both at an individual level and at a batch level (Hernández et al., 2013). Moreover, many epidemiological characteristics of *Salmonella* spread remain highly uncertain, for instance: the dose–response relationship between the environmental contamination and the infection probability of healthy pigs (Boughton et al., 2007; Loynachan and Harris, 2005), the excretion rate of shedders (Ivanek et al., 2012; Martín-Peláez et al., 2009; Tanaka et al., 2014), or the rate of stressed non-shedding carriers reverting to excretion (Scherer et al., 2008). This prevents drawing definite conclusions regarding the relative impact of factors on the risk of carcass contamination (Rostagno and Callaway, 2012).

The complex interplay between biological and management processes affecting *Salmonella* transmission appeals for a modelling approach to

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evaluate the impact of different factors at different levels of the production chain (Hotes et al., 2012; Smid et al., 2012). Mechanistic models have been successfully implemented at a farm level (Berriman et al., 2013; Hill et al., 2015; Lurette et al., 2008). Transport and lairage are usually not represented, with the notable exception of an EFSA scientific report (VLA, DTU, RIVM, 2010), which performed a quantitative microbial risk analysis of the pork production chain to investigate the effect of interventions at different points of the food chain (Schaffner and Doyle, 2008). It resulted in a hierarchy of control measures and an estimation of their impact on the public health risk of salmonellosis. The model describing transmission during transport and lairage was recently detailed (Simons et al., 2015).

In line with these communications, an exhaustive exploration of the interactions between management conditions and epidemiological settings in a batch during transport and lairage was carried out. The aim of this study was to assess their relative impact on the epidemiological status of pigs at slaughter under different transmission regimes, while considering the internal carriage and cutaneous contamination, as both can lead to (cross-)contamination during slaughter. The impact of the slaughter processes on carcass contamination is outside the scope of this study.

2. Material and methods

2.1. Model description

This work presents a discrete-time stochastic epidemiological model that follows a single batch from farm to slaughter considering three stages: waiting at farm (stage F), transport by truck (stage T) and waiting at lairage (stage A), as shown in Fig. 1a. The time spent in each stage is given by the stage duration t_X. The batch is characterised by its epidemiological state $B(t)$ at time t, describing the number of healthy (S), latent (E), actively shedding (I) and non-shedding carrier (R) pigs (Fig. 1b), and by its average cutaneous contamination $C(t)$, which represents the average skin soiling of a pig. Its initial state at time $t_0 = 0$ is defined by three parameters: batch size $b_0 = S(t_0) + E(t_0) + I(t_0) + R(t_0)$, which remains constant over time, *Salmonella* prevalence at farm $p_0 = \frac{I(t_0)+R(t_0)}{b_0}$ and initial cutaneous contamination c_0. At each stage $X \in \{F, T, A\}$, pens are characterised by their final environmental contamination Q_X, initialised by q_X.

The model considers three stochastic processes governing the evolution of the variables from the beginning ($t_{b,X}$) to the end ($t_{e,X} = t_{b,X} + t_X$) of each stage: excretion, transmission and skin soiling (Fig. 1b). Note that the beginning of the waiting at farm corresponds to the initial time ($t_{b,F} = t_0 = 0$) and that stages are connected without lapses (for instance, $t_{e,F} = t_{b,T}$).

To determine the final environmental contamination Q_X, the amount of *Salmonella* shed by active shedders using random samples taken from a normal distribution ($\mathcal{N}$) was computed with:

$$Q_X = q_X + \mathcal{N}\left(\varepsilon, \frac{\varepsilon}{10}\right) I(t_{b,X})\, t_X \tag{1}$$

where ε is the excretion rate. The standard deviation of the excretion rate is set arbitrarily to $\varepsilon/10$, so that the different levels of ε explored in the sensitivity analysis do not overlap. Occasional samples of negative numbers, which very seldom occurred, were replaced by zero.

In the following equations, we dropped the stage subscript X for $t_{X,b}$ and $t_{X,e}$, as there was no possible ambiguity. For each stage, the model updated the number of pigs in each epidemiological state (Fig. 1b) as follows:

$$\begin{cases} S(t_e) &= S(t_b) - N_{S\to E}(t_b, t_e) \\ E(t_e) &= E(t_b) + N_{S\to E}(t_b, t_e) - N_{E\to I}(t_b, t_e) \\ I(t_e) &= I(t_b) + N_{E\to I}(t_b, t_e) - N_{I\to R}(t_b, t_e) + N_{R\to I}(t_b, t_e) \\ R(t_e) &= R(t_b) + N_{I\to R}(t_b, t_e) - N_{R\to I}(t_b, t_e) \end{cases}. \tag{2}$$

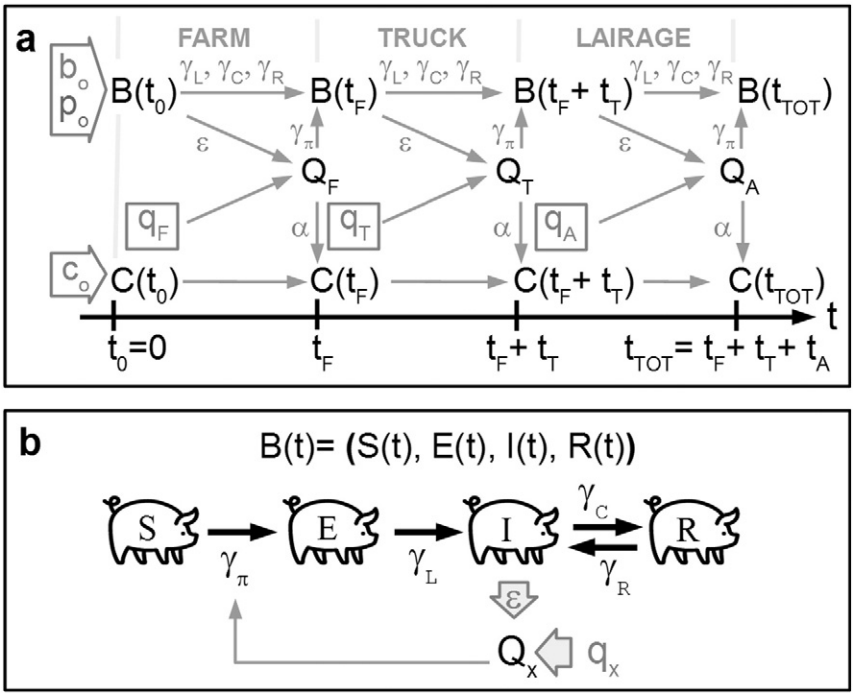

Fig. 1. Outline of the stochastic compartmental model representing *Salmonella* dynamics in a batch from farm to slaughter. (a) The model derives the environmental contamination (Q_X), the epidemic state (B) and the average cutaneous contamination (C) of the batch at each stage (X: F = farm, T = transport and A = lairage), from the batch size (b_0), prevalence at farm (p_0), initial cutaneous contamination (c_0) and environmental contaminations (q_X); it considers *Salmonella* excretion (ε), contamination (γ_π), infection dynamics (γ_L, γ_C and γ_R) and skin soiling (α). (b) The epidemic model considers four infection states (S = healthy, L = latent, I = active shedder and C = non-shedder carrier); faecal–oral transmission (γ_π) is driven by environmental contamination (Q_X), resulting from the initial contamination (q_X) and from shedding (ε); the other transition rates between states (γ_L, γ_C and γ_R) only depend on the stage duration (t_X).