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Quantitative risk assessment of *Campylobacter* in broiler chickens – Assessing interventions to reduce the level of contamination at the end of the rearing period

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ABSTRACT

The European Food Safety Authority (EFSA) has estimated that a proportion ranging from 20% to 30% of campylobacteriosis in humans may be attributed to the consumption of broiler meat and a reduction in the numbers of *Campylobacter* in the intestines of infected birds at slaughter by 3 log units would reduce the public health risk by at least 90%. In this study, a stochastic model was implemented to reproduce the dynamics of *Campylobacter* transmission in broiler flocks and explore the effects of several management conditions and/or on-farm mitigation strategies on the estimated level of contamination of infected flocks at slaughter. Results were expressed as 'proportion of highly contaminated flocks' (%HCFs) and estimated as a function of the proportion of infected birds in the flock the day of final depopulation and the individual level of contamination in infected birds. The effects of the mitigation strategies aimed at reducing the level of contamination in infected birds were modelled assuming that those effects are exerted on the distribution describing the bacterial load in infected birds. The impact of management conditions such as the adoption of enhanced biosecurity measures (B+) and/or partial depopulation during the production cycle (T+) were quantified using results of an extensive epidemiological study conducted in UK. A standard broiler flock was reproduced and used as baseline to make comparisons and simulate the effects of the mitigation strategies of interest. The baseline model predicted 18.8% probability of HCFs at slaughter. A positive effect ranging from −32.44% to −4.78% was attributed to B+ while T+ had negative effect ranging from +17.55% to +86.70%. When both the effects were tested simultaneously (B+T+), results were not conclusive with %HCFs ranging from −20.21% to +77.65%. When mitigation strategies operating on *Campylobacter* concentration in intestine were tested, a reduction of 100% and 99.6% in %HFCs were estimated following a generic treatment with bacteriocins and bacteriophages. Reduction in %HCFs as a function of immunization measures were explored and a reduction of 15% in the rate of transmission led to a %HCFs at slaughter reduced by almost 50%. The model was developed to be flexible, easily reproducible, updatable and adaptable to several baseline scenarios. The main parameters and assumptions underlying the baseline model were tested and a sensitivity analysis was performed to identify and discuss the impact that the uncertainty in the baseline information might have on the outcomes.

1. Introduction

Campylobacter is a major cause of foodborne disease worldwide (Havelaar et al., 2015). The pathogen is believed to be responsible for about nine million cases of human campylobacteriosis per year in countries of the European Union (EU), with an estimated cost to the EU economy of approximately EUR 2.4 billion per year (EFSA, 2015). Chicken meat is a well-known source of *Campylobacter*; in 2010 the European Food Safety Authority (EFSA) estimated that between 20% and 30% of the total cases of campylobacteriosis across the EU can be attributed to the handling, preparation and consumption of broiler meat while 50%–80% may be attributed to the chicken reservoir as a whole (EFSA, 2010). Following a request from the European Commission, the Panel on Biological Hazards in

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2011 issued a scientific opinion on *Campylobacter* in broiler meat production: the control options and performance objectives and/or targets at different stages of the broiler meat chain. The major conclusions were: (i) there is a linear relationship between prevalence of *Campylobacter* in broiler flocks and public health risk and (ii) reducing the numbers of *Campylobacter* in the intestines of chickens at slaughter by 3 log CFU/g units would reduce the public health risk by at least 90% (EFSA, 2011). The opinion concluded that controlling *Campylobacter* in primary broiler production would result in greater public health benefits than interventions at later stages in the food chain. Although the linearity of the relationship should be considered a simplification and interpreted cautiously, a recent review supports the hypothesis that mitigation strategies aimed at reducing the level of contamination of the birds entering the slaughterhouse would result in significant reduction of the risk for human health (Meunier, Guyard-Nicodème, Dory, & Chemaly, 2016). Increased understanding of the dynamics of within flock infection and of the likely impact of interventions on the level of contamination is therefore a public health priority.

Following these considerations, the aim of this study was to quantify the effect of farm-level mitigation strategies on the level of contamination of broiler flocks at depopulation. The proportion of Highly Contaminated Flocks (*%HCFs*) sent to slaughter was used as the unit of comparison. The threshold used to define a flock as 'Highly' contaminated was previously formulated by Georgiev at al. (Georgiev, Beauvais, & Guitian, 2016) and used in their epidemiological study aimed at exploring factors associated with the risk of a broiler flock being highly colonized at slaughter in the UK. Three categories can be distinguished amongst the strategies that were explored: (i) management practices aimed at reducing chicken's exposure to the pathogen (enhancement of biosecurity, avoidance of partial depopulation, early final depopulation), (ii) interventions aimed at increasing the resistance of broiler chickens to colonization (e.g. through vaccination or use of feed additives) and (iii) mitigation strategies aimed at reducing the pathogen's load in the caecal contents of infected birds (bacteriophage therapy and bacteriocins). Factors that reflect the level of biosecurity (e.g. adopting rodent control around the broiler house, changing of footwear and clothes before entering the houses or improvement of the hygiene barriers), adoption of the thinning practice and the slaughter age, have been frequently identified as risk factors for *Campylobacter* colonization in broilers at slaughter (Allain et al., 2014; Bouwknegt et al., 2004; Georgiev et al., 2016; Hansson, Engvall, Vagsholm, & Nyman, 2010; Torralbo et al., 2014). Not surprisingly, control strategies exerting effects on those factors are placed in first position in the hierarchy of control methods reported by EFSA (EFSA, 2011). However, it should be noted that while factors like changing footwear or improving hygiene barriers are easier and relatively cheap to handle, avoiding thinning and earlier depopulation need rigorous cost-benefit analysis.

On the other hand, although results of experiments assessing the efficiency of mitigation strategies aimed at increasing resistance to colonization or reducing the level of the pathogen in caeca are encouraging (Meunier et al., 2016; Robyn, Rasschaert, Pasmans, & Heyndrickx, 2015), further studies to obtain more reproducible results are needed before effective applications of those measures on large scale.

As suggested by Robyn et al., lowering or delaying *Campylobacter* colonization in broiler flocks is likely to be more effective by combining measures directed to prevent the introduction of *Campylobacter* into the flock with measures aimed at lowering *Campylobacter* survival in infected broilers (Robyn et al., 2015).

In our model, the assessment was made by developing a baseline probabilistic model aimed at capturing the dynamics of the within flock transmission of *Campylobacter* in a typical broiler chicken flock and comparing the proportion of highly contaminated flocks obtained under baseline conditions with that obtained when different strategies were implemented. The study includes the findings of an epidemiological study conducted to support the activities of the UK's Food Standards Agency (FSA) and the UK Joint Working Group on *Campylobacter* that generated estimates of the strength of association between management conditions and likelihood of flock colonization at high levels (Georgiev et al., 2016).

2. Materials and methods

2.1. The baseline model

The baseline model, outlined in Fig. 1, was aimed to estimate the proportion of flocks with average contamination level higher than 5.09 log/CFU g as a function of (i) the within flock prevalence (*WFP*) and (ii) the individual level of contamination (log CFU/g) in colonized birds. The baseline model was implemented with the available information and/or data included in studies related to broiler chicken raised in intensive systems in the UK (Georgiev et al., 2016; Goddard, Arnold, Allen, & Snary, 2014). The assessment of the mitigation strategies affecting the pathogen's load in the caecal contents of infected birds was made by adopting the overall effects of the interventions already summarized by EFSA (EFSA, 2011).

One of the main factors driving the model outcome, the *WFP*, can be expressed as the ratio between the number of birds colonized with *Campylobacter* over the total number of birds in the flock. This value is calculated at the day of final depopulation or clearance (*dpday*) and assumed to be dependent on two main factors:

1. The age or day of the cycle at which the flock became colonized
2. The spread of *Campylobacter* within the flock following colonization measured as the rate at which non-colonized birds become colonized

In our model, the first day of colonization defines the moment at which the spread starts, which is in turn dependent on a number of biological variables such as the total number of birds in the flock (*Nb*) and the number of infected birds at t_0 (It_0).

2.1.1. The age at which the flock became infected

The dynamics describing the broiler becoming colonized by *Campylobacter* and the time at which this occurs in a typical broiler flock are largely unknown. Longitudinal studies of broiler flocks raised under commercial conditions, have reported that *Campylobacter* is rarely detected before 10–14 days after the beginning of the production cycle (Bull et al., 2006; Evans & Sayers, 2000; Jacobs-Reitsma, van de Giessen, Bolder, & Mulder, 1995) and for modelling purposes, the first day at which the flock become colonized has been proposed to be adequately described as a uniform random variable between fourteen days and the day of depopulation (FAO/WHO, 2009; Hartnett, Kelly, Newell, Wooldridge, & Gettinby, 2001). While the assumption of the minimum age of flock infection is biologically plausible (i.e. presence of passive immunity) and supported by empirical data, assuming that infection is equally likely to occur on each day of the cycle after day 10 is in conflict with field evidence. Applying a Bayesian model to several longitudinal datasets on *Campylobacter* infection in UK broiler flocks, Goddard et al., estimated that the time at which a flock becomes infected with *Campylobacter* ranges between 10 and 45 days, with a most likely value around 30–35 days (Goddard et al., 2014); thus, we assume the first day of colonization ($Cday^{+}$) can be described as: