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Modeling cross-contamination during poultry processing: Dynamics in the chiller tank

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ABSTRACT

Understanding mechanisms of cross-contamination during poultry processing is vital for effective pathogen control. As an initial step toward this goal, we develop a mathematical model of the chilling process in a typical high speed Canadian processing plant. An important attribute of our model is that it provides quantifiable links between processing control parameters and microbial levels, simplifying the complexity of these relationships for implementation into risk assessment models. We apply our model to generic, non-pathogenic *Escherichia coli* contamination on broiler carcasses, connecting microbial control with chlorine sanitization, organic load in the water, and pre-chiller *E. coli* levels on broiler carcasses. In particular, our results suggest that while chlorine control is important for reducing *E. coli* levels during chilling, it plays a less significant role in the management of cross-contamination issues.

1. Introduction

Poultry contamination by bacterial pathogens such as *Salmonella*, *Campylobacter* and *Escherichia coli* O157:H7, continues to pose a serious threat to public health both in Canada and on the global scale. According to the World Health Organization, 25% of foodborne outbreaks are closely associated with cross-contamination events involving deficient hygiene practices, contaminated equipment, contamination via food handlers, processing, or inadequate storage (Carrasco, Morales-Rueda, & Garcia-Gimeno et al., 2012). As processing has been highlighted as a pivotal juncture in the supply chain, both for preventing and potentially promoting cross-contamination, researchers have conducted numerous studies, attempting to determine pathogen prevalence and concentration at various processing stages. However, the underlying mechanisms of cross contamination are still poorly understood and, furthermore, many studies evaluating the efficacy of intervention strategies during processing have presented inconsistent and even contradictory results. One reason for such issues is that studies were conducted at the lab or pilot scale under specific conditions that leave their results difficult to synthesize (Bucher et al., 2012).

In this work, part one of a series of studies, we develop a mathematical model to gain insight into the main mechanisms of chlorine decay and cross-contamination during the chilling process. This approach is important because of its ability to test mechanistic hypotheses as well as to help streamline experiments that would other wise be expensive both financially and temporally. More specifically, modeling informed insights can be used as cost-effective tools to help describe the mechanisms driving cross-contamination, and to establish unambiguous, quantifiable links between processing control parameters (such as chiller water temperature, wash time, chlorine concentration, carcass to water volume ratio, etc.) and pathogen prevalence and concentration. In turn, the quantified connections between control parameters and pathogen dynamics can provide invaluable information in terms of testing control strategies to keep pathogen levels below thresholds.

While our focus is the chiller process of a typical modernized Canadian poultry inspection program plant (high speed), our model can be easily generalized to chiller processes in other locales. Also,

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the modeling framework and techniques can be modified to describe similar mechanisms in the process of defeathering, evisceration and scalding. We describe the background and modeling formulation in Section 2. In Section 3 we apply our model to generic, non-pathogenic *E. coli* contamination of broiler carcasses, discuss detailed parameter estimation, and perform sensitivity analysis. Using the results of the sensitivity analysis, we discuss thresholds within which cross-contamination and chlorine control play a lesser role as well as when cross-contamination may pose a more significant risk. Also, in Section 3, we compare model predictions for *E. coli* levels on poultry exiting the chiller tank when free chlorine (FC) input is used at 50 mg/l or not at all. These results are given in terms of USDA baseline values. In addition, we examine the dynamics of FC inactivation via the organic load in chiller red water, *i.e.*, chiller water that has been exposed to poultry carcasses, organic material and possibly pathogens. In the final section, we suggest some quantified rules of thumb for managing cross-contamination issues and discuss the feasibility of developing more complex models and of simplifying the complexity of cross-contamination models for relatively easy implementation.

2. Background and chiller model

Canada has a variety of poultry processing operations, ranging from smaller traditional type processing to state of the art, high speed operations. In this work, we consider a typical modernized poultry processing plant (high speed), which covers most of the Canadian slaughter production (based on personal communication with CFIA officers, which we will reference from now on as [P]). Essentially, our processing framework involves a poultry slaughter establishment which operates under the CFIA approved Modernized Poultry Inspection Program (MPIP); see CFIA (2014) for more information. This perspective leads to several assumptions that guide our model formulation. These include (1) the typical weight of a carcass is 2 kg; (2) the typical processing speed is 180 carcasses/min; (3) the average dwell time of carcasses in the chiller tank is 45 min; (4) red water is not recycled, rather the set up involves fresh water intake at the beginning of the chiller tank, with overflow at the end; (5) a maximum of 50 ppm (mg/l) of free chlorine (FC) is added (if any) at the beginning of the chiller tank, and mixed with incoming fresh water; and (6) due to model simplification and a lack of data, we assume that organic matter and microbes do not bind/attach to the tank surfaces.

Our model is built around two main types of mechanisms: (i) those that involve typical processing procedures for immersion chilling in high speed poultry processing facilities in Canada and (ii) bacteria transfer, bacteria inactivation, and water chemistry dynamics during the chilling process. Refer to Table 2 for a list of parameters corresponding to type (i) and (ii). To be clear, the parameters involved with the particular processing assumptions and dynamics, as in (i), are what specifies our model for Canadian poultry programs. The mechanisms under type (ii) are general mechanisms that are expected in a typical large-scale immersion chilling procedure that is utilized during poultry processing in many locales, not just Canada. Therefore, in this section as well as Section 3, where we apply our model to generic *E. coli* contamination, data used to quantify the type (ii) mechanisms need not necessarily be Canadian.

We now formulate the chiller model in several steps.

2.1. The carcass dynamics and total suspended solids

We assume that the incoming rate of chicken carcasses to the tank is N (kg/min) and the chickens spend on average $1/d_p$ (min) in the tank. These two assumptions lead to the following equation for P, the total kg of chicken carcasses in the tank at time $t \geq 0$ (min):

$$P' = N - \varepsilon d_p P, \tag{1}$$

where

$$\varepsilon = \begin{cases} 0, & t \leq \dfrac{1}{d_p} \\ 1, & t > \dfrac{1}{d_p}. \end{cases}$$

Note that ' is the derivative with respect to time and the function ε ensures that no carcasses will leave the tank before the "average" wash time $1/d_p$ has elapsed.

As the chickens enter and move through the chiller tank, they release high amounts of organic material (in the form of blood, fat, protein, *etc.*) into the water. Such material is important because it alters chiller water chemistry as well as microbial counts (Russell, 2012). We represent the organic material in the chiller tank at time $t > 0$ by J (kg). In order to relate this to the total suspended solids (concentration), we consider J/T_V, where T_V is the total tank volume in ml. For simplicity, we assume that the amount of organic material coming in to the water is proportional to the incoming rate of chicken carcasses N (kg/min) and this is represented by $q \in (0,1)$. Note that in reality, the amount of organic material shed from individual carcasses may be independent of one another. Also, we assume, via the flow through the tank, that the organic material spends on average $1/d_p$ minutes in the tank. Therefore we build the following equation for J:

$$J' = qN - \varepsilon d_p J. \tag{2}$$

2.2. Average microbial load on carcasses and organic material in the tank

One of the key purposes of the model is to understand the dynamics of the average microbial load on both the poultry and the organic material in the chiller tank. To do so, we represent the average microbial load (CFU/(kg ml)) on the chicken and organic material in the tank at time $t > 0$, by v_p and v_j, respectively. Notice that the units for v_p and v_j are (CFU/(kg ml)) since we scale the average bacteria load per kg by the tank volume T_V. For modeling purposes, it is convenient to scale by the tank volume and this scaling should not be connected with bacterial concentration measurements taken from typical rinse procedures used to quantify the microbial load on a pre or post-chill carcass. For instance, the USDA conducted studies using a 400 ml carcass rinse in order to determine *E. coli* levels on individual poultry carcasses during processing and reported their results in units CFU/ml (USDA, 2012).

We assume that the chickens enter the chiller process with an average level of σ CFU/kg. Upon entering the tank, a certain fraction of this contamination level initially sheds into the chiller water. Let this fraction be ρ and so $0 < \rho < 1$. Also, as the carcasses move through the chiller tank, we suppose that continued microbial shedding occurs at a rate bv_p, where b (1/min) is the shedding parameter (*i.e.*, the shedding rate is proportional to the current average contamination level on the poultry). In addition, bacterial attachment occurs via contact between a carcass and microbials in the chiller water. If we let W (CFU/ml) be the microbial concentration in the chiller water at time t, then we assume this attachment occurs at a rate βW, where β (1/(kg min)) is the binding parameter.