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Robustness of a cross contamination model describing transfer of pathogens during grinding of meat

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Abstract

This study aimed to evaluate a cross contamination model[1] for its capability of describing transfer of *Salmonella* spp. and *L. monocytogenes* during grinding of varying sizes and numbers of pieces of meats in two grinder systems. Data from 19 trials were collected. Three evaluation approaches were applied: *i*) Acceptable Simulation Zone method compared observed with simulated transfer, *ii*) each trial was fitted and parameters were integrated in a Quantitative Microbiological Risk Assessment model, *iii*) the Total Transfer Potential was calculated from fitted parameters. Risk estimates revealed that grinding was influenced by sharpness of grinder knife, specific grinder and grinding temperature.

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Keywords: microbial transfer; foodborne pathogens; model assessment; risk; meat processing.

1. Introduction

Møller et al. (2012)[1] published a model capable of describing the observed transfer of *S.* Typhimurium DT104 during grinding of pork. It is not known whether the model is equally capable of describing transfer of different pathogens in other meat matrices using different grinding systems. Therefore, the aim of this study was to evaluate

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the capability of this model to properly describe the transfer of both *Salmonella* spp. and *L. monocytogenes* when grinding different types of meat (pork and beef), using two different types of grinders and variable sizes and numbers of meat pieces to be minced.

2. Material and methods

2.1. Experimental design

As indicated in Table 1, microbial transfer was investigated in relation to types of meat (beef and pork), piece sizes (50 to 324 g) and number of pieces subjected to grinding (10 to 100), as well as three bacterial pathogens (*S.* Enteritidis, *S.* Typhimurium DT104 and *L. monocytogenes*).

Table 1. Aspects challenged in each of the performed experiments and in the published datasets

Trial	Meat Type	Inoculation		Pieces of meat		Temperature of processing (°C)
		Pathogens	Concentration (log_{10} CFU/piece)	Size (g)	Number	
1	beef[a]	*S.* Enteritidis cocktail[c]	6.85[d]	50	90	19 - 27
2	beef[a]	*S.* Enteritidis cocktail	6.86[d]	50	90	19 - 27
3	beef[a]	*S.* Enteritidis cocktail	7.48[d]	50	80	19 - 27
4	beef[a]	*S.* Enteritidis cocktail	7.74 - 8.26	50	80	19 - 27
5	beef[a]	*S.* Enteritidis cocktail	7.92 - 8.00	50	80	19 - 27
6	beef[a]	*S.* Enteritidis cocktail	7.74 - 8.30	50	80	19 - 27
7	beef[a]	*S.* Enteritidis cocktail	6.80 - 7.65	50	24	19 - 27
8	beef[a]	*S.* Enteritidis cocktail	6.78 - 8.04	50	24	19 - 27
9	pork[a]	*S.* Enteritidis 54	6.33 - 8.48	196 ± 35	100	22 - 27
10	pork[a]	*S.* Enteritidis 54	8.11 - 8.77	196 ± 25	10	22 - 27
11	pork[a]	*S.* Enteritidis 54	8.07 - 8.82	186 ± 29	96	22 - 27
12	pork[a]	*S.* Enteritidis 54	7.70 - 8.50	157 ± 26	15	22 - 27
13	pork[b]	*S.* Typhimurium DT104	8.32 - 9.00	170 ± 46	25	22
14	pork[b]	*S.* Typhimurium DT104	8.71 - 8.92	229 ± 63	25	22
15	pork[b]	*S.* Typhimurium DT104	8.33 - 9.10	224 ± 61	35	22
16	pork[b]	*S.* Typhimurium DT104	8.61[e]	274 ± 37	44	22
17	pork[b]	*L. monocytogenes*	8.76[e]	324 ± 53	45	22
18[f]	pork[b]	*S.* Typhimurium DT104	9.10 - 9.52	236 ± 64	45	22
19[f]	pork[b]	*S.* Typhimurium DT104	8.87 - 9.33	241 ± 49	45	4
20[f]	pork[b]	*S.* Typhimurium DT104	8.71 - 9.22	230 ± 49	95	4

[a] processing in a semi-industrial grinder in stainless steel and tin (Beccaro® equipamentos industriais Ltda, Brazil (Model Picador PB-10I)
[b] processing in a semi-industrial grinder in stainless steel (la Minerva® food service equipment, Italy (Model AE22)
[c] a strain of *S.* Enteritidis isolated from beef and another *S.* Enteritidis strain isolated from chicken legs were tested in this cocktail.
[d] for modelling purposes, the input of the pathogen was estimated based on counts directly from the culture.
[e] for modelling purposes, the average of the input of the pathogen to all five contaminated pieces of meat was applied.
[f] data obtained from Møller et al. (2012)[1].

Following the methods of Møller et al. (2012)[1], five pieces of experimentally contaminated pieces were ground, followed by non-contaminated pieces. Individual portions of each ground piece were collected and analyzed.

2.2. Model

Parameter values of the he cross contamination model proposed and explained by Møller et al. (2012)[1] (equation.1) were estimated by fitting the observed values from each of the twenty trials (Table 1) by minimizing the Residual Sum of Squares (RSS), using the Solver function in MS Excel (Microsoft® Office Excel® 2007).

$$\begin{cases} M_i = (1-a_1)(1-a_2)\,P_i + (b_1\,gr_{1,i-1}) + (b_2\,gr_{2,i-1}) \\ gr_{1,i} = a_1\,P_i + (1-b_1)\,gr_{1,I-1} \\ gr_{2,i} = a_2\,P_i + (1-b_2)\,(1-c_3)\,gr_{2,i-1} \end{cases} \quad \text{(Equation 1)}$$