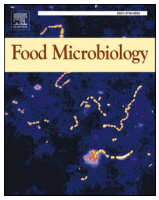
Food Microbiology 115 (2023) 104338

Contents lists available at ScienceDirect

Food Microbiology

journal homepage: www.elsevier.com/locate/fm



Growth models for *Salmonella*, *E. coli* O157:H7 and *L. monocytogenes* give different predictions for pathogen growth in cut leafy greens transportation, but are consistent in identifying higher risk conditions

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ARTICLE INFO

Keywords:
Salmonella
E. coli O157:H7
L. monocytogenes
Predictive microbiology
Leafy greens

ABSTRACT

Leafy greens are frequently implicated in foodborne disease outbreaks and cut-leafy greens are a food that requires time and temperature control for safety. Predictive microbiology uses mathematical models to predict the growth of bacteria based on environmental conditions. The objective of our study was to compare published square root growth models for *Salmonella* (n = 6), pathogenic *E. coli* (n = 6) and *Listeria monocytogenes* (n = 4) using real world transport temperature data. Data from trucks transporting fresh-cut leafy greens during cross-country shipments were used as temperature inputs to the models. Bacterial growth was computed using the temperatures from each probe in every truck over the duration of transit, which resulted in 12–18 growth predictions per truck for each model. Each model generally gave significantly different predictions than other models for the same organism. The exception was for the two *Salmonella* models predicting the least growth and the two *Salmonella* models predicting the most growth which gave predictions that were not significantly different. Although different models tended to give different predictions, their ability to rank risk by truck was generally consistent across models. While absolute risk might be dependent upon choice of model, relative risk is independent of model choice.

1. Introduction

Leafy greens are frequently implicated in foodborne disease outbreaks. The US Food and Drug Administration (FDA) list of outbreak investigations shows multiple outbreaks every year associated with some type of leafy greens (Center for Food Safety and Applied Nutrition, 2022). Confirmed single etiology outbreaks linked to leafy greens reported that Norovirus was most commonly implicated followed by *Escherichia coli* O157:H7 and *Salmonella* (Herman et al., 2015). *Listeria monocytogenes* has also been linked to leafy greens recalls with several recent outbreaks (Center for Food Safety and Applied Nutrition, 2022; US Food and Drug Administration, 2016). *L. monocytogenes* is particularly concerning because it can grow even at commonly accepted appropriate refrigerated temperatures (Walker et al., 1990).

Leafy greens can become contaminated with pathogens by a variety of means including contaminated irrigation water, improperly composted manure used for fertilizer, and by the feces of animals. Contamination can occur also during processing, including washing, cutting and storage (Herman et al., 2015). Refrigeration at 5 °C or less will prevent the growth of *Salmonella* and pathogenic *E. coli* that may be present on leafy greens (Abdul-Raouf et al., 1993; Koseki and Isobe, 2005; US Food and Drug Administration, 2016) and will restrict the growth of *L. monocytogenes* also. Storage of leafy greens at 5 °C or above may allow pathogens to multiply, increasing the risk of foodborne disease (Li et al., 2001). The FDA Model Food Code identifies cut-leafy greens as a food that requires time and temperature control for safety (US Food and Drug Administration, 2000). The need for temperature control includes control during the shipment of fresh-cut leafy greens by tractor trailers or other means. If the tractor trailer loads are subjected to temperature above 5 °C, they may be rejected by distribution centers or wholesale markets on arrival (Cantwell and Suslow, 2002; Chang and Fang, 2007; Franz et al., 2010; Kim et al., 2008; Sant'Ana et al., 2012). Temperature must be controlled carefully, however temperatures below ~0 °C can lead to damage of plant tissues by freezing. This freezing will

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https://doi.org/10.1016/j.fm.2023.104338
Received 4 April 2023; Received in revised form 5 June 2023; Accepted 10 July 2023
Available online 12 July 2023
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Table 1
A summary of temperature probe data from 16 trucks shipping fresh-cut leafy greens during cross-country shipment collected by Brown et al. (2016).

Truck Number	Probe Temperature (°C)					Number of Observations
	Minimum	Maximum	Mean	Standard Deviation	Median	
1	**1.50** [a]	7.94	**3.59**	1.21	**3.28**	16,737
2	0.56	5.44	2.71	0.61	2.67	**30,201**
3	0.61	7.50	2.44	0.95	2.33	21,920
4	−0.28	7.61	2.06	0.96	2.06	19,824
5	0.78	**9.67**	3.03	**1.43**	2.72	18,630
6	0.61	6.17	2.32	0.54	2.33	15,646
7	−0.22	7.33	1.83	0.88	1.83	23,236
8	−0.72	*5.17* [b]	1.66	0.95	1.61	26,883
9	−1.22	7.06	*0.90*	1.16	*0.61*	27,559
10	0.50	5.67	2.61	0.95	2.61	17,242
11	0.56	6.50	2.62	*0.48*	2.61	24,840
12	0.83	7.17	2.50	0.58	2.50	14,112
13	0.50	6.50	2.22	0.60	2.17	14,256
14	*−2.39*	6.78	2.21	1.09	2.17	24,210
15	−0.78	8.56	1.63	1.00	1.50	9504
16	−0.83	*5.17*	1.53	1.01	1.72	*7480*

[a] Highest values within a column are **bolded and underlined**.
[b] Lowest values within a column are *italicized and underlined*.

lead to quality loss and a potential for greater subsequent microbial growth in the damaged tissue after the temperature rises again (Courcol et al., 1982).

Predictive microbiology uses mathematical models to predict the growth of bacteria based on environmental conditions (Ross and McMeekin, 2003). Multiple growth models have been developed to predict the growth of *Salmonella* spp. (Gibson et al., 1988; Koseki and Isobe, 2005; Mishra et al., 2017; Puerta-Gomez et al., 2013; Sant'Ana et al., 2013; 2012; Veys et al., 2016), *E. coli* O157:H7 (Buchanan et al., 1993; Danyluk and Schaffner, 2011; Koseki and Isobe, 2005; McKellar and Delaquis, 2011; Puerta-Gomez et al., 2013; Veys et al., 2016), and *L. monocytogenes* (Buchanan and Phillips, 1990; Koseki and Isobe, 2005; Mishra et al., 2017; Sant'Ana et al., 2013; 2012) in leafy greens.

Despite the wide availability of predictive models, many of which are substrate specific, the literature offers very little guidance on methods to compare and select the appropriate model from amongst a list of potentially valid choices using real world temperature datasets. The objective of our study was to compare the pathogen growth models cited above using the temperatures recorded during transportation of fresh-cut leafy greens. The outcome can improve risk analysis by indicating which models are more (or less) conservative for each of the three bacteria.

2. Material and methods

2.1. Temperature data

Transport temperature data from trucks containing fresh-cut leafy greens during cross-country shipment as reported Brown et al. (2016) were provided by those authors. Briefly, temperature probes were placed at numerous locations within fresh-cut leafy green transport trucks originating from Salinas, California and Yuma, Arizona. A total of 16 shipments were monitored throughout 2010 and 2011, and sensors recorded temperatures at intervals that did not exceed 5 min, for a total of 213,280 data points. Each truck had between 12 and 18 sensors, and the sensor probe positions varied by truck. Sensors were placed in the front, middle and rear of each trailer, with two locations monitored at each position. Sensors were also placed on each sidewall next to each monitored position. Additional sensors at the middle center were also used for some shipments. Brown et al. (2016) indicate the temperatures were recorded using Temptale 4 programmable temperature loggers (Sensitech, Beverly MA). According to Sensitech (https://www.sensitech.com/en/products/monitors/conventional/), the sensors are accurate to ± 0.55C. For the purposes of this study, the recorded temperatures were used without any corrections for accuracy.

2.2. Models

Bacteria growth was modeled using the square root or Ratkowsky growth model (Ratkowsky et al., 1982), which has the form $\sqrt{\mu} = b(T - T_0)$, using parameters appropriate for each bacterium. The model computes the common log change of colony forming units (CFU), where T is the temperature in degrees Celsius (°C) and T_0 is a model specific minimum temperature parameter in °C. The parameter b is the empirically derived regression coefficient of the temperature on the square root of the growth rate (Ratkowsky et al., 1982).

Relevant growth model parameters T_0 and b were selected from the literature for *Salmonella*, *E. coli* O157:H7, and *L. monocytogenes*. Six *Salmonella* models, six *E. coli* O157:H7 models, and four *L. monocytogenes* models were identified. Lag time models were not used in this analysis. Models were selected based on their substrate (i.e., leafy greens), although one traditional broth model from the early literature was included for each species (Supplemental Table 1).

Supplemental Table 1 shows that the number of strains ranged from only a single strain to one model which analyzed data from 17 different studies. The substrates used to create the model tended to be predominantly leafy greens although some of the models were developed with sterile laboratory media. The predominant primary model used was the Baranyi model but, some of the earlier literature use the Gompertz model and several papers used the three-phase linear model. Supplemental Fig. 1 provides a visualization of the square root model parameters from Table 1. It's clear from Supplemental Fig. 1 that the *L. monocytogenes* models tend to have lower T_0 values as might be expected given the psychotropic nature of the organism. The other pattern that is apparent is that the models developed in broth tend to cluster towards the right-hand portion of the graph indicating that these models are more conservative (predict higher growth) since they tend to have higher b parameters (faster increase in growth rate with increasing temperature).

Some calculations were performed to standardize the parameters into the same units. Two models that used natural logarithms instead of common (base-10) logarithms in their original sources, had the given parameter b divided by the square root of the natural log of 10, or b/1.5174, to convert b into common logarithm units (details in the appendix). For the two models where the parameter b was not given in square root units, the square root of b was used to convert it for comparison with the other models. One model reported its parameter b for daily (instead of hourly) logarithmic growth. To compare with the other

Table 2
Standardized square root model parameters for *Salmonella*, *E. coli* O157:H7 and *L. monocytogenes* from the published literature. Values are given using the same number of significant figures as reported in the original publication. Highest values within an organism within a column are bolded and underlined. Lowest values within an organism, within a column are italicized and underlined.

Organism	Square root model parameters [a]		Source
	b	T_0 (°C)	
S. typhymurium	0.0172 [b]	5.88	Puerta-Gomez et al. (2013)
Salmonella	**0.037**	**6.27**	Gibson et al. (1988)
Salmonella spp.	0.027	5.42	Veys et al. (2016)
Salmonella spp.	0.033	4.96	Koseki and Isobe (2005)
S. enterica	*0.0132* [c]	−0.571	Mishra et al. (2017)
S. enterica	0.0178	*−4.6*	Sant'Ana et al. (2013)
E. coli O157:H7	0.0246 [b]	**4.76**	Puerta-Gomez et al. (2013)
E. coli O157:H7	*0.0126* [d]	2.628	Danyluk and Schaffner (2011)
E. coli O157:H7	**0.033**	4.45	Koseki and Isobe (2005)
E. coli O157:H7	0.032	2.67	Buchanan et al. (1993)
E. coli O157:H7	0.023	*1.2*	McKellar and Delaquis (2011)
E. coli O157:H7	0.028	1.58	Veys et al. (2016)
L. monocytogenes	0.0152 [c]	**0.599**	Mishra et al. (2017)
L. monocytogenes	*0.0144*	−1.6	Sant'Ana et al. (2013)
L. monocytogenes	**0.027**	−0.44	Buchanan and Phillips (1990)
L. monocytogenes	0.016	*−4.26*	Koseki and Isobe (2005)

[a] Significant figures are reported as per the original published manuscript.
[b] Converted from the published parameter by taking the square root.
[c] Converted from originally stated parameter in natural logarithm to common logarithm.
[d] Converted from originally stated parameter in log CFU/day to log CFU/hour.

models, this parameter was divided by $\sqrt{24}$. A comparison of the predictions using both the transformed and untransformed parameters confirmed identical predictions. Use of the transformed parameters facilitates comparison between models.

Temperature data from each probe in each truck was used as inputs to each growth models. The incremental growth for each time interval was calculated for each model for each truck where the time interval was 5 min. When a temperature of less than the model T_0 was encountered, the predicted growth for that time interval was set to a 0 log CFU increase. Growth was computed using the temperatures from each probe in every truck over the duration of transit, which resulted in 12–18 growth predictions per truck for each model.

2.3. Data analysis

The predicted log CFU increases results were compared statistically using the R statistical software package (R Core Team, 2021) and the data science package TidyVerse (Wickham et al., 2019). The predicted growth at each probe location within a truck and across all trucks for each model were used to calculate means and maxima. Predicted increases in pathogen concentration by truck for different models as well as predicted increases in pathogen concentration across all trucks for different models were calculated.

The Shapiro-Wilk normality test (Shapiro and Wilk, 1965) revealed a lack of normality when the models were separated into categories by bacteria. Differences in the multiple models within each category, were therefore detected using Friedman's test (Friedman, 1937), a nonparametric, one-way, repeated measures Analysis of Variance (ANOVA). A significant Friedman test was followed up by pairwise Wilcoxon signed-rank tests (Wilcoxon, 1945) to identifying which groups were different. We used the Bonferroni correction (Bland and Altman, 1995) to compensate for any increase in Type I errors. Kendall's W determined the effect size to assess agreement among the models (Kendall and Smith, 1939) ranging from zero (no trucks have a consistent ranking across models), to one (all trucks have a consist ranking across models).

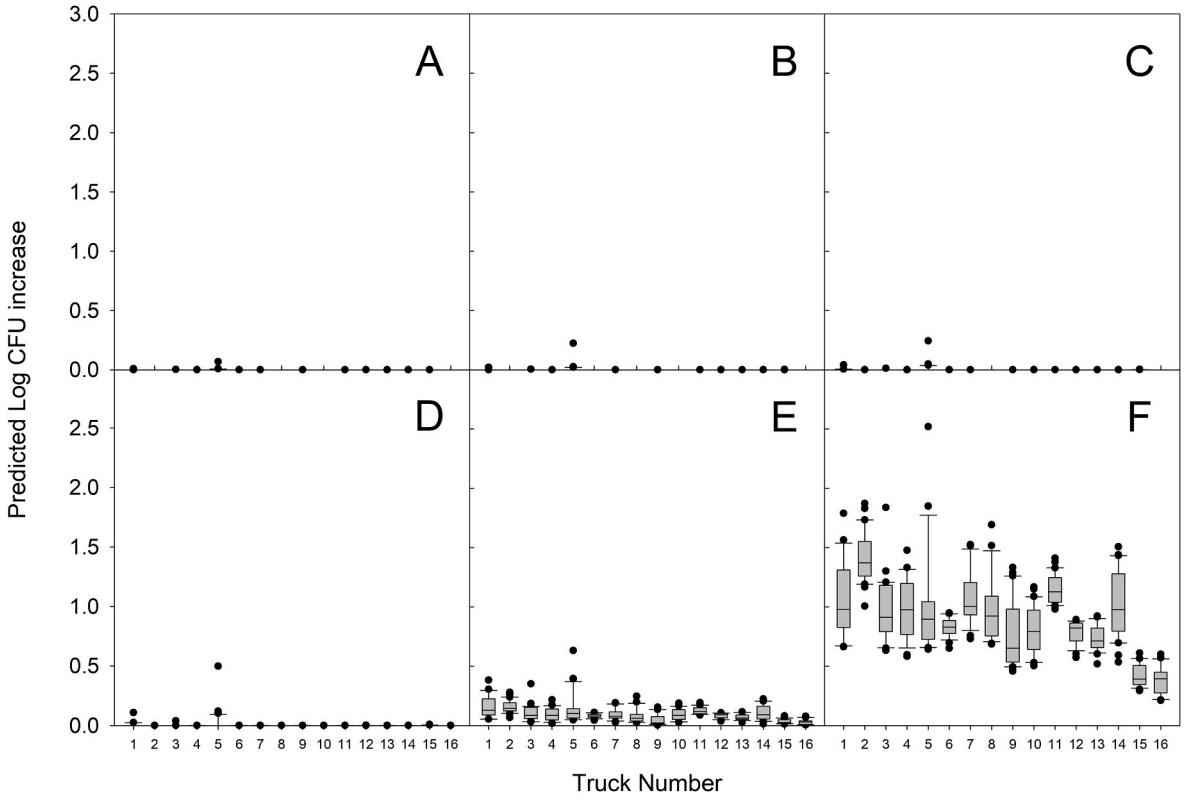

Fig. 1. Predicted increases in *Salmonella* concentration by truck for 6 different models: (A) Puerta-Gomez et al. (2013); (B) Gibson et al. (1988); (C) Veys et al. (2016); (D) Koseki and Isobe (2005); (E) Mishra et al. (2017); and (F) Sant'Ana et al. (2013).

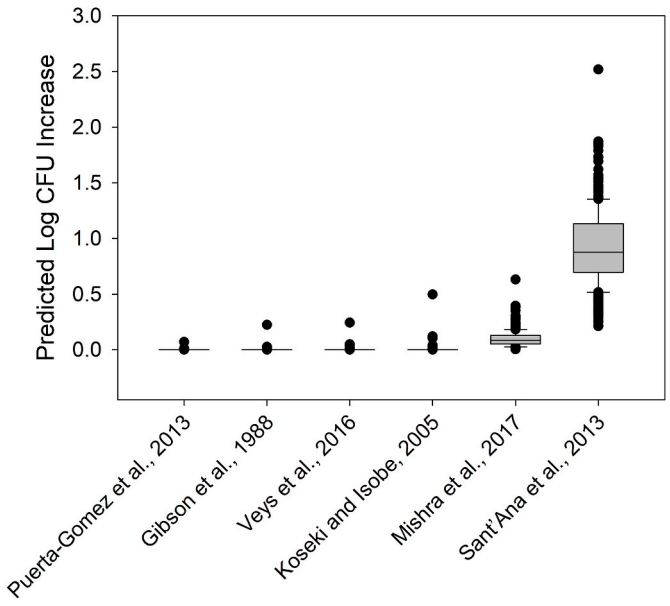

Fig. 2. Predicted increases in *Salmonella* concentration across all trucks for 6 different models: Puerta-Gomez et al. (2013); Gibson et al. (1988); Veys et al. (2016); Koseki and Isobe (2005); Mishra et al. (2017); and Sant'Ana et al. (2013).

3. Results and discussion

3.1. Temperature observations

As shown in Table 1, Truck 1 contained probes that recorded the highest minimum temperature (1.5 °C), the highest mean temperature (3.59 °C), and the highest median temperature (3.28 °C) across all 16 trucks. Truck 2 had the greatest number of observations (>30,000). Truck 5 contained probes which reported the maximum temperature (9.67 °C), as well as the greatest standard deviation (1.43 °C), across all 16 trucks. Trucks 8 and 16 contained probes which reported the lowest maximum temperature (5.17 °C), while truck 9 reported the lowest mean temperature (0.90 °C), as well as the lowest median temperature (0.61 °C) of all 16 trucks. Truck 11 had probes which recorded the smallest standard deviation of any of the 16 trucks (0.48 °C). Truck 14 contained a probe which reported the lowest minimum temperature of all 16 trucks (−2.39 °C). Truck 16 had the smallest total number of observations (<7500).

3.2. Model parameters

As seen in Table 2, amongst the *Salmonella* models Gibson et al. (1988), had the highest values for b and T_0, while Mishra et al. (2017) had the lowest value for b and Sant'Ana et al. (2013) had the lowest value for T_0. Amongst the *E. coli* O157:H7 models Koseki and Isobe (2005) reported the highest b value and Puerta-Gomez et al. (2013) the highest T_0, while Danyluk and Schaffner (2011) and McKellar and Delaquis (2011) had the lowest of the same, respectively. Amongst the L. *monocytogenes* models Buchanan and Phillips (1990) had the highest b, and Mishra et al. (2017) the highest T_0. Sant'Ana et al. (2013) had the lowest b, while Koseki and Isobe (2005) reported the lowest T_0.

3.3. Salmonella spp. models

The predicted increases in *Salmonella* concentration by truck for six different models (Gibson et al., 1988; Koseki and Isobe, 2005; Mishra et al., 2017; Puerta-Gomez et al., 2013; Sant'Ana et al., 2013; Veys et al., 2016) are shown in Fig. 1. The models shown in panels A–D (Puerta-Gomez et al., 2013; Gibson et al., 1988; Veys et al., 2016; and Koseki and Isobe, 2005 respectively) all have very low mean predicted growth, with most trucks essentially showing no increase. Truck 5 shows the most predicted growth across all trucks for these four models ranging from 0.07 to 0.50 log CFU. The predictions for the Mishra et al. model (Fig. 1E) show modest growth across most trucks, with a maximum predicted increase of less than 0.5 log CFU. The Sant'Ana et al. model predictions are by far the greatest, and most trucks show at least 0.5 log CFU increase, and every truck shows some increase. As with the other models, the greatest growth is predicted in truck 5 which shows a maximum increase of 2.5 log CFU. It is interesting to note that despite this one prediction for truck 5, there are several other trucks that have higher average log increases, since these trucks have more sensors that are on average warmer than the sensors in truck 5.

The Friedman test for average growth for each truck confirms that the models predict different levels of growth in different trucks ($p < 0.0001$) i.e., different trucks are different within a model. The Kendall W effect size is 0.95, which indicates the ranking of trucks by models is quite consistent, in other words the worst truck is always the worst truck no matter the model.

Fig. 2 shows the model predictions grouped by model across all trucks, and shows the same trends observed in Fig. 1. The two models predicting the least growth (Gibson et al. and Puerta-Gomez et al.) and the two models predicting the most growth (Mishra et al. and Sant'Ana et al.) are not significantly different from one another. The other two models (Veys et al. and Koseki and Isobe) are significantly different from one another and are also significantly different from the two models

Table 3
Evaluation of different mathematical models for the prediction of *Salmonella* spp., *E. coli* O157:H7 and *L. monocytogenes* growth in leafy greens based on data collected in 16 trucks using pairwise Wilcoxon signed-rank tests with Bonferroni correction.

Pathogen	Source	Predicted growth in 16 trucks (log CFU)		
		Mean [a]	Standard deviation	Maximum [b]
Salmonella	Puerta-Gomez et al. (2013)	0.0003 A	0.0034	0.0689
	Gibson et al. (1988)	0.0009 A	0.0109	0.2234
	Veys et al. (2016)	0.0012 B	0.0123	0.2437
	Koseki and Isobe (2005)	0.0033 C	0.0257	0.4977
	Mishra et al. (2017)	0.1022 D	0.0684	0.6322
	Sant'Ana et al. (2013)	1.0754 D	0.3338	2.5189
E. coli O157:H7	Puerta-Gomez et al. (2013)	0.0019 A	0.0164	0.3128
	Danyluk and Schaffner (2011)	0.0040 B	0.0151	0.2234
	Koseki and Isobe (2005)	0.0061 C	0.0363	0.6732
	Buchanan et al. (1993)	0.0509 D	0.0959	1.4240
	McKellar and Delaquis (2011)	0.0924 E	0.1040	1.2039
	Veys et al. (2016)	0.1149 F	0.1286	1.5880
L. monocytogenes	Mishra et al. (2017)	0.0592 A	0.0588	0.6208
	Sant'Ana et al. (2013)	0.2167 B	0.1106	0.9498
	Buchanan and Phillips (1990)	0.5822 C	0.2749	2.5713
	Koseki and Isobe (2005)	0.7578 D	0.2521	1.9255

[a] Superscripts within a pathogen grouping indicate a statistically significant difference in the mean predicted pathogen growth in 16 trucks.
[b] The maximum predicted increase observed amongst all probe locations and trucks for the specific model.

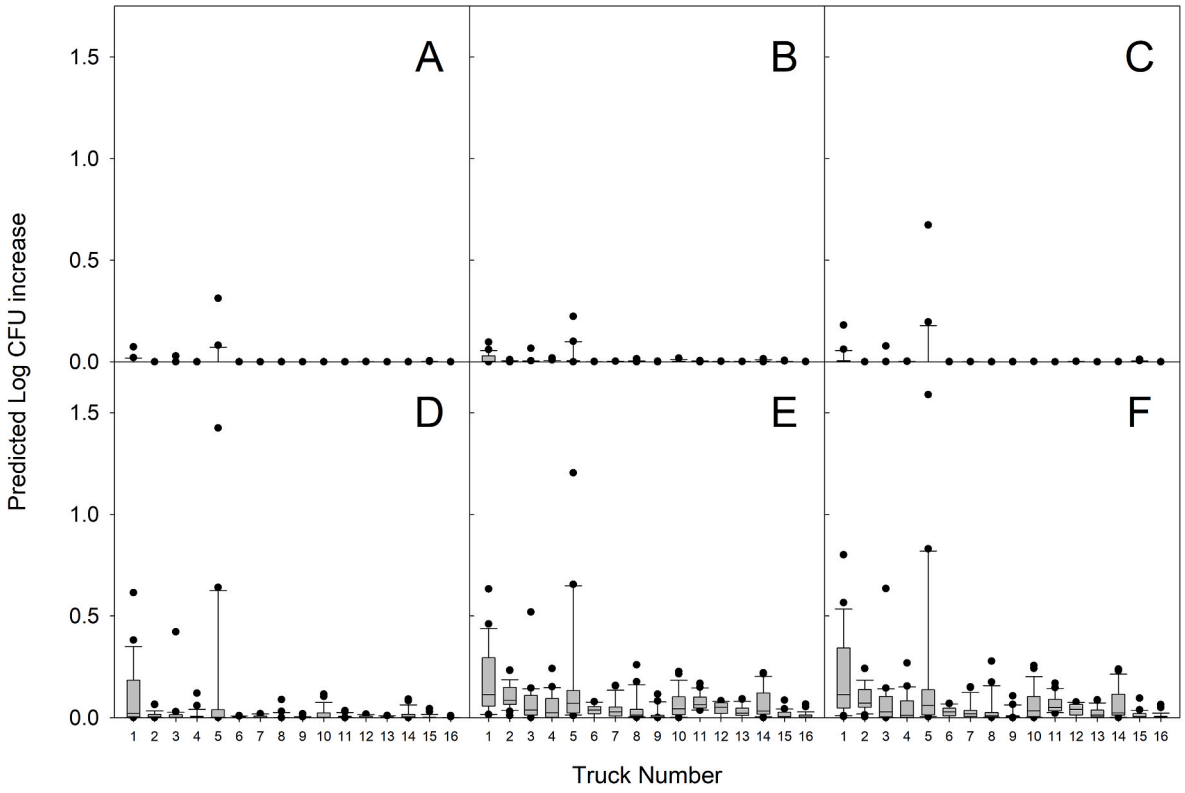

Fig. 3. Predicted increases in *E. coli* O157:H7 concentration by truck for 6 different models: (A) Puerta-Gomez et al. (2013); (B) Danyluk and Schaffner (2011); (C) Koseki and Isobe (2005); (D) Buchanan and Phillips (1990); (E) McKellar and Delaquis (2011); and (F) Veys et al. (2016).

predicting the least growth and the two predicting the most growth. These data are summarized in Table 3, where predicted mean growth values sharing the same capital letter within a microorganism indicate no significant difference, while a different letter indicates statistically significant difference ($p < 0.001$). Ranking the models by increasing mean predictions corresponds with ranking the model by maximum predicted growth as well, where predictions from Puerta-Gomez et al. result in the lowest maximum and Sant'Ana et al. the highest.

As seen in Table 2, all six models use a parameter b with similar magnitude ($0.0132 \leq b \leq 0.033$). However, the two models with the most predicted growth use much lower values for the minimum temperature (T_0) parameter than the remaining four models. The Sant'Ana et al. model uses −4.6 °C as the minimum temperature that *Salmonella* can grow, which is about 4 °C lower than the Mishra et al. model, and the Mishra et al. model uses −0.571 °C, which is about 5 °C lower than the remaining four models. Both of these models assume minimum temperature (T_0) parameter well below the commonly accepted limit for *Salmonella* growth of 5.2 °C (National Advisory Committee on Microbiological Criteria for Foods, 2010). The Mishra et al. and the Sant'Ana et al. models are much more fail-safe (i.e., predicted more growth) than the other four models, which have minimum temperatures more consistent with this commonly accepted minimum.

3.4. *Escherichia coli O157:H7 models*

When probe temperatures from the 16 trucks were used as inputs to the six *E. coli* O157:H7 models (Buchanan and Phillips, 1990; Danyluk and Schaffner, 2011; Koseki and Isobe, 2005; McKellar and Delaquis, 2011; Puerta-Gomez et al., 2013; Veys et al., 2016), the log growth predictions for each truck are shown in Fig. 3. The graphs are arranged (Fig. 3A–F) by model in order of increasing predicted mean logarithmic growth. Truck 5 shows consistently greater predicted growth than the other trucks as seen with the *Salmonella* models. Although the Danyluk and Schaffner model (Fig. 3B) predicts the least amount of growth for truck 5, the lowest overall predicted mean log growth across all trucks is given by the Puerta-Gomez et al. model.

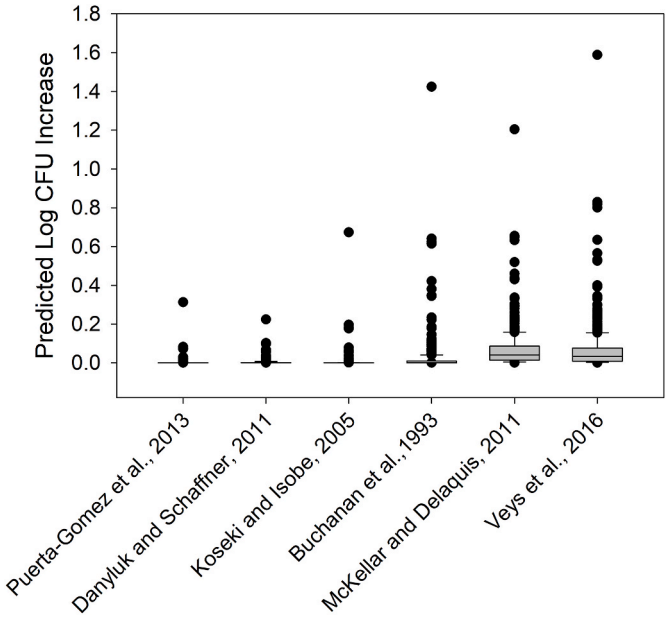

Fig. 4. Predicted increases in *E. coli* O157:H7 concentration across all trucks for 6 different models: Puerta-Gomez et al. (2013); Danyluk and Schaffner (2011); Koseki and Isobe (2005); Buchanan and Phillips (1990); McKellar and Delaquis (2011); and Veys et al. (2016).

Table 3 shows the mean and maximum predicted logarithmic growth for each *E. coli* model. The results of the pairwise Wilcoxon signed-rank tests with Bonferroni correction indicate each model gives a distinct

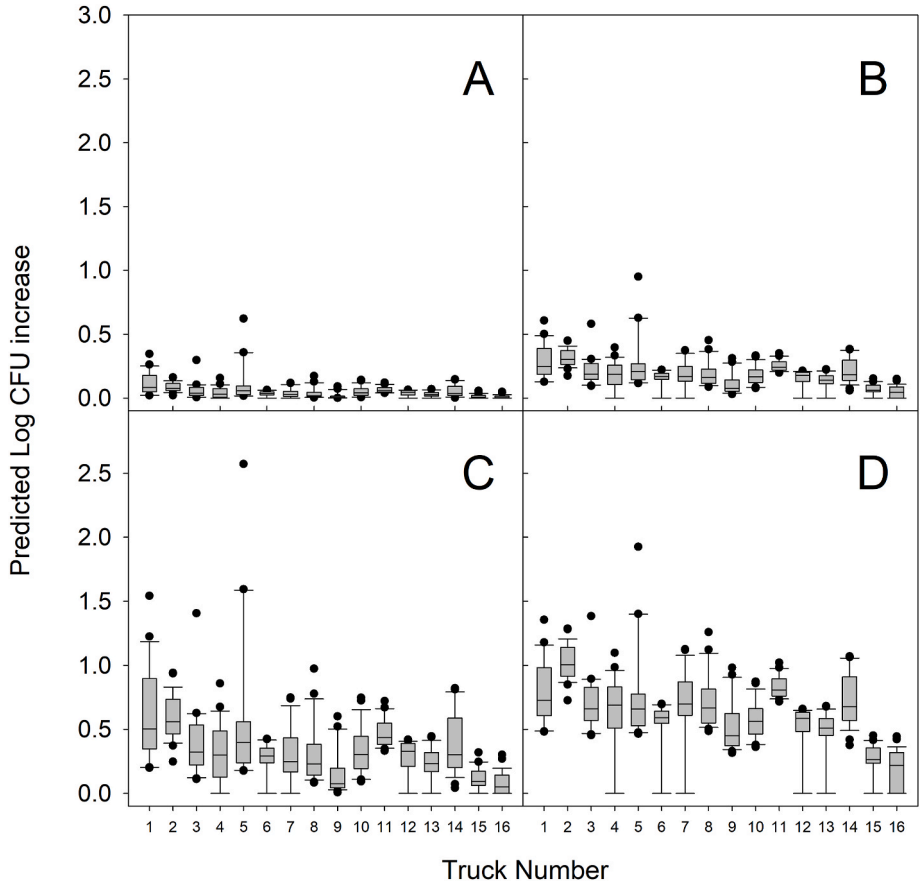

Fig. 5. Predicted increases in *Listeria monocytogenes* concentration by truck for 4 different models: (A) Mishra et al. (2017); (B) Sant'Ana et al. (2013); (C) Buchanan and Phillips (1990) and (D) Koseki and Isobe (2005).

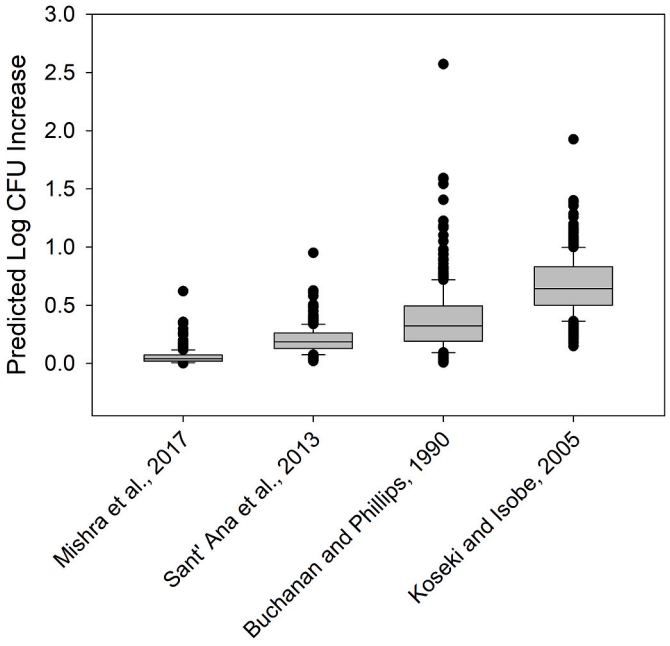

Fig. 6. Predicted increases in *Listeria monocytogenes* concentration across all trucks for 4 different models: Mishra et al. (2017); Sant'Ana et al. (2013); Buchanan and Phillips (1990) and Koseki and Isobe (2005).

prediction. Each of the six *E. coli* models gives statistically significantly different results from every other model ($p < 0.001$), as shown by the different letters in Table 3.

The Friedman test on the average growth predicted for each truck supports the observation in Table 3 that the *E. coli* models predict significantly different mean log growth across the 16 trucks ($p < 0.0001$). The Kendall W effect size for the *E. coli* models is 0.95, which indicates the ranking of the models is quite strong, almost the same as the *Salmonella* models (differing at the 3rd decimal place). Fig. 4 compares the *E. coli* model predictions across all trucks, and compliments the data in Table 3, with the McKellar and Delaquis and Veys et al. models predict more growth than the other four models, with the maximum single greatest growth seen for one location with the Veys et al. model (1.59 log increase), followed by the Buchanan et al. model (1.42 log increase). As shown in Fig. 4, there are a few probes locations with >1 log CFU predicted growth for the three models with the highest predictions (Buchanan et al., 1993; McKellar and Delaquis, 2011; Veys et al., 2016), but even these most liberal models generally show less than a one large increase. The three more conservative models (Puerta-Gomez et al., 2013; Danyluk and Schaffner, 2011; Koseki and Isobe, 2005) almost always show less than a 0.5 log increase.

3.5. *Listeria monocytogenes* models

When temperature sensor data from the 16 trucks were analyzed using the four *L. monocytogenes* models (Buchanan and Phillips, 1990; Koseki and Isobe, 2005; Mishra et al., 2017; Sant'Ana et al., 2013), the results by model (Panel A–D) and by truck are shown in Fig. 5, while Fig. 6 compares the models aggregating all trucks. The Friedman test on the average growth for each truck (data not shown) supports the data in

Table 3 (which uses pairwise Wilcoxon signed-rank tests with Bonferroni correction) indicating that each of the four models predicts significantly different growth that each of the other models ($p < 0.0001$). The Kendall W effect size is 0.97, which indicates the relationship of the trucks across the models is even a bit more consistent than models for the other two organisms.

There appear to be clear differences between each of four models as seen in Figs. 5 and 6 as well as Table 3. As shown in Table 1, the slope parameter (b) for three models (Mishra et al. Sant'Ana et al. and Koseki and Isobe models) are similar (0.0152, 0.0144, and 0.016, respectively). The Mishra et al. model has the highest minimum temperature (0.599 °C) and predicts the least growth while Koseki and Isobe, with the lowest minimum temperature predicts the most growth. The Sant'Ana et al. and Buchanan and Phillips models do not follow this pattern. The Buchanan and Phillips model has the highest slope value (0.027) which offsets its minimum temperature (−0.44 °C), while the Sant'Ana et al. model has the lowest slope (0.0144) and an intermediate minimum temperature (−1.6 °C).

4. Conclusion

Our results show that for the 16 models analyzed, model predictions for a given organism tended to be significantly different than predictions from other models for the same organism. This means that if models are to be used for predicting the absolute level of risk (i.e., a specific log increase), then model choice is of critical importance. We observed that the temperature minimum parameter of the square root model (T_0) tended to be quite important in the overall model predictions. Models with lower minimum temperature parameters generally predicted higher levels of increase. This is not surprising given the real-world data sets used as inputs to the model. Since temperature control of perishable foods tends to be generally good, models that predict growth at lower conditions will tend to predict more growth than models which do not predict growth at lower temperature conditions. The b parameter for the square root model which influences the growth rate of the organism above the temperature minimum tended to be of lesser importance, which is also consistent with the choice of the real world dataset used to make the model predictions. Despite these important differences between models, our analysis also shows that the ability of different models to rank different shipping conditions (e.g., trucks) was generally quite consistent. This means if the objective is to identify riskier conditions relative to one another the choice of the specific model is less important. Future research should continue to examine these implications using real world data sets to determine the suitability of models for predicting absolute and relative risk.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This work was supported by the U.S. Department of Agriculture [grant number 2011-51110-31027] and Rutgers University Dining.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.fm.2023.104338.

AppendixNatural Logarithm to Common Logarithm

Compute the slope parameter b of a model given in natural logarithms (base e, which is Euler's number, and often abbreviated as "ln") to common logarithms (base 10).

Given the equation $\sqrt{\mu} =$, square both sides to get $\mu = (b(T - T_0))^2$ where the slope b is in natural logarithms per hour. Then $e^{(b(T-T_0))^2} = 10^{(x(T-T_0))^2}$, and solve for x to get the slope in common logarithms per hour.

Take the natural log of both sides, which gives $(b(T - T_0))^2 = ((x(T - T_0))^2) * \ln(10)$.

Algebraically, $\frac{(b(T-T_0))^2}{\ln(10)} = ((x(T - T_0))^2)$.

$$\frac{b^2}{\ln(10)} = x^2$$

$$x = \frac{b}{\sqrt{\ln(10)}} \approx \frac{b}{1.5174}$$

Hence for each b with units in natural logarithms, divide the b by $\sqrt{\ln(10)}$ to get the b in units of base-10 logarithms.

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