EVALUATION OF PREDICTING PERFORMANCES OF EXTENDED LOGISTIC MODEL AND BARANYI MODEL FOR THE GROWTH OF *SALMONELLA ENTERITIDIS* IN MINCED BEEF

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ABSTRACT

The aim of this study was to evaluate the performances of two growth models for prediction of *Salmonella Enteritidis* in ground beef, namely the extended logistic model and the ComBase web edition Baranyi model. Performances of the growth models were evaluated by using various statistical criteria, namely the square root of the mean of the square error (*RMSE*), calculation of the residuals, and student *T*. test. It was found that both models described well the growth curves for *Salmonella Enteritidis* at various initial doses, constant and dynamic temperatures. In addition, no significant differences were observed between the estimated values of data points at various initial doses and at constant and dynamic temperatures with the two models ($p>0.05$) except at the initial dose of 2 log (CFU/g) that was significant ($p<0.05$). The residuals for Salmonellae described by both models at various growth conditions were very small; all residuals for the data points were less than 0.5 log CFU/g. This shows that all points were in the acceptable prediction zone between -1 log and 0.5 log CFU/g. In addition, the averages of *RMSE* values at various initial doses were very low, which were 0.06 and 0.07 (log CFU/g) for the extended logistic and Baranyi model, respectively. Similarly, the averages of *RMSE* values at various constant temperatures were low, with averages being 0.08 and 0.12 (log CFU/g) for the extended logistic and Baranyi model, respectively. The *RMSE* values at low and high range dynamic temperatures were very low, being 0.16, 0.15 with the extended logistic model and 0.12, 0.07 with Baranyi model, respectively. The results of statistical analysis showed that there was no significant difference in the performances of the two growth models, suggesting that the models were equally suitable for describing the growth of *Salmonella Enteritidis* at various initial doses, constant and dynamic temperatures.

Keywords: *salmonella enteritidis*, minced beef, extended logistic, the ComBase web edition Baranyi

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1. INTRODUCTION

The concept of predictive microbiology is that a detailed knowledge of the growth of microorganisms in food products enables objective evaluation of the microbiological safety and quality of foods (Dens *et al.*, 1999). Following the understanding of this microbial ecology, the goal of predictive microbiology come with the power of developing mathematical equations that describe the behavior of microorganisms under different environmental factors (physical, chemical, competitive), which enable predictions of growth and/or survival of an organism of concern. Simply, predictive microbiology models may be used to estimate changes in the size of a microbial population in a food product as a function of environmental parameters such

as temperature (McMeekin *et al*., 1993). The most commonly used growth models in food microbiology are of two types: empirical (algebraic expressions), and growth rate models (almost all variants of the continuous logistic equation) which called the Verhulst or mechanistic model (Peleg and Corradini, 2011). Empirical models are built up to summarize or describe the data in mathematical curve (curve fitting). The mechanism produced this data is unknown or poorly understood. Examples are the logistic models. When the underlying mechanism is known or available, in this case mechanistic or deterministic or theoretical models can be constructed to represent this mechanism (Draper, 2006). Juneja *et al.* (2009) compared the performances of two empirical and two mechanistic models for describing the growth rate of Salmonellae in irradiated ground beef, but only at constant temperatures. Performances of these models were evaluated by using various statistical criteria. All the chosen models fitted well to the growth data of Salmonellae based on these criteria. The results of statistical analysis showed that there was no significant difference in the performances of the four primary models, suggesting that the models were equally suitable for describing isothermal bacterial growth. In addition, Yılmaz (2011) compared the performance of the Baranyi model for prediction of the effect of plant essential oils on growth potential of Salmonellae in fish products stored under aerobic conditions with those of the empirical modified Gompertz and logistic models and Huang models. Recently, the growth kinetics of *Salmonella Enteritidis* in minced beef has been studied using the extended logistic model developed by Fujikawa *et al*. (2003; 2004) (unpublished data). The authors in their study successfully predicted growth of *Salmonella Enteritidis* in raw ground beef at various initial doses, constant and dynamic temperatures. Moreover, they developed a secondary model for the prediction of growth of *Salmonella Enteritidis* in raw ground beef by modeling the initial dose of the pathogen and temperature with the combination of primary growth model and a polynomial model (secondary), the secondary model developed reincorporated into the equation of the primary model to produce the tertiary model. Here in the present study the aim was that the estimated or predicted data with the extended logistic model (unpublished data) compares with that of online ComBase Baranyi model, empirical and mechanistic, for evaluating their performances for the prediction of growth of *Salmonella Enteritidis* in raw ground beef.

2. MATERIALS AND METHODS

2.1. The extended logistic model

The growth data, three trials at various initial doses, constant and dynamic temperatures, used in the present study was previously studied with the extended logistic model (unpublished data). Salmonella cell preparation, Salmonella inoculation, storage of inoculated ground beef, bacterial cell counts were done in the same manner as for ground chicken and liquid egg products (Zaher and Fujikawa, 2011; Sakha and Fujikawa, 2012; 2013). Averages of Salmonella counts for the three trials of various initial doses or the constant temperature experiments or the three samples of the dynamic temperature experiments were calculated for analysis (Zaher and Fujikawa, 2011; Sakha and Fujikawa, 2012; 2013). Salmonella counts of the samples during the storage were then analyzed with the extended logistic model, which is expressed as follows (Fujikawa *et al*., 2003; 2004):

$$\frac{dN}{dt} = rN\{1-(\frac{N}{N_{\max}})^{m}\}\{1-(\frac{N_{\min}}{N})^{n}\} \quad (1)$$

Here N is the population of a microorganism (CFU/g) at time t (h), r is the rate constant of growth (1/h), N_{max} is the

maximum population (CFU/g), and N_{min} is the initial population (CFU/g). *m* and *n* (>0) are parameters related to the curvature of the deceleration phase and the period of the lag phase, respectively.

The equation was solved numerically with the 4th-order Runge-Kutta method. Numerical data of Salmonella counts were analyzed by a computer program to fit to the growth model, which was developed using a spreadsheet software program, Microsoft Excel (Fujikawa and Kano, 2009). Here microbial populations estimated by the model (CFU/g) were then transformed to logarithm to make a growth curve.

Growth at a dynamic temperature was predicted using the values of parameters in equation (1) studied at constant temperatures (Fujikawa *et al*., 2003; 2004; Zaher and Fujikawa, 2011). The value for (*r*) at the measured temperature of the time interval during an experiment was obtained from the square root model (McMeekin *et al.,* 1993).

2.2. ComBase DMFit web edition Baranyi model:

The same growth data, at various initial doses, constant and dynamic temperatures, estimated by the extended logistic model were then evaluated by web edition Baranyi model. DMFit web edition is a web-based application to fit bacterial curves where a linear phase is preceded and followed by a stationary phase. The models of the ComBase Predictor which can be accessed via the ComBase web site (http://www.combase.cc) were developed using DMFit (Baranyi and Roberts, 1994).

This edition of DMFit allows the user to view a graphical representation of microbiological growth / survival data and fit a growth/survival model to the data to obtain parameter estimates for maximum growth/death rate, lag time (or shoulder), initial cell count, final cell count, and estimate standard errors on these parameters

2.2.1. ComBase Models

Bacterial curves can be fitted to two different types of models, the first is the model of Baranyi and Roberts, and the second one is the trilinear model, biphasic models and linear models. In the present study the comparison carried out with model of Baranyi and Roberts. The model of Baranyi and Roberts (1994) describes a sigmoid bacterial curve. The main difference between this model and other sigmoid curves like Gompertz, Logistic, etc. is that the mid-phase is close to linear unlike those classical sigmoid curves which have a pronounced curvature there. The model of Baranyi and Roberts has 4 main parameters (Initial Value, lag/shoulder, maximum rate, Final Value) and 2 curvature parameters: mCurv and nCurv which describe the curvature of the sigmoid curve respectively at the beginning and at the end of the growth phase. In this version, the values of mCurv and nCurv depend on the model selected by the user: When selecting model of Baranyi and Roberts (no lag), the curvature parameter mCurv is set to zero, the model describes only the growth/death and the stationary phase. When model of Baranyi and Roberts (complete model) is selected, default values are used for mCurv and nCurv: mCurv =10 and nCurv =1 (Baranyi and Roberts, 1994):

2.3. Secondary models

Secondary models for the rate constant of growth or maximum growth rates (r or μ_{max}) and N_{max} were developed to express the effect of various initial doses, constant temperatures on these parameters. Similarly, the parameters of the secondary model were estimated using the *RMSE*, the coefficient of regression and the student *T*. test.

2.4. Statistical analysis

Performance of the mathematical model was evaluated with (i) the square root of the mean of the square error, *RMSE* between log-transformed cell concentrations estimated with the model (log N_{est}) and those observed (log N_{obs}) at the observation points, which is described below and (ii) the

residual, which is the value of log N_{obs} minus log N_{est}, for each observation point during the growth (*Oscar, 2009*). (iii) The student *T*. test has been used to clarify if there were significant or non-significant differences between the estimated data with both models at the same time of observation points at various initial doses, constant and dynamic temperatures.

$$RMSE = \sqrt{\frac{\sum_{i=1}^{k} (\log N_{iobs} - \log N_{iest})^2}{k}} \quad (2)$$

Here *k* is the total number of observation points in a growth curve. Statistical analysis of data including regression analyses was performed with Microsoft Excel.

3. RESULTS

3.1. Prediction performances at various initial doses

Growth kinetics of *Salmonella Enteritidis* (a cocktail of four strains) in raw ground beef at various initial doses of *Salmonella Enteritidis* was first compared using the extended logistic and Baranyi & Roberts models. Salmonella was injected into ground beef at various initial doses ranging from 2.3 to 5.3 log CFU/g and then stored at a given temperature of 24℃. The growth curves were precisely described with the two growth model. There were no significant difference between the estimated values of data points with the two models (p>0.05), except at the initial dose of 2 (log CFU/g) it was significant (p<0.05). The values of *RMSE* were very low for logistic and Baranyi models (table 1A, B), and there were no significant differences (p>0.05) between *RMSE* values of logistic and Baranyi models. Also, the residuals for Salmonella described by both models were very small; all residuals for the data points were less than 0.5 log CFU/g. This shows that all points were in the acceptable prediction zone between -1 log and 0.5 log (Figure 1).

The values of the rate constant of growth (r) with the extended logistic were similar among them, ranging from 0.60 to 0.70 (1/h), therefore, the average was calculated and used in the growth model. Similarly, with Baranyi & Roberts model the values of (r) were similar among them, ranging from 0.20 to 0.30 (1/h) (table 1). Although that statistically, there were significant differences (p<0.05) between the values of (r) resulted by the two model.

Also, the lag periods in the growth curves of the extended logistic model were also similar, ranging from 1.6 to 3.1 h (unpublished data). However, the N_{max} values in the stationary phase calculated with both models were clearly higher at the higher initial doses. Values for N_{max} for extended logistic were 7.2, 8.3, 8.8, and 9.1 log CFU/g at the initial doses of 2.3, 3.3, 4.1, and 5.3 log CFU/g, respectively (unpublished data), while those calculated with Baranyi model were 7.14, 8.29, 8.73 and 9.13 at the initial doses of 2.21, 3.20, 4.11, and 5.24 log CFU/g, respectively. It important to mention that Baranyi & Roberts model always use its own initial doses, which were a little bit lower or equal to the observed initial doses in the present study.

The relationship between the values of initial dose (I) and the values of N_{max}, calculated with the extended logistic model, was expressed with a cubic equation with I *(*equation 3) (unpublished data).

$$N_{max} = 0.030I^3 - 0.52I^2 + 3.2I + 2.2 \quad (3)$$

While, the cubic equation expressed this relationship from the N_{max} values resulted from Baranyi & Roberts model (equation 4) was as follow:

$$N_{max} = 0.091I^3 - 1.21I^2 + 5.7 + 0.50 \quad (4)$$

The equation (3) could precisely describe the data points with the coefficient of regression of 0.999. Moreover, equation (4) could also precisely describe the data points

with the coefficient of regression of 1.00 (Figure 2).

A growth curve of Salmonellae in ground beef at a given value of *I* was then estimated with equation 2 to validate the polynomial model for N_{max}. The value for *I* in the experiment was measured to be 3.8 log CFU/g and thus the N_{max} value was estimated to be 8.6 log CFU/g with equation 3. Other parameter values in the growth model (equation 1) were the averages from the values of the curves studied at different initial doses. Namely r=0.64, m=0.58, and n=8.5. With those parameter values, a growth curve was predicted and the curve was very close to the observed data. The *RMSE* value for the curve was as low as 0.12 log (CFU/g). This result showed that the polynomial model with *I* was applicable to estimate N_{max} at a constant temperature (unpublished data). On the other hand, Baranyi model similarly predicted well the growth curve at initial dose of 3.73 log CFU/g and the N_{max} value was estimated to be 8.6 log CFU/g (Figure 3). The *RMSE* value for the curve was as low as 0.09 log (CFU/g).

3.2. Prediction performances at constant temperatures.

The growth kinetics of *Salmonella Enteritidis* in the ground beef was then compared using the extended logistic and Baranyi models at constant temperatures ranging from 8˚C to 36˚C. Here the values for *I* were constant (3.2 log CFU/g) at these temperatures. No Salmonellae growth was observed at 8˚C model. Growth curves of Salmonella in the ground beef at the constant temperatures were all sigmoidal and well described with the growth (unpublished data). The *RMSE* were very low ranging between 0.06 to 0.10 log CFU/g (Table 2A). The Baranyi model also showed good fitting for *Salmonella Enteritidis* growth curves at different temperatures resulted in low values of *RMSE* ranged between 0.08 to 0.15 log CFU/g (Table 2B), which were significantly different from the values by the logistic model (p<0.05). Also, the residuals for Salmonella described by both models were very small; all residuals for the data points were less than 0.5 log CFU/g (Figure 4A, B). Moreover, No significant differences were noticed between the estimated values of data points with the two models (p>0.05) at various constant temperatures. The values of r for Salmonella in the beef calculated with the Baranyi models were well described with the square root model (Fig. 5). Linear regression lines for r of Salmonella calculated with the extended logistic and Baranyi models were described by equations 5 and 6, respectively. Here T is temperature (˚C).

$$\sqrt{r} = 0.0401(T - 3.47) \quad (5)$$

$$\sqrt{r} = 0.0264(T + 4.55) \quad (6)$$

The coefficients of determination for the extended logistic and Baranyi models were 0.995 and 0.985, respectively. The values for N_{max} for Salmonella calculated with the extended logistic model were described as a line broken at 28.3˚C, which is shown in equation 7 (unpublished data).

$$\log N_{max} = 0.158T + 4.67 \quad 12 \le T < 28.3$$
$$= 9.15 \quad 28.3 \le T \le 36 \quad (7)$$

The values for N_{max} calculated with Baranyi model were described also as a line broken at 28.3˚C (Fig. 6) (equation 8).

$$\log N_{max} = 0.1557T + 4.66 \quad 12 \le T < 28.3$$
$$= -0.0038T + 9.09 \quad 28.3 \le T \le 36 \quad (8)$$

3.3. Prediction performances at dynamic temperatures

The values for *m* and *n* for Salmonella at these temperatures were almost constant, being 0.47 and 6.4 as the averages, respectively (unpublished data). Using the above equations (equations 5, 7) and the averages of the parameters of the growth model (equation 1), growth curves of Salmonella were predicted at dynamic temperatures. Here the value for *I* was constant (3.2 log CFU/g). The extended logistic growth model could well predict

Salmonella at both low and high dynamic temperatures. The *RMSE* values for *Salmonella* were very low, which were 0.16 and 0.15, respectively (unpublished data). On the other hand, Baranyi model also resulted in good prediction for Salmonella at low and high dynamic temperatures (Fig. 7).The *RMSE* values were very low, which were 0.12 and 0.07, respectively. The residuals resulted from both models at low and high dynamic temperatures were very small; all residuals for the data points were less than 0.5 log CFU/g (Figure 8). Moreover, No significant differences were noticed between the estimated values of data points with the two models (p>0.05) at low and high dynamic temperatures.

Table 1: Growth characteristics of *Salmonella Enteritidis* described with the extended logistic and Baranyi models in raw ground beef at various initial doses.

A.Extended logistic model					B. Baranyi model				
N_{min}[a]	r [b]	Lag	N_{max}[c]	*RMSE*[d]	N_{min}	r	Lag	N_{max}	*RMSE*
2.3	0.59	3.1	7.24	0.08	2.21	0.27	3.23	7.14	0.08
3.3	0.71	2.29	8.27	0.06	3.20	0.29	2.17	8.29	0.08
4.1	0.63	1.62	8.8	0.02	4.11	0.26	1.44	8.73	0.05
5.3	0.55	1.91	9.14	0.06	5.24	0.23	1.61	9.13	0.08

a. N_{min} is the initial population (CFU/g)
b. ***r*** is the rate constant of growth (1/h)
c. $\boldsymbol{N_{max}}$ is the maximum population (CFU/g)
d.RMSE the square root of the mean of the square error

Figure 1: Residual plots for the populations of Salmonella along through the storage period. Symbols: solid Symbols expressed with the extended logistic model and open Symbols expressed with the Baranyi model. Symbols: ●, $10^{2.3}$; ■, $10^{3.3}$; ▲, $10^{4.2}$; ♦, $10^{5.3}$

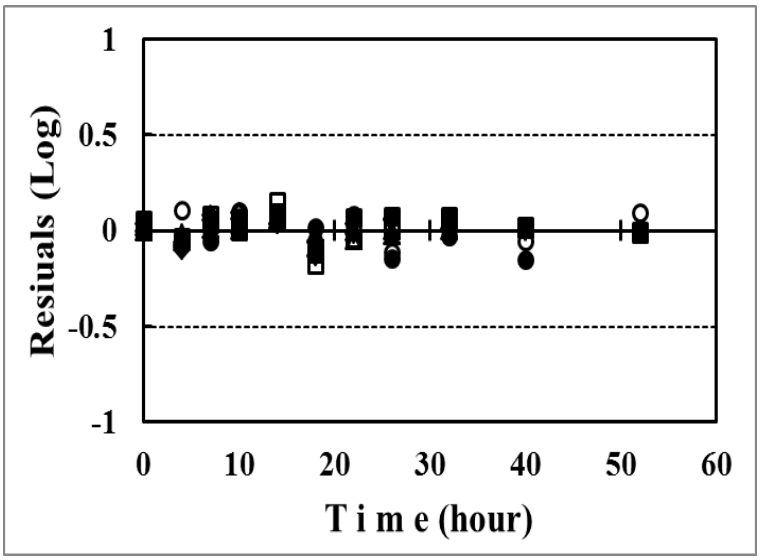


Fig. 2: The initial dose dependency of the values for N_{max}. The N_{max} values were described with Baranyi model.

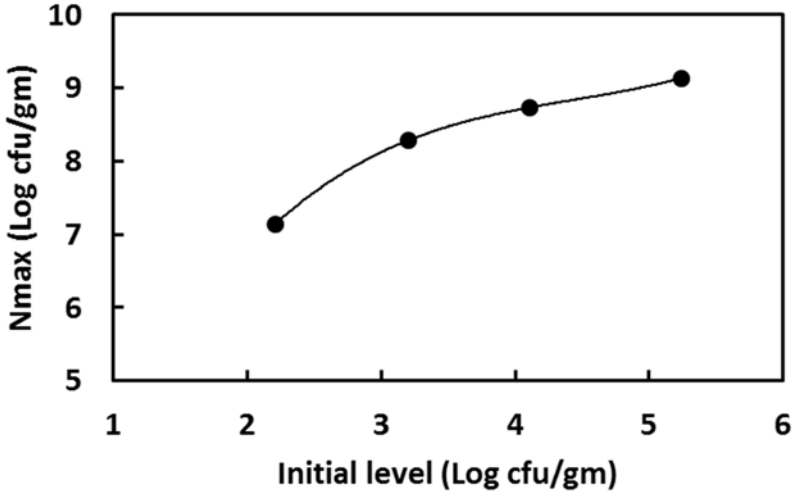


Fig. 3: Predictions of the pathogen at the initial dose of $10^{3.8}$ CFU/g. closed circles are measured values. Growth curves are described with Baranyi model.

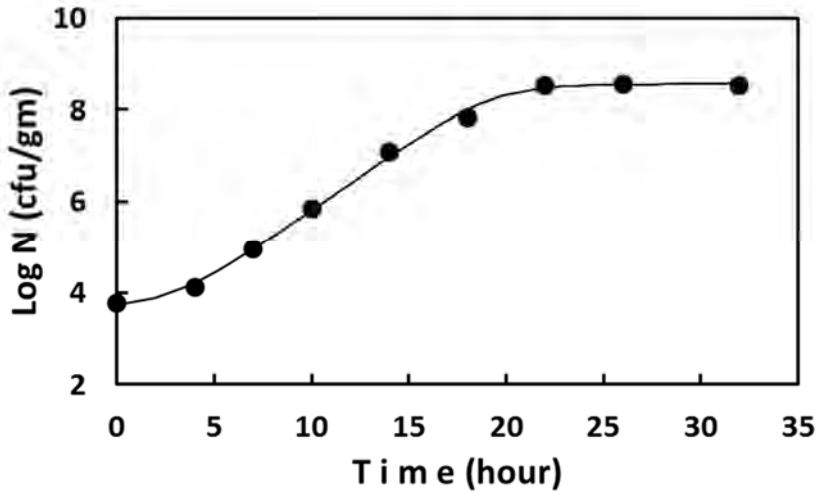


Table 2: Growth characteristics of *Salmonella Enteritidis* described with the extended logistic and Baranyi models in raw ground beef at various temperatures.

	A.Extended logistic model				B.Baranyi and Roberts model			
Temp.	r [a]	Lag (h)	N_{max} [b]	*RMSE* [c]	r	Lag (h)	N_{max}	*RMSE*
8ºc					0.002	*	2.93	
12 ºc	0.12	22.4	6.43	0.08	0.05	19.7	6.38	0.11
16 ºc	0.23	7.06	7.38	0.11	0.10	6.48	7.35	0.13
20 ºc	0.41	3.5	7.79	0.06	0.17	3.27	7.76	0.10
24 ºc	0.71	2.6	8.27	0.06	0.29	2.17	8.29	0.08
28 ºc	0.97	2.44	9.16	0.08	0.39	2.04	8.98	0.14
32 ºc	1.44	1.74	9.16	0.07	0.55	1.23	8.96	0.15
36 ºc	1.58	1.72	9.12	0.10	0.61	1.26	8.95	0.15

*no lag model (this curve cannot be described except by no lag Baranyi model)

a. $\boldsymbol{r}$ is the rate constant of growth (1/h) b. $\boldsymbol{N_{max}}$ is the maximum population (CFU/g)

c. *RMSE* the square root of the mean of the square error

Figure 4A, B: Residual plots for the populations of Salmonella along through the storage period at different temperatures. Symbols A: ●, 12; ■, 16; ▲, 20. Symbols B: ●, 24; ■, 28; ▲, 32; ♦, 36. Solid Symbols expressed with the extended logistic model and open Symbols expressed with the Baranyi model.

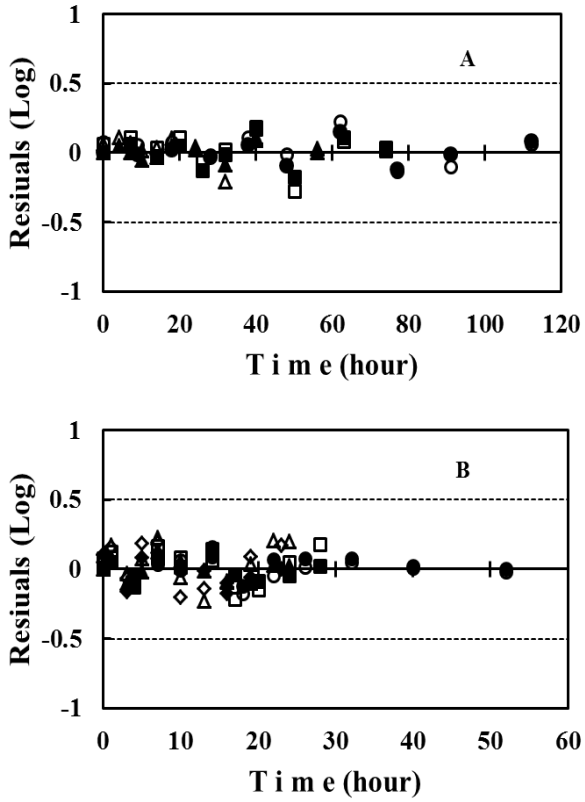


Figure 5: Square root models for the rate constant of growth for the Salmonella described with the Baranyi model. Line is the regression.

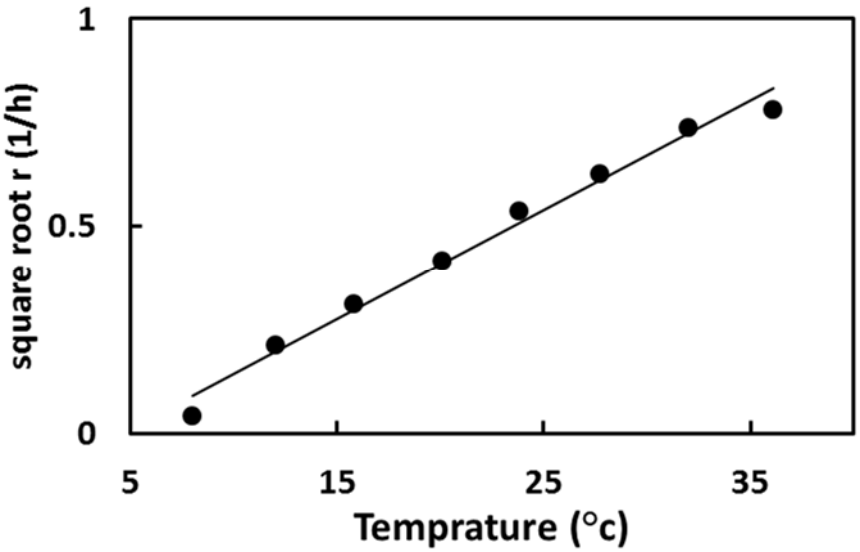


Figure 6: The maximum population for Salmonella at various constant temperatures described with the Baranyi model. Line is the regression.

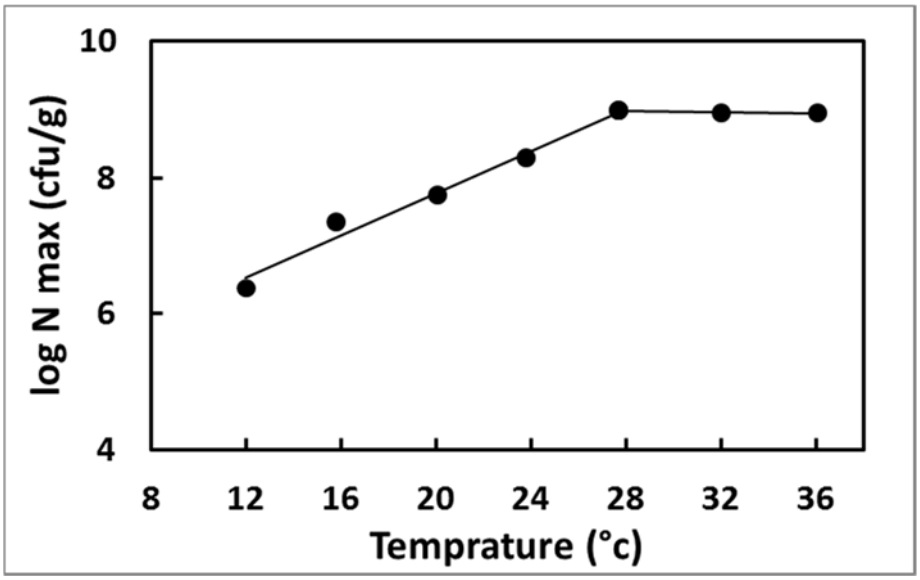


Fig. 7A, B: Prediction of growth of *Salmonella* in ground beef at low (A) and high (B) dynamic patterns of temperature. Closed circles are observed values of *Salmonella*. Growth curves are described with the Baranyi model (solid line). The dotted line shows the measured temperature of ground beef.

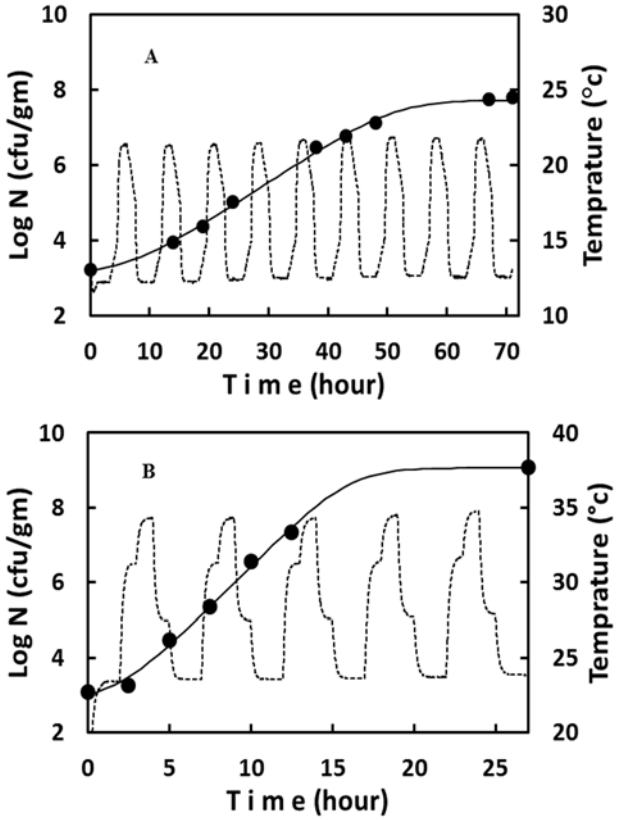
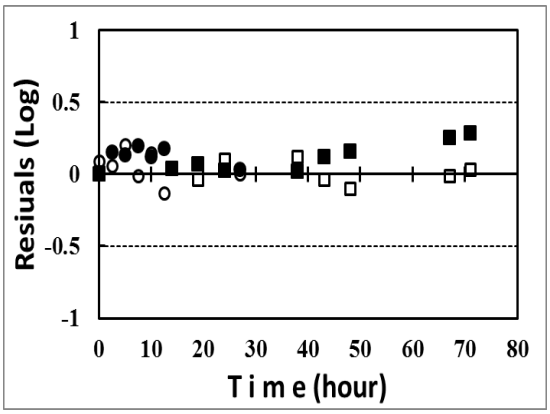


Fig. 8: Residual plot for the population of *Salmonella* along through the storage period at low (●) and high (■) dynamic patterns of temperature. Solid symbols expressed with the extended logistic model and open Symbols expressed with the Baranyi model.



4. DISCUSSION

Control of both pathogenic and spoilage microbe in a variety of foods is important to guarantee food safety and quality. Currently, the majority of food industry relies on conventional microbiological methods or rapid microbial techniques for quantification of microbial growth in food products. The traditional microbiological techniques are time-consuming. Rapid enumeration techniques, although relatively fast, are expensive and require necessary pre-enrichment steps to yield a detectable response. On the other hand, predictive mathematical models can provide the estimates of the growth of foodborne pathogen in a food matrix in a real time situation（Velugoti *et al.,* 2011). There are three categories to classify mathematical models. First based on the microbiological event categorized into kinetic and probability models (Roberts, 1989); the second based on modeling approach categorized into Empirical and Mechanistic ways (Roels and Kossen, 1978); third based on the variables considered into primary, secondary and tertiary (Whiting and Buchanan, 1993). Baranyi and Roberts published papers (1993, 1994, and 1995) that gave a good mathematical basis for mechanistic modelling of the lag phase. The Baranyi-model has subsequently been cited in more than 300 papers, and has become the most widely used primary growth model (Baranyi and Roberts, 2004).

It is worthy to mention that Baranyi model has an essential problem in its concept of modeling microbial growth. That is, the model built on the assumption that the concentration of a substance or substances critical to microbial growth would increase exponentially in a cell during the whole growth period, which is biologically impossible (Baranyi and Roberts, 1995). In addition, Baranyi and Roberts (2004) stated that purely mechanistic models are very rare in practical applications. Models in daily use are, in fact, between the two, using mechanistic elements when possible and completing them with empirical approaches when only observations are available, which apply on Baranyi and Roberts model, namely it describes the transition phases, for either the growth or death situation, in a way that can be also used for a fluctuating environment.

Sakha and Fujikawa (2012) compared the performances of the extended logistic and Baranyi models for describing the growth of the same strains used in the present study of Salmonella, but in pasteurized and unpasteurized liquid egg. They found that Baranyi model predicted well most of the growth curves at various initial doses and constant temperatures. The results at different initial doses showed that the *r* and

N_{max} values calculated by the Baranyi model were dependent on the initial dose, while the values of lag phase were reversely related to it. However, with the extended logistic model only N_{max} values were clearly dependent on the initial doses, therefore this relationship expressed by secondary model and validated experimentally well. Moreover, the values of *r* resulted with the extended logistic model were nearly double those produced with the Baranyi model. The growth kinetics of *Salmonella Enteritidis* in the ground beef at constant temperatures ranging from 8˚C to 36˚C showed that there were no Salmonella growth observed at 8˚C, therefore the extended logistic model cannot describe it, while the Baranyi model described it when selected to fit data with no lag phase, but the complete Baranyi model could not also describe it. The *r* values calculated with the extended logistic and Baranyi models were dependent on storage temperatures, but the magnitudes of *r* values described with Baranyi model were about half those described with the extended logistic model. N_{max} values described with both models were dependent on storage temperatures ≤28°c. In addition, the maximum N_{max} value obtained by the extended logistic was greater than this obtained by Baranyi model, being 9.16 and 8.98 logs CFU/g, respectively. In addition, lag phase values were reversely related to storage temperatures ≤28°c. These differences between the same growth parameters in the two models probably due to those experimentally determined growth parameters might be influenced not only by the chosen growth model but also by procedural details (Peleg and Corradini, 2011).

Generally, the results of statistical criteria used in the present study to evaluate the performances of the models showed that both models described well, but not equally, the growth of Salmonella in minced beef at various initial doses, constant and dynamic temperatures. In more details, the extended logistic model gave better prediction, smaller values of *RMSE*, especially at various initial doses and constant temperatures than the Baranyi model. However, at dynamic temperatures Baranyi model has smaller values of *RMSE* than the extended logistic model. These findings agree with those reported by Sakha and Fujikawa (2012) and Juneja *et al.* (2009), that both models were similarly able to describe bacterial growth. In contrast to this result was Yılmaz (2011) who found that the modified Gompertz and logistic models can be used more effectively than the semi mechanistic Huang and Baranyi models to predict the effect of plant essential oils on growth potential of Salmonellae in fish products. Also, Draper (1988) considered that the mechanistic models is more preferable than the empirical ones, as they usually contain fewer parameters, fit the data better and extrapolate more sensibly. While, the field of validity of an empirical model is much narrower than that of a theoretical model because they can be applied only at specific experimental conditions and cannot be extrapolated out of the field of investigation (Leguerinel and Mafart, 2008).

Another third mathematician's interpretation, that an agreement between prediction and observation alone only supports the modeling approach, but by itself it does not confirm the validity of the underlying assumptions, especially if alternative models, based on different assumptions can also explain and predict the same results (Peleg and Corradini, 2011). They proposed that agreement between prediction and observation is a necessary condition but not sufficient. Consequently, a slightly better fit of a particular model to a specific set of experimental growth results should not be interpreted as evidence of this model's superiority over alternative models. Unless a large database consisting of several organisms tested repeatedly is employed, the relative merits of different mathematical models might be better judged by utilitarian criteria (by its

mathematical simplicity, flexibility, the number of its adjustable parameters and, where appropriate, whether they have intuitive meaning and not based on the statistical criteria alone. Finally, depending on the vision of Peleg and Corradini (2011), the competition between models will continue in developing to be more flexible, simple and useful.

5. REFERENCES

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تقييم أداء النموذج اللوجستي االجديد ونموزج بارني للتنبؤ بنمو السالمونيلا انتريتيديس في اللحم البقري المفروم

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الملخص العربي

تستخدم النماذج الرياضية التنبؤية لحساب التغييرات الكمية في اعداد الميكروبات الممرضة اثناء عمليات التصنيع والتخزين والتوزيع عن طريق تتبع سلوك هذه الميكروبات في اي وقت تحت تاثير العوامل البيئية المختلفة مثل درجات الحرارة. وكنتيجة لذلك تمكن مستخدمي هذه النماذج من تقييم تأثير هذه العمليات على السلامة الميكروبيولوجية والجودة للغذاء وبالتالي تستطيع هذه النماذج ان تمدنا بالمعلومات الكافية لتقييم العمر الافتراضي وكذلك سلامة الغذاء. استهدفت هذه الدراسة تقييم أداء اثنين من نماذج التنبؤ بالنمو وذلك للتنبؤ بنمو السالمونيلا انتريتيديس في اللحم البقري المفروم، وهم النموذج اللوجستي االجديد ونموزج بارني (اصدارالانترنت). وتم تقييم أداء نماذج النمو باستخدام المعايير الإحصائية المختلفة، وهي الجذر التربيعي لمتوسط مربع الخطأ (*RMSE*)، وحساب المتبقيات، بالإضافة إلى اختبار T الاحصائي. وقد تبين أن كلا النموذجين قد وصفوا جيدا منحنيات نمو السالمونيلا انتريتيديس عند االحقنات الأولية المختلفة، وعند درجات الحرارة الثابتة والديناميكية. كما، لم يلاحظ أي فروق ذات دلالة إحصائية بين القيم المقدرة لنقاط البيانات باستخدام النموذجين عند مختلف الحقنات الأولية وكذلك عند درجات الحرارة الثابتة والديناميكية ($p>0.05$) باستثناء في الحقنات الأولية ٢ لوغ (مستعمرة ميكروبية/جم) وكان فارق كبيرا ذو دلالة إحصائية ($p<0.05$). وكانت قيم المتبقيات للسالمونيلا التي وصفها كلا النموذجين في ظروف النمو المختلفة صغيرة جدا. وكانت جميع المتبقيات لنقاط البيانات أقل من ٠,٠٥ لوغ (مستعمرة ميكروبية/جم) وهذا يدل على أن جميع نقاط البانات المقدرة من النموذجين كانت في منطقة التنبؤ المقبولة وهي بين -١ لوغ (مستعمرة ميكروبية/جم)٠,٠٥ لوغ (مستعمرة ميكروبية/جم). أيضا، كانت متوسطات القيم *RMSE* عند الحقنات الأولية المختلفة منخفضة جدا، والتي كانت ٠,٠٦ و ٠,٠٧ (مستعمرة ميكروبية/جم) لنموذج النمو اللوجستي الجديد ونموذج بارني، على التوالي. وبالمثل، كانت متوسطات قيم RMSE عند مختلف درجات الحرارة الثابتة منخفضة، والتي كانت متوسطاتها هي ٠,٠٨ و ٠,١٢ لوغ (مستعمرة ميكروبية/جم) لنموذج النمو اللوجستي الجديد ونموذج بارني، على التوالي. وكانت قيم *RMSE* ايضا منخفضة جدا عند نطاق درجات الحرارة الديناميكية المنخفضة والمرتفعة، وكانت ٠,١٦، ٠,١٥ لوغ (مستعمرة ميكروبية/جم) لنموذج النمو اللوجستي الجديد و ٠,١٢، ٠,٠٧ لوغ (مستعمرة ميكروبية/جم) لنموذج بارني، على التوالي. وقد أظهرت نتائج التحليل الإحصائي أنه لا يوجد اختلاف كبير في الأداء بين نماذج النمو الاثنين، مما يشير إلى أن النماذج كانت الي حد كبير مناسبة بالتساوي لوصف نمو السالمونيلا انتريتيديس عند االحقنات الأولية المختلفة، وعند درجات الحرارة الثابتة والديناميكية.

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