

Comparison of Prediction Capability of Primary Models for Detection of Chicken Meat Spoilage

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ABSTRACT

The main objective of the present work is to compare the prediction capability of different primary models known as the modified Gompertz, modified logistic and Baranyi models to simulate the effect of temperature on aerobically-stored raw and marinated chicken meat spoilage using one-step modelling approach. For this purpose, total viable count (TVC) growth data were extracted from the published work for aerobically-stored raw and marinated chicken meat. The fitting capability of the global models was compared by taking into account root mean square error (RMSE) and adjusted coefficient of determination (adjusted-R²). Statistical indices, RMSE and adjusted-R² values were found to be maximum 0.299 and minimum 0.970, respectively for each of the primary models and both of the chicken products. The prediction performance of the global models were evaluated with the r_{max} values that were independently published for aerobically-stored raw chicken meat, and RMSE values with lower than 5.11×10^{-2} revealed that one-step modelling approach can be reliably employed to predict TVC in aerobically-stored raw chicken meat.

Keywords: Global model, Microbiological quality, Growth kinetic, Chicken meat spoilage, Predictive microbiology

Tavuk Eti Bozulmasının Tespiti İçin Birincil Modellerin Tahmin Kabiliyetinin Karşılaştırılması

ÖZ

Bu çalışmanın temel amacı, depolama sıcaklığının aerobik olarak depolanan çiğ ve marine edilmiş tavuk eti bozulmasına etkisini tek adımlı modelleme yaklaşımı kullanarak simüle etmek için modifiye Gompertz, modifiye lojistik ve Baranyi modelleri olarak bilinen farklı birincil modellerin tahmin kabiliyetini karşılaştırmaktır. Bu amaç doğrultusunda, toplam canlı popülasyonu (TVC) çoğalma verileri, aerobik olarak depolanmış çiğ ve marine edilmiş tavuk eti için yayımlanmış çalışmadan elde edilmiştir. Global modellerin uydurma kabiliyeti, kök ortalama kare hatası (RMSE) ve düzeltilmiş belirleme katsayısı (düzeltilmiş-R²) dikkate alınarak karşılaştırıldı. İstatistiksel indeksler, RMSE ve düzeltilmiş-R² değerleri, birincil modellerin her biri ve her iki tavuk ürünü için sırasıyla maksimum 0.299 ve minimum 0.970 olarak bulundu. Global modellerin tahmin performansı, aerobik olarak depolanan çiğ tavuk eti için farklı çalışmadan elde edilen r_{max} değerleri ile değerlendirildi ve 5.11×10^{-2} 'den küçük RMSE değerleri, aerobik olarak depolanan çiğ tavuk etindeki toplam canlı popülasyonunu tahmin etmek için tek adımlı modelleme yaklaşımının güvenilir bir şekilde kullanılabileceğini ortaya koydu.

Anahtar Kelimeler: Global model, Mikrobiyolojik kalite, Çoğalma kinetiği, Tavuk eti bozulması, Tahminsel mikrobiyoloji

INTRODUCTION

Meat is one of the most important sources of nutrition [1]. Poultry meat is widely consumed due to being relatively cheap and having low fat content compared to red meat, and its consumption has recently increased extensively in the world [2, 3, 4]. But the shelf-life of raw poultry is quite limited, and short-shelf life is a big problem for the poultry industry [5]. Hence, extending the shelf-life of raw meat without any adverse effect on its quality is important. One of the most preferred ways to extend the shelf-life and enhance sensory quality for the muscle-origin foods such as meat and fish is marination process of soaking the food products in a usually acidic solution [6].

Predictive food microbiology is a recent field in food microbiology employing mathematical functions to describe responses of microorganisms in food products to different environmental conditions. These functions enable scientists to guess the behaviour of pathogens and spoilage microorganisms under different combined factors [7]. The main purpose of predictive food microbiology is to assure both food safety and food quality with mathematical models under different conditions. The most widely used mathematical functions in predictive food microbiology are primary and secondary models [8]. The modified Gompertz, modified logistic and Baranyi models are commonly employed primary models which were fitted to growth data as a function of time under static environmental conditions. Secondary models are applied to determine the relationship between environmental factors (e.g., temperature, pH and water activity) and the maximum growth rate or duration of lag phase which play a key role in description of growth behaviour. Among different environmental conditions, temperature has a very important effect on bacterial growth performance. In this regard, namely Ratkowsky model is the most popular secondary model to model the effect of temperature on maximum growth rate [9].

Primary models used in predictive food microbiology suitably enable to simulate the bacterial growth data as a function of time at static environmental conditions. But for real life, environmental conditions are not always static, and the temperature is the most likely changed environmental factor with time [10]. Hence, integrating primary and secondary models considering changing temperature effect on food products is important [7].

Two-step modelling approach is traditionally applied in the predictive food microbiology as a separately fitting of primary and secondary models to the growth data and kinetic parameters respectively; however, it is known that two-step modelling approach has some drawbacks. Being sequentially performed nonlinear regression two times is the main disadvantage that leads to be accumulation and propagation of errors for two-step modelling approach [11]. In other words, the sequentially performed primary and secondary model fittings usually reduce the overall prediction ability of the model and widen ambiguity of estimated parameter. The

mentioned situation is particularly encountered when the degree of freedom of the model is low [12]. Due to these drawbacks of two-step modelling approach, alternatively, a one-step modelling approach can be employed while simulating microbial behaviour in predictive food microbiology. In this approach, primary and secondary modelling is implemented simultaneously, and the use of one-step modelling approach enhances prediction power and provides more precise coefficients and robust confidence interval than the two-step modelling approach [13, 14]. When it appears to lack of sufficient microbiological data for secondary model, one-step modelling approach is much more considerably important to simulate bacterial growth behaviour [15, 16].

The simulation of bacterial growth behaviour with one-step modelling approach is a fairly new method in predictive food microbiology, and only some food products such as liquid eggs [17], potato salad [18] and oyster mushroom [16] were used as a food matrix to be performed one-step modelling approach. But there is no study pertaining to the simulation of microbial growth data of TVC for chicken meat considering one-step modelling approach. In this regard, employing one-step modelling approach to simulate bacterial growth data for marinated and unmarinated chicken meat is necessary and important to fulfil the gap in the predictive food microbiology field.

MATERIALS and METHODS

Data Collection

The total viable count (TVC) growth data were collected from the published work for aerobically-stored chicken meat [6]. Following experimental procedure for the determination of TVC and marination process were clarified in detail in their studies [6]. The growth data for isothermal storage temperatures (4, 10 and 15°C) were directly obtained from the presented growth tables. In the current study, fourteen growth data were collected separately for different isothermal storage temperatures (4, 10 and 15°C) and different types of chicken meat (marinated and unmarinated), which means eighty-four growth data were used to develop models at isothermal storage temperature in the range of 4 and 15°C. Additionally twenty growth rate data which were collected from published work for aerobically-stored raw chicken meat [5] were employed to assess the prediction capability of developed models for different temperatures.

Modelling

One-step Modelling

The most popular primary models employed in the predictive food microbiology are the modified Gompertz, modified logistic and Baranyi models which can be defined by Equations (1) (2) and (3), respectively [19, 20]:

$$x(t) = x_0 + (x_{\max} - x_0) \cdot \exp \left\{ -\exp \left[\frac{r_{\max} \cdot e}{(x_{\max} - x_0)} \cdot (\lambda - t) + 1 \right] \right\} \quad (1)$$

$$x(t) = x_0 + \frac{(x_{\max} - x_0)}{\left\{ 1 + \exp \left[\frac{4 \cdot r_{\max}}{(x_{\max} - x_0)} \cdot (\lambda - t) + 2 \right] \right\}} \quad (2)$$

$$x(t) = x_0 + r_{\max} \cdot F(t) - \frac{1}{\ln(10)} \cdot \ln \left[1 + \frac{e^{r_{\max} \cdot \ln(10) \cdot F(t)} - 1}{10^{(x_{\max} - x_0)}} \right] \quad (3)$$

F(t) is the adjustment function that is described by Baranyi and Roberts, [20]:

$$F(t) = t + \frac{1}{v} \ln \left(e^{-r_{\max} \cdot \ln(10) \cdot t} + e^{-r_{\max} \cdot \ln(10) \cdot \lambda} - e^{(-r_{\max} \cdot \ln(10) \cdot t - \mu_{\max} \cdot \lambda)} \right) \quad (4)$$

where t is the storage time (h), x(t) is the count of bacterial populations (log₁₀ CFU/g) at time t, x₀ is the initial count of bacterial populations (log₁₀ CFU/g), x_{max} is the maximum count of bacterial populations (log₁₀ CFU/g), r_{max} is the maximum bacterial growth rate (log₁₀ CFU/h) and λ is the duration of lag phase (h).

Ratkowsky model was applied to define r_{max} as a function of storage temperature with the Equation (5):

$$\sqrt{r_{\max}} = b_1(T - T_0) \quad (5)$$

where T is the storage temperature (°C), T₀ is the theoretical lowest bacterial growth temperature (°C), r_{max} is the maximum bacterial growth rate (log₁₀ CFU/h), b₁ is the regression coefficient.

Additionally, λ was correlated with r_{max} with respect to temperature using the Equation (6) [21]:

$$\lambda = \frac{b_2}{r_{\max}(T)} \quad (6)$$

where b₂ is the regression coefficient, r_{max}(T) is a function of temperature.

The global model was simultaneously fitted to bacterial growth data and temperature of storage, and each of the parameters was calculated by means of NonLinearModel command which uses Levenberg Marquardt algorithm in the Matlab 8.3.0.532 (R2014a) software (MathWorks Inc., Natick, MA, USA). Determination of suitable starting values in nonlinear regression procedure is necessary step to estimate the accurate parameters. The starting values for the parameters, x₀ and x_{max} were selected as the minimum and maximum concentration of bacterial populations considering the entire temperature range, respectively.

Randomly choosing starting points for the parameters, b₁, b₂ and T₀ might lead the estimated parameters to possible local optimal points around global one. Therefore, the starting points of these parameters were selected by using ga command which uses genetic algorithm in Global Optimization Toolbox of Matlab software. Following successful iteration process for the nonlinear regression procedure, the global optimum values of the parameters were obtained.

Comparison of Goodness of Fit of Global Models

The comparison of the global models' estimation capabilities was evaluated by taking into consideration the root mean square error (RMSE) and the adjusted coefficient of determination (adjusted-R²) values using Equations (7) and (8), respectively:

$$RMSE = \sqrt{\sum_{i=1}^n \frac{(\text{observed}_i - \text{fitted}_i)^2}{n - s}} \quad (7)$$

$$\text{adjusted-R}^2 = 1 - \left(\frac{n - 1}{n - s} \right) \left(\frac{SSE}{SST} \right) \quad (8)$$

where observed_i is the experimental count of bacterial populations, fitted_i is the predicted count of bacterial populations n is the number of experiments, s is the number of parameters of the model, SSE is the sum of squares of errors and SST is the total sum of squares.

Validation of Global Models

Verification of the global models developed in the predictive food microbiology is a necessary step to evaluate the prediction power of the models. In this regard, the prediction performance of the global models developed considering isothermal storage temperatures was assessed via independent experimental data which was performed for aerobically-stored raw chicken meat [5]. In validation step, the comparison of experimental

growth rate data with the predicted growth rate data were done with RMSE values of the global models. The global model with the lowest RMSE value was defined as the best model to predict growth rate data of TVC in aerobically-stored raw chicken meat.

RESULTS and DISCUSSION

Modelling of TVC in Raw Chicken Meat at Isothermal Storage Conditions

The observed growth data of TVC in aerobically-stored raw chicken meat [6] were fitted to the global models

being modified Gompertz, modified logistic and Baranyi models (Figure 1). The initial population of TVC was $5.10 \pm 0.30 \log_{10}$ CFU/g for each storage temperatures, while the maximum populations of TVC were 10.00 ± 0.40 , 10.10 ± 0.30 and $10.40 \pm 0.20 \log_{10}$ CFU/g for the storage temperatures of 4, 10 and 15°C, respectively. The maximum bacterial populations were observed on the storage days of 8, 6 and 5 for the chicken meat aerobically-stored at 4, 10 and 15°C, respectively. These results revealed that the growth potential of TVC in aerobically-stored chicken meat was enhanced with the increasing storage temperature.

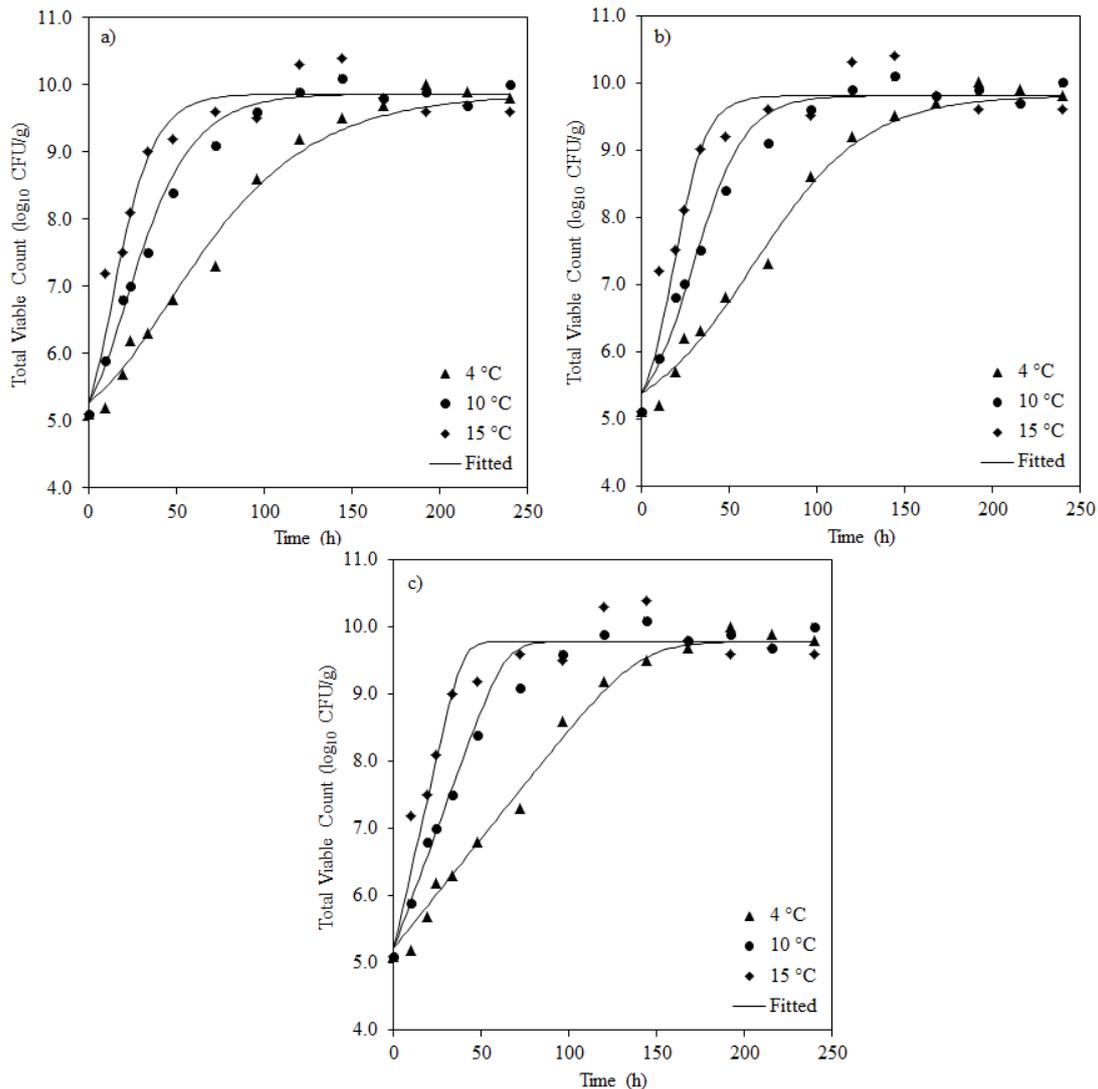


Figure 1. Growth data of TVC in raw chicken meat aerobically stored at 4, 10 and 15°C to fit to the (a) modified Gompertz model, (b) modified logistic model and (c) Baranyi model using one-step modelling approach

The minimum populations of TVC were calculated as 4.95 ± 0.12 , 4.80 ± 0.12 and $5.23 \pm 0.11 \log_{10}$ CFU/g for the modified Gompertz, modified logistic, Baranyi models, respectively (Table 1). The estimated minimum counts were reported to be 5.12 ± 0.20 , 5.26 ± 0.12 and $5.67 \pm 0.22 \log_{10}$ CFU/g by Lytou et al. [6] for the storage

temperatures of 4, 10 and 15°C, respectively. These results indicated that the modified Gompertz and Baranyi models integrated with one-step modelling approach gave better prediction performance compared to the estimated minimum bacterial populations previously reported by Lytou et al. [6].

Table 1. Parameters of the primary and secondary models used for the description of bacterial growth behaviour of TVC in the raw chicken meat at different isothermal conditions based on the one-step modelling approach

Data Source	Primary Models	Model parameters ^a					RMSE	adjusted-R ²
		X ₀ (log ₁₀ CFU/g)	X _{max} (log ₁₀ CFU/g)	T ₀ (°C)	b ₁	b ₂		
Lytou et al. [6]	Modified Gompertz	4.95±0.12	9.87±0.07	-8.95±1.10	1.54 × 10 ⁻² ±1.08 × 10 ⁻³	0.00±0.00	0.278	0.974
	Modified Logistic	4.80±0.12	9.82±0.07	-8.68±1.07	1.56 × 10 ⁻² ±1.09 × 10 ⁻³	0.00±0.00	0.299	0.970
	Baranyi	5.23±0.11	9.79±0.06	-8.44±0.96	1.45 × 10 ⁻² ±9.29 × 10 ⁻⁴	0.00±0.00	0.282	0.973

^a Estimated values ± standard errors. RMSE: root mean square error; adjusted-R²: adjusted coefficient of determination.

The maximum populations of TVC were found to be 9.87±0.07, 9.82±0.07 and 9.79±0.06 log₁₀ CFU/g for the modified Gompertz, modified logistic and Baranyi models, respectively (Table 1). Experimentally obtained maximum populations were averagely 10.17 log₁₀ CFU/g in the temperature range of 4 and 15°C, and its estimation were reported as 9.84±0.12, 9.86±0.16 and 9.79±0.17 log₁₀ CFU/g for the storage temperatures of 4, 10 and 15°C, respectively by Lytou et al. [6]. These results simply mean that each of the primary models developed in the current study estimated better than the model used by Lytou et al. [6].

The secondary model's parameter, T₀ was estimated as -8.85±1.10, -8.68±1.07 and -8.44±0.96°C for the modified Gompertz, modified logistic and Baranyi models, respectively. Regarding this parameter, it is important to underline that the estimated T₀, which is the temperature-intercept of the Ratkowsy model, only represents the theoretical minimum temperature and it actually can be considerably higher than this estimation [22].

As considered the secondary model parameters (b₁, b₂ and T₀), r_{max} and λ parameters could be found. With increasing the storage temperature from 4 to 15°C, the r_{max} increased from 0.040 to 0.136, from 0.039 to 0.137 and from 0.033 to 0.116 log₁₀ CFU/h for the modified Gompertz, modified logistic and Baranyi models, respectively (Figure 2). Additionally, none of the global models that are employed in this study gave λ values meaning the microorganisms are already ready to grow even before storage for the chicken at the storage temperature between 4 to 15°C. This result is in agreement with the findings of the work of Lytou et al. [6] who did not report any λ value for TVC in chicken meat.

The prediction power of the global models being different primary models (the modified Gompertz, modified logistic and Baranyi models) was compared taking into consideration their RMSE and adjusted-R² (Table 1). RMSE and adjusted-R² were found to be maximum 0.299 and minimum 0.970, respectively for each primary model. The coefficient of determination (R²) was reported as maximum 0.967 (adjusted-R² = 0.957) for the model that are used by Lytou et al. [6]. These results demonstrated that each of the global models used in this work gave better goodness of fit than the model developed by Lytou et al. [6] to simulate growth data of TVC in aerobically-stored chicken meat.

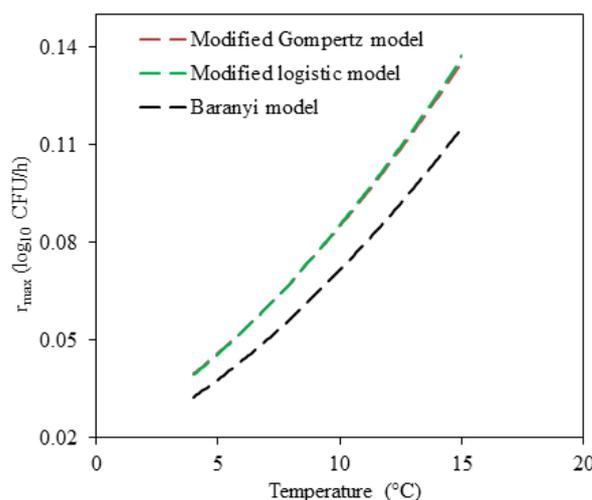


Figure 2. The effect of storage temperature on the maximum growth rate of TVC obtained from the one-step modelling approach

Modelling of TVC in Marinated Chicken Meat at Isothermal Storage Conditions

The experimental growth data of TVC in marinated and aerobically-stored chicken meat [6] were also fitted to the global models (Figure 3). The initial population of TVC was 4.50±0.30 log₁₀ CFU/g for each storage temperatures, while the maximum populations of TVC were 8.00±0.10, 8.80±0.10 and 8.90±0.10 log₁₀ CFU/g for the storage temperatures of 4, 10 and 15°C, respectively. These results demonstrated that marination process has a lethal effect on TVC in chicken meat at the level of 0.60 log₁₀ CFU/g and decreased growth potential of TVC in aerobically-stored chicken meat.

The minimum populations of TVC were calculated as 4.29±0.12, 3.73±0.30 and 4.32±0.11 log₁₀ CFU/g for the modified Gompertz, modified logistic, Baranyi models, respectively (Table 2). The estimated minimum counts were reported to be between 4.25±0.13 and 3.95±0.21 by Lytou et al. [6] for the storage temperatures in the range of 4 and 15°C. These results demonstrated that the modified Gompertz and Baranyi models integrated with one-step modelling approach gave better prediction performance compared to the estimated minimum bacterial populations previously reported by Lytou et al. [6].

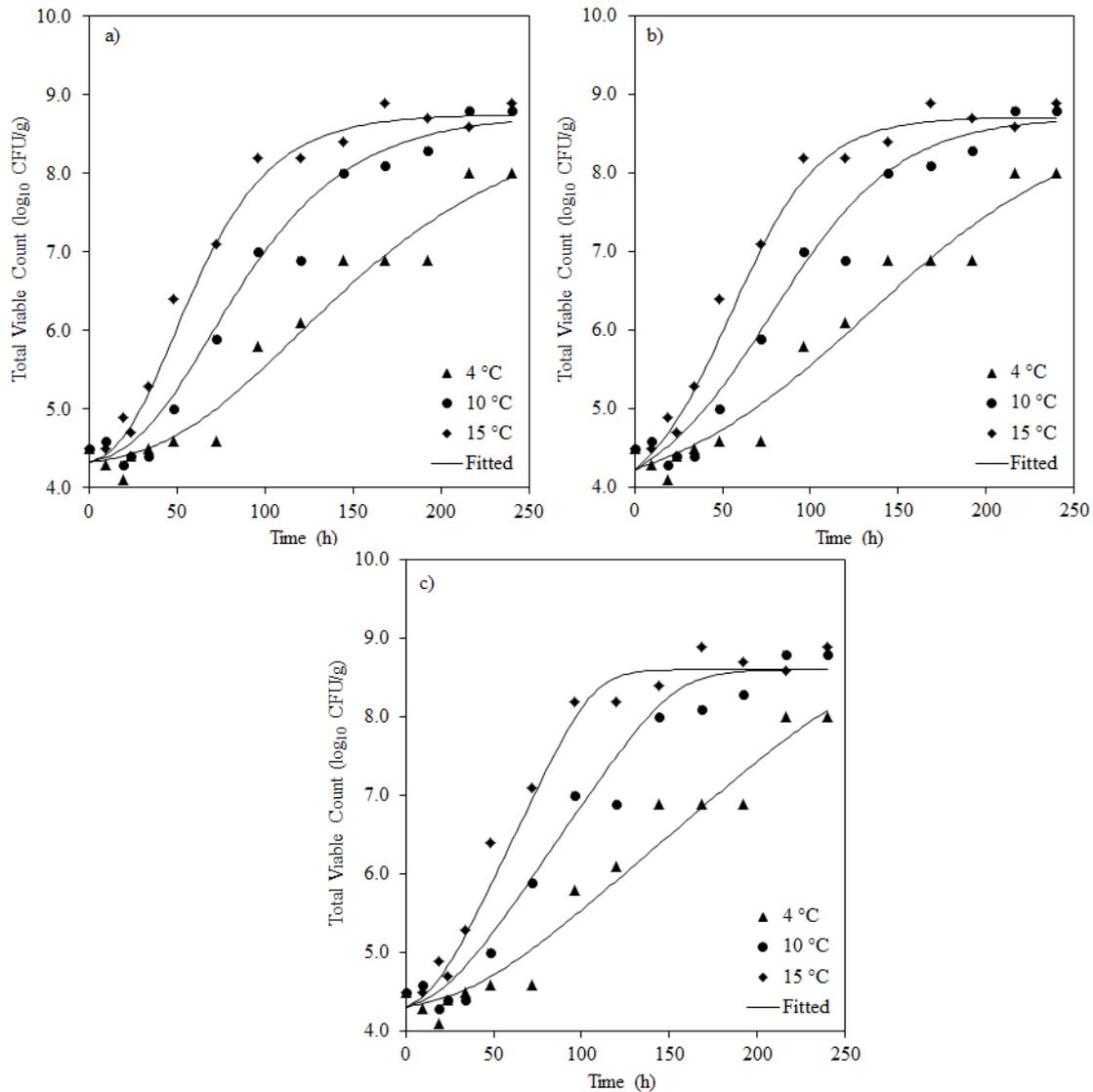


Figure 3. Growth data of TVC in marinated chicken meat aerobically stored at 4, 10 and 15°C to fit to the (a) modified Gompertz model, (b) modified logistic model and (c) Baranyi model using one-step modelling approach

Table 2. Parameters of the primary and secondary models used for the description of bacterial growth behaviour of TVC in the marinated chicken meat at different isothermal conditions based on the one-step modelling approach

Data Source	Primary Models	Model parameters ^a					RMSE	adjusted-R ²
		X ₀ (log ₁₀ CFU/g)	X _{max} (log ₁₀ CFU/g)	T ₀ (°C)	b ₁	b ₂		
Lytou et al. [6]	Modified Gompertz	4.29±0.12	8.75±0.11	-15.49±1.54	7.57 × 10 ⁻³ ±5.73 × 10 ⁻⁴	0.92±0.28	0.254	0.979
	Modified Logistic	3.73±0.30	8.72±0.11	-15.71±1.65	7.25 × 10 ⁻³ ±5.77 × 10 ⁻⁴	0.22±0.49	0.273	0.975
	Baranyi	4.32±0.11	8.61±0.10	-15.84±1.60	7.03 × 10 ⁻³ ±5.44 × 10 ⁻⁴	0.73±0.27	0.283	0.973

^a Estimated values ± standard errors. RMSE: root mean square error; adjusted-R²: adjusted coefficient of determination.

With increasing the storage temperature from 4 to 15°C, the r_{max} increased from 0.022 to 0.053, from 0.020 to 0.050 and from 0.019 to 0.047 log₁₀ CFU/h for the modified Gompertz, modified logistic and Baranyi models, respectively (Figure 4a). On the other hand, estimated λ values decreased from 42.4 to 17.3, from

10.9 to 4.5 and from 37.6 to 15.6, for the modified Gompertz, modified logistic, Baranyi models, respectively (Figure 4b). These results demonstrated that r_{max} of TVC chicken meat was considerably decreased and λ values started to be appeared with marination process.

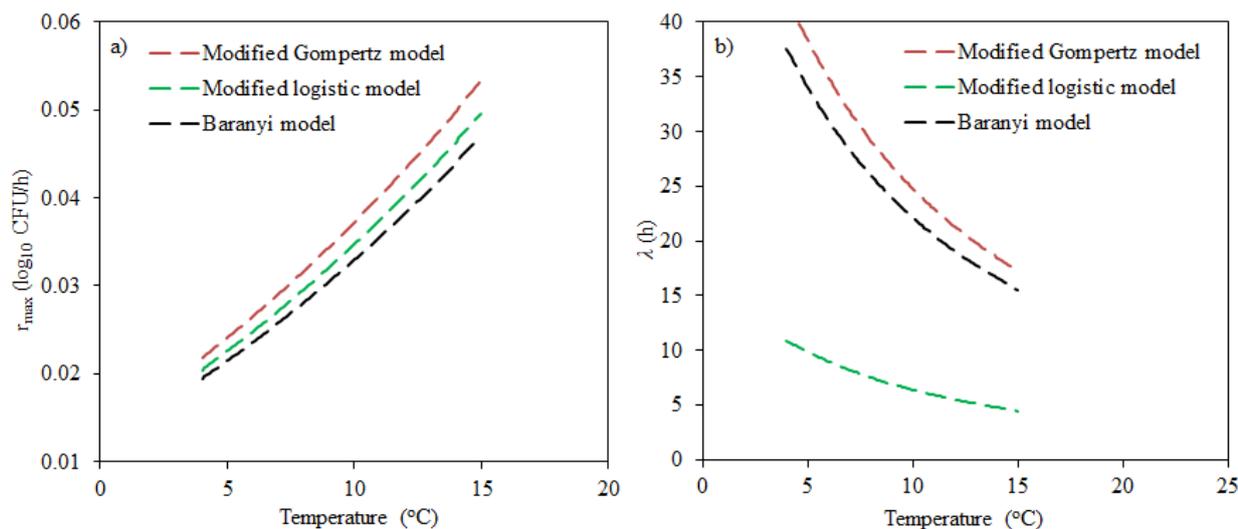


Figure 4. Values of (a) the maximum growth rate (r_{max}) and (b) the lag phase duration (λ) of TVC in marinated chicken meat as a function of storage temperature estimated using the Ratkowsky model

RMSE and adjusted- R^2 were found to be lower than 0.283 and higher than 0.973, for each global model. The coefficient of determination (R^2) was reported as maximum 0.963 (adjusted- $R^2 = 0.952$) for the model that are used by Lytjou et al. [6]. These results revealed that each of the global models used in this work gave better goodness of fit than the model developed by Lytjou et al. [6] to simulate growth data of TVC in aerobically-stored marinated chicken meat.

Validation of the Global Models

The observed growth data of TVC in aerobically-stored raw and marinated chicken meat were compared the predicted growth data with the global models involving the modified Gompertz, modified logistic and Baranyi models (Figure 5). As can be seen from the Figure 5, each of the global models successfully described the observed growth data of TVC in aerobically-stored raw and marinated chicken meat.

However, verification of the models that are developed in the predictive food microbiology is required for the purpose of employing reliably them to be simulation tool; therefore the prediction power of the global models was evaluated with the indices of RMSE. For the validation step, independent maximum growth rate data of TVC were collected from the work of Dominguez and Schaffner, [5] conducted for the chicken meat aerobically-stored at the temperature between 5 and 15°C. The maximum growth data were predicted via the all global models involving different primary models, and they were compared with the experimentally observed the maximum growth data published [5] (Table 3). RMSE values were found to be 4.88×10^{-2} , 4.92×10^{-2} and 5.11×10^{-2} for the modified Gompertz, modified logistic and Baranyi models, respectively. These results confirmed that the one-step modelling approach exhibited considerably improved prediction power no matter which primary model is used. As the spoilage of chicken meat is directly linked with TVC population, the validated global model involving the modified Gompertz model exhibited a high potential as a prediction tool to be employed for the prediction of chicken meat spoilage.

Table 3. Predicted and observed TVC growth rates in the raw chicken meat at different isothermal conditions.

Storage temperature (°C)	Observed r_{max} (\log_{10} CFU/h) ^a		Predicted r_{max} (\log_{10} CFU/h) ^b		
			Modified Gompertz	Modified logistic	Baranyi
5	0.0251	0.0267	0.0461	0.0458	0.0380
7	0.0394	0.0549	0.0602	0.0602	0.0502
10	0.0435	0.0522	0.0850	0.0854	0.0715
12	0.0779	0.2424	0.1039	0.1046	0.0879
15	0.1268	0.1365	0.1358	0.1372	0.1156

^a Observed and predicted r_{max} values (\log_{10} CFU/h) obtained from Dominguez and Schaffner, [5].

^b Predicted r_{max} values (\log_{10} CFU/h) calculated with different one-step modelling approach

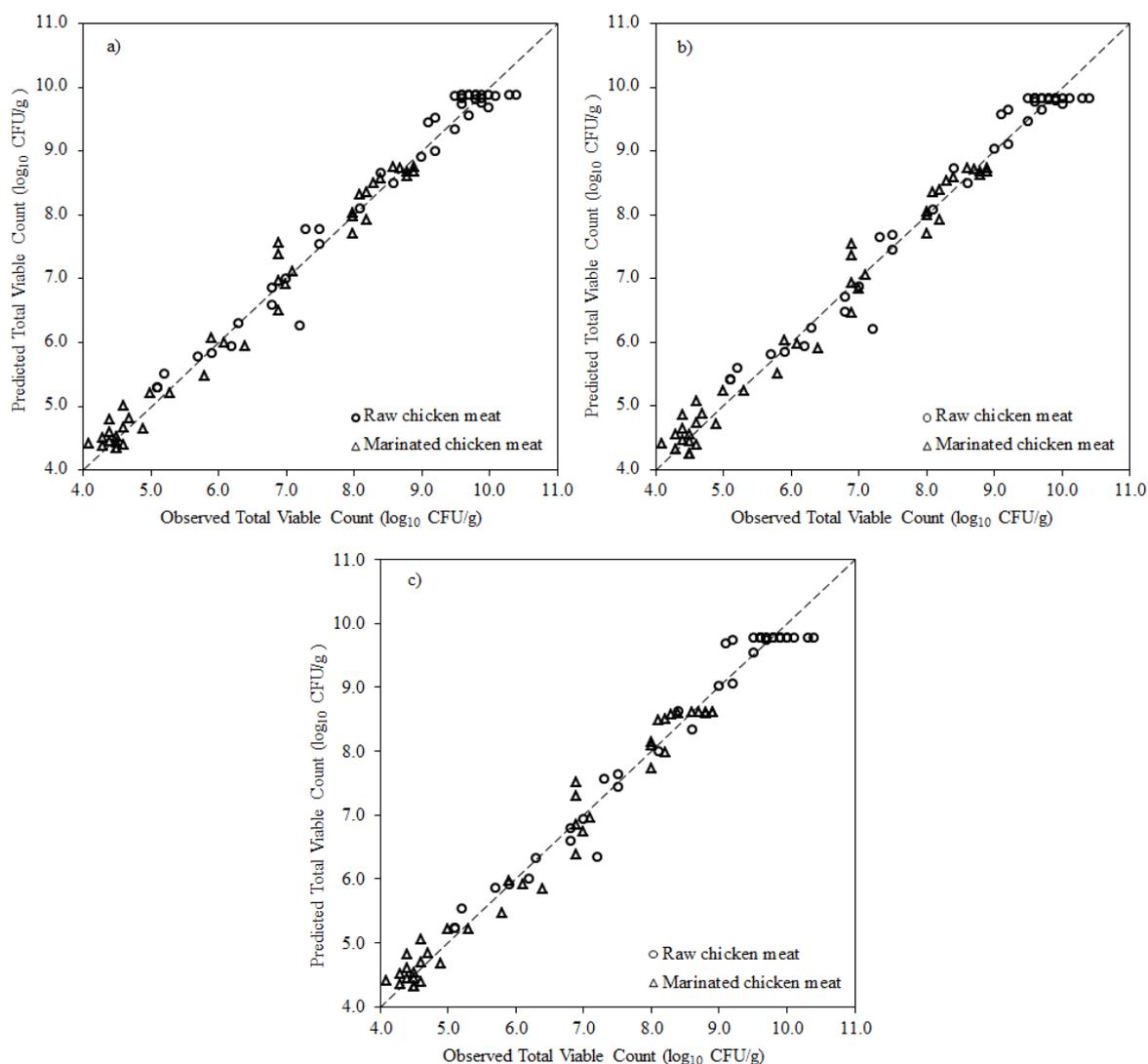


Figure 5. The correlation between observed TVC populations in chicken meat aerobically stored at 4, 10 and 15°C and the fitted TVC populations with (a) modified Gompertz model, (b) modified logistic model and (c) Baranyi model using one-step modelling approach.

CONCLUSIONS

The one-step modelling approach improved the prediction capability of all of the primary models which were published for the quantitative description of TVC population in aerobically-stored chicken meat. However, the modified Gompertz model has the best goodness of fit to predict the TVC population as a function of time and storage temperature if their initial population is known for raw and marinated chicken meat. Therefore, one-step modelling approach involving the modified Gompertz model has a high potential to be used as a prediction tool for the detection of chicken meat spoilage based on TVC population.

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