



Comparison of Secondary Models for Modelling the Growth of *Salmonella* in Leafy Greens

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ABSTRACT

This study evaluated the performance of three mathematical models—the Ratkowsky square-root, Arrhenius-type, and Cardinal models—in describing the temperature-dependent growth of *Salmonella enterica* in leafy greens. Therefore, data on the maximum growth rate ($\mu_{\max}$) of *Salmonella enterica* in leafy greens under different temperature conditions were collected from peer-reviewed scientific publications available in databases. The Integrated Pathogen Modeling Program (IPMP) software was then used for modelling and analysis. The results indicated that the sub-optimal Ratkowsky model most accurately captured growth rates below the organism's optimum temperature, with parameters $a=0.02$ and $T_{\min}=7.3^{\circ}\text{C}$ estimated with high precision. In contrast, the model's supra-optimal parameters were weakly constrained due to limited high-temperature data. Despite achieving strong explanatory power ($R^2=0.90$), the Arrhenius-type and Cardinal models had significant parameter uncertainty over the whole temperature range, which limited their usefulness. These findings support the use of simpler, empirically grounded models in predictive microbiology when thermal data are incomplete. Future research should prioritize gathering data at higher temperatures to better characterize growth decline in the supra-optimal range.

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Introduction

Foodborne illnesses remain a major global public health concern, affecting an estimated 48 million people annually and causing approximately 128,000 hospitalizations, and 3000 deaths in the USA (Warmate & Onarinde, 2023). In addition to the human toll, these illnesses impose significant economic burdens due to medical costs, lost productivity, and food recalls (Hoffmann et al., 2024). A key strategy to mitigate such impacts involves the ability to accurately identify, monitor, and predict the growth or survival of pathogenic microorganisms in food products (Aladhadh, 2023). However, conventional microbiological methods used for such purposes are often labor-intensive, time-consuming, and costly (Yu et al., 2025). Moreover, the data generated from these traditional approaches are typically not cumulative or easily transferable across different food systems (Kumar et al., 2024; Tarlak, 2023).

To address these limitations, predictive microbiology has emerged as a valuable tool, offering mathematical models to forecast microbial behavior under varying environmental and processing conditions (Taiwo et al., 2024; Tarlak, 2023). These models enable researchers and

food safety professionals to assess microbial risks without relying solely on experimental methods. Predictive models are generally categorized into three types: primary, secondary, and tertiary. Primary models describe microbial growth over time (e.g., using Baranyi or Gompertz equations), while secondary models quantify the influence of environmental variables—such as temperature, pH, and water activity—on the parameters derived from primary models, particularly the maximum specific growth rate ($\mu_{\max}$) and lag phase duration (Baranyi et al., 2024; Huang, 2013, 2014; Taiwo et al., 2024). The creation of a useful interface for forecasting is made easier by the tertiary models, which are produced by integrating the previous two models into a computer program such as IPMP. For non-expert end users, including hazard analysts, researchers, and those with little understanding of microbiological prediction, to effectively utilize these tools, it is imperative that complex predictive models be made simpler and easier to understand (Kumar et al., 2024).

Numerous secondary models have been developed to describe the temperature dependence of microbial growth, including the Ratkowsky square-foot model, the Huang

square-foot model, the Cardinal Temperature Model, and the Arrhenius-type model (Huang et al., 2011b; Huang, 2014; Li et al., 2008; Mertens et al., 2012; Tarlak, 2023). Despite their widespread use, these models vary in complexity, biological interpretability, and fit quality depending on the organism and food matrix in question (Huang et al., 2011a; McMeekin et al., 2013). In the context of leafy greens, which present a complex and variable surface environment conducive to pathogen attachment and growth, choosing an appropriate model becomes especially critical.

This study aimed to compare the performance of several widely used secondary models—namely the Ratkowsky square-root, Huang square-root, Cardinal, and Arrhenius-type models—in describing the temperature-dependent growth rate of *Salmonella* in leafy greens collected from literature. The study also sought to identify the most appropriate modeling approach for use in quantitative microbial risk assessments (QMRAs) and food safety decision-making related to fresh produce by evaluating model fit, predictive accuracy and biological interpretability.

Materials and Methods

Data Collection

Maximum growth rate data ($\mu_{\max}$) of *Salmonella enterica* in leafy greens under varying temperature conditions were collected from peer-reviewed scientific publications available in databases such as Scopus and Web of Science. Only studies that reported quantitative *Salmonella* growth rates on leafy greens (e.g., lettuce,

spinach, arugula) at known isothermal conditions were included. Studies that did not report exact growth rates or experimental conditions (e.g., pH, initial inoculum, temperature) were excluded to ensure consistency.

To maintain data quality and comparability, the following criteria were applied:

- Growth data must be derived from isothermal experiments.
- Leafy greens must be the primary food matrix.
- The strain of *Salmonella* used must be identified or commonly reported (e.g., *S. Typhimurium*, *S. Enteritidis*).
- $\mu_{\max}$ values must be estimated using a recognized primary growth model (e.g., Baranyi or Gompertz).

Data from multiple studies presented in Table 1 were extracted and compiled into a dataset comprising maximum specific growth rates ($\mu_{\max}$) at different temperatures (ranging from 5°C to 40°C, depending on study availability).

Modeling Approach

The collected $\mu_{\max}$ values were used to evaluate the performance of four commonly used secondary models, including suboptimal Ratkowsky square-root (Eq. 1), full temperature range Ratkowsky square-root (Eq. 2), suboptimal Huang square-root (Eq. 3), full temperature range Huang square-root (Eq. 4), Cardinal (Eq. 5), suboptimal Arrhenius-type (Eq. 6), and full temperature range Arrhenius-type (Eq. 7) models that describe microbial growth rate as a function of temperature (Huang, 2014):

Table 1. A list of published studies

Bacteria	Food product	Temperature range (°C)	References
<i>Salmonella</i> Enteritidis ATCC BAA-708 and ATCC 4931,	Lettuce	5-25	(Koseki & Isobe, 2005)
<i>Salmonella</i> Typhimurium ATCC 29057, 29629, and 29630	Lettuce	7-30	(Sant'Ana et al., 2012)
<i>Salmonella</i> Typhimurium 277 and 386, <i>Salmonella</i> Enteritidis ATCC 13076	Baby spinach	10-37	(Puerta-Gomez et al., 2013)
<i>Salmonella</i> Typhimurium LT2	Cabbage	15-35	(Yoon et al., 2014)
<i>Salmonella</i> Typhimurium ATCC 19585, ATCC 43971, and phage type DT104	Lettuce	5-37	(Veys et al., 2016)
<i>Salmonella</i> Enteritidis SE86, <i>Salmonella</i> Typhimurium L12031, <i>Salmonella</i> Typhimurium 1T2, <i>Salmonella</i> Anatum, <i>Salmonella</i> Newport, <i>Salmonella</i> Saint Paul	Lettuce	5-40	(De Oliveira Elias et al., 2018)
<i>Salmonella</i> Enteritidis SE86, <i>Salmonella</i> Typhimurium L12031 and LT2, <i>Salmonella</i> Anatum, <i>Salmonella</i> Newport, <i>Salmonella</i> Saint Paul	Lettuce	10-25	(Park et al., 2019)
<i>Salmonella</i> Typhimurium	Iceberg lettuce	15	(Tarlak et al., 2020)
<i>Salmonella</i> Reading VI 51763	Lettuce	12-36	(Xiao et al., 2021)
<i>Salmonella</i> Typhimurium SA62, Z62, Z95, Z9, X79, Z27, HZC3, X54, X100 and X63	Lettuce	5-25	(Ndraha et al., 2022)
<i>Salmonella enterica</i> 1060117v and 1060271v	Lettuce	9-18	(Cuggino et al., 2023)
<i>Salmonella</i> Thompson	Cabbage	5-36	(Son et al., 2024)
<i>Salmonella</i> Typhimurium ATCC 13311, <i>Salmonella</i> Enteritidis KCMM 12021, <i>Salmonella</i> Enteritidis			

$$\sqrt{\mu_{max}} = a(T - T_{min}) \quad (1)$$

Where, μ_{max} , a , T , and T_{min} refer to the maximum growth rate (h^{-1}), a coefficient, temperature ($^{\circ}C$), and the estimated minimum growth temperature ($^{\circ}C$), respectively.

$$\sqrt{\mu_{max}} = a(T - T_0)[1 - e^{b(T-T_{max})}] \quad (2)$$

Where, b and T_{max} refer to the coefficient and estimated maximum growth temperature ($^{\circ}C$), respectively.

$$3\sqrt{\mu_{max}} = a(T - T_{min})^{0.75} \quad (3)$$

$$\sqrt{\mu_{max}} = a(T - T_{min})^{0.75}[1 - e^{b(T-T_{max})}] \quad (4)$$

$$\mu_{max} = \frac{\mu_{opt}(T-T_{max})(T-T_{min})^2}{[(T_{opt}-T_{min})(T-T_{opt})-(T_{opt}-T_{max})(T_{opt}+T_{min}-2T)](T_{opt}-T_{min})} \quad (5)$$

Where, μ_{opt} refers to te optimum growth rate at the optimum temperature (T_{opt}).

$$\mu_{max} = a(T + 273.15)\exp\left\{-\left[\frac{\Delta G'}{R(T+273.15)}\right]^n\right\} \quad (6)$$

Where, R , $\Delta G'$, and n refer to the gas constant (8.134 J/mol), type of kinetic energy related to bacterial growt and coefficient, respectively.

$$\mu_{max} = a(T + 273.15) \exp\left\{-\left[\frac{\Delta G'}{R(T+273.15)}\right]^n\right\} [1 - e^{b(T-T_{max})}] \quad (7)$$

Each model was fitted to the temperature- μ_{max} dataset using non-linear regression analysis in IPMP software. The parameters of each model (e.g., T_{min} , T_{max} , T_{opt}) were provided by the software.

Model Evaluation Criteria

The performance of each model was evaluated using the following statistical indicators:

- Coefficient of determination (R^2 ; Eq. 8): to assess the proportion of variance explained by the model.

$$R^2 = 1 - \frac{SSR}{SST} \quad (8)$$

where, SSR and SST represent the sum squares of residuals and total sum of squares, respectively.

- Root Mean Square Error (RMSE Eq. 9): to measure the average deviation between predicted and observed values.

$$RMSE = \sqrt{\frac{SSE}{N-p}} \quad (9)$$

Where, N and p represent the number of observations and number of model parameters, respectively.

- Akaike Information Criterion (AIC): to account for model complexity and fit.

$$AIC = n * \ln\left(\frac{SSE}{N}\right) + 2 * (p + 1) + \frac{2 * (p+1) * (p+2)}{N-p-2} \quad (10)$$

Residuals were analyzed to check for systematic deviations, and biological relevance of the estimated parameters (e.g., realistic minimum and optimum growth temperatures) was also considered in model evaluation.

All modeling and statistical analyses were conducted in the Integrated Pathogen Modeling Program (IPMP, 2013), and graphical outputs were generated using SigmaPlot software (version 11.0, San Jose, CA, USA). The IPMP is a tertiary model created by the USDA Agricultural Research Services (ARS) as a software tool for predictive microbiology data analysis and model creation

Results

Table 2 shows how well four different models performed Suboptimal and Full Huang square-root, Suboptimal and Full Ratkowsky square-root, Suboptimal and Full Arrhenius-type, and the Cardinal model measured by RMSE, R^2 , and AIC. Among these models, the suboptimal and full Huang square-foot models did not work. This result may be due to data collected at high temperatures because this model was developed to improve the prediction of growth rate close to the lower boundary of the growth temperature; it adds a temperature-dependent term to the square-foot model. For cold-tolerant microbes that are pertinent to the storage of refrigerated food, this model is very helpful (Ratkowsky et al., 1983).

The Cardinal model achieved the best predictive accuracy, returning the lowest RMSE (0.080), closely followed by the suboptimal Arrhenius-type (0.084) and full Arrhenius-type (0.090) models. In contrast, both Ratkowsky models showed considerably higher RMSE values (>0.10), indicating less precise predictions. The Arrhenius-type models and the Cardinal model all attained high explanatory power, with $R^2 = 0.90$, meaning they explained 90% of the variance in the data. Both Ratkowsky models lagged, with $R^2 = 0.85$, showing weaker performance in capturing data variability. When considering model simplicity alongside fit, the suboptimal Arrhenius-type model performed best, with the lowest AIC (-87.448), reflecting the most favorable trade-off. The full Arrhenius-type (-78.491) and Cardinal (-75.826) models followed. In comparison, the Ratkowsky models had higher AIC values, making them less desirable overall. Comparing suboptimal versus full versions revealed that adding complexity generally worsened performance: RMSE increased, AIC rose, and R^2 remained unchanged, suggesting overfitting without real benefits. In summary, the suboptimal Arrhenius-type model offers the most balanced performance, combining low prediction error, high explanatory power, and efficient complexity. The Cardinal model is nearly as strong in accuracy and explanatory ability but is less optimal in terms of parsimony. Ratkowsky-based models consistently trail behind on all metrics.

The *Salmonella* growth rate data were subjected to the full Ratkowsky square-root model, which incorporates both supraoptimal and suboptimal temperature components. Table 3 displays the parameter estimates and related statistics. A statistically significant t-value of 5.815 and a p-value of 3.41×10^{-5} were obtained by estimating the parameter a at 0.02 with a standard error of 0.003.

Table 2. Performance of secondary growth models in predicting *Salmonella* growth

Model	Root means square error (RMSE)	The coefficient of determination (R^2)	Akaike information criterion (AIC)
Suboptimal Ratkowsky square root	0.108	0.85	-79.558
Full Ratkowsky square root	0.115	0.85	-72.558
Suboptimal Huang square-root	-	-	-
Full Huang square-root	-	-	-
Suboptimal Arrhenius-type	0.084	0.90	-87.448
Full Arrhenius-type	0.090	0.90	-78.491
Cardinal	0.080	0.90	-75.826

Table 3. Parameter estimates for the models fitted to *Salmonella* growth rate data.

Parameters	Value	Std-Error	t-value	p-value	95% Confidence interval (CI) (Lower)	95% Confidence interval (CI) (Upper)
Full Ratkowsky square-root model						
a	0.02	0.003	5.815	3.41E-05	0.013	0.027
T_{max}	72.651	4.05E+10	0	1.00E+00	-8.6E+10	8.62E+10
b	0.746	9.27E+08	0	1.00E+00	-2E+09	1.98E+09
T_{min}	7.35	2.017	3.643	2.40E-03	3.05	11.65
Suboptimal Ratkowsky square-root model						
a	0.02	0.002	9.344	4.15E-08	0.016	0.025
T_{min}	7.35	1.805	4.072	7.93E-04	3.542	11.158
Full Arrhenius-type model						
a	0.184	2.356	0.078	9.39E-01	-4.868	5.237
T_{max}	40.503	25302205	0	1.00E+00	-5.4E+07	54267873
$\Delta G'$	3572.704	5084.106	0.703	4.94E-01	-7331.62	14477.03
b	6.568	3.25E+08	0	1.00E+00	-7E+08	6.97E+08
n	4.575	11.18	0.409	6.89E-01	-19.404	28.554
Suboptimal Arrhenius-type model						
a	0.05	0.246	0.203	8.42E-01	-0.471	0.571
$\Delta G'$	3117.196	1583.172	1.969	6.65E-02	-238.979	6473.37
n	6.049	7.939	0.762	4.57E-01	-10.781	22.878
Cardinal model						
T_{max}	42.952	2.72E+07	0	1	-5.83E+07	5.83E+07
T_{opt}	42.954	1.74E+06	0	1	-3.72E+06	3.72E+06
T_{min}	0.85	6.105	0.139	0.891	-12.243	13.943
μ_{opt}	0.889	1.29E+06	0	1	-2.78E+06	2.78E+06

The range of the 95% CI for a was 0.013 to 0.027. In addition to showing statistical significance, the estimated value of the parameter, T_{min} (theoretically minimum temperature), was 7.35°C with a standard error of 2.017, resulting in a t-value of 3.643 and a p-value of 2.40×10^{-3} . T_{min} has a 95% confidence interval between 3.05°C and 11.65°C. Nevertheless, the parameters, T_{max} (theoretical maximum temperature) and b (shape parameter), showed very high standard errors (about 10^9 and 10^8 , respectively), leading to t-values that were near zero and p-values that were almost one. Because there were insufficient data points in the supraoptimal temperature range, the 95% confidence intervals for these parameters were incredibly broad, ranging from negative to positive values, indicating that they could not be accurately assessed. On the other hand, the data was fitted to the suboptimal Ratkowsky square-root model, which only contains parameters, a and T_{min} . With a t-value of 9.344 and a p-value of 4.15×10^{-8} , the estimated value of parameter a was 0.02 with a standard error of 0.002, showing significant statistical significance. The parameter of a had a 95% CI between 0.016 and 0.025. A t-value of 4.072 and a p-value of 7.93×10^{-4} were obtained by estimating the parameter, T_{min} , at 7.35°C with a standard error of 1.805, which likewise indicated

statistical significance. T_{min} had a 95% confidence interval between 3.542°C and 11.158°C, aligning with the expected growth limits of *Salmonella* reported by Tarlak et al. (2020) and Mishra et al. (2017). According to these results, the suboptimal model offers accurate and statistically significant estimates for both, a and T_{min} , while the complete model's values for T_{max} and b are extremely unclear because there is no data in the supraoptimal temperature range, according to a comparison of the full and suboptimal models. Because it provides more accurate parameter estimates and is better supported by the existing data, the suboptimal Ratkowsky square-root model is therefore chosen to describe *Salmonella* growth at temperatures below the optimum.

In order to evaluate the temperature dependency of microbial growth, the Arrhenius-type model was applied to the *Salmonella* growth rate data in both its complete form and as a suboptimal model (Table 3). A lack of statistical significance was shown by the estimated value of the parameter, a , in the entire Arrhenius-type model, which was 0.184 with a standard error of 2.356, resulting in a t-value of 0.078 and a p-value of 0.939. Besides, since there were insufficient data points in the supraoptimal temperature range, the parameter T_{max} was estimated to be

40.503°C with a extremely large standard error of 25,302,205, yielding a t-value of 0 and a p-value of 1.00. This suggests that the parameter was not correctly calculated. Similarly, a lack of statistical significance was also shown by the estimated value of the parameter $\Delta G'$ (activation energy), which was 3,572.704 with a standard error of 5,084.106, resulting in a t-value of 0.703 and a p-value of 0.494. Likewise, a t-value of 0 and a p-value of 1.00 indicate that the parameter, b , was not reliably calculated, with an estimated value of 6.568 and a standard error of 325,000,000. In addition, with a t-value of 0.409 and a p-value of 0.689, the estimated value of the parameter n was 4.575 with a standard error of 11.18, indicating that it was not statistically significant.

A t-value of 0.203 and a p-value of 0.842, indicating a lack of statistical significance, were obtained from the estimation of the parameter a at 0.05 with a standard error of 0.246 in the suboptimal Arrhenius-type model, which only contains the parameters a , $\Delta G'$, and n . The range of 95% confidence intervals for a was -0.471 to 0.571. By estimating the parameter $\Delta G'$ to be 3,117.196 with a standard error of 1,583.172, a t-value of 1.969 and a p-value of 0.066 were obtained, indicating a marginal statistical significance. $\Delta G'$ had a 95% confidence interval between -238.979 and 6,473.37. With a t-value of 0.762 and a p-value of 0.457, the estimated value of n was 6.049 with a standard error of 7.939, suggesting that it was not statistically significant. The suboptimal model yields more accurate estimates for the parameters $\Delta G'$ and n with the former nearing statistical significance, when the full and suboptimal Arrhenius-type models are compared. However, the parameter of a in both models is not statistically significant, and the paucity of data in the supraoptimal temperature range means that the parameter T_{max} in the whole model is still poorly estimated. Because it provides more accurate parameter estimates and is better supported by the existing data, the suboptimal Arrhenius-type model is therefore recommended for explaining *Salmonella* growth at temperatures below the optimum.

Furthermore, the effects of temperature on microbial development were evaluated using the Cardinal model on the *Salmonella* growth rate data. Table 3 displays the parameter estimates and related statistics. The theoretical maximum temperature, T_{max} , in the Cardinal model was estimated to be 42.952°C with a standard error of 27,200,000. This resulted in a t-value of 0 and a p-value of 1.00, suggesting that the lack of data points in the supraoptimal temperature range made it impossible to reliably estimate the parameter. In addition, the paucity of data points in the ideal temperature range suggests that the parameter, T_{opt} , was not consistently determined. It was estimated at 42.954°C with a standard error of 1,740,000, resulting in a t-value of 0 and a p-value of 1.00. Likewise, there was no statistical significance found when the parameter, T_{min} (theoretical minimum temperature), was calculated to be 0.85°C with a standard error of 6.105, resulting in a t-value of 0.139 and a p-value of 0.891. T_{min} has a 95% confidence interval between -12.243 and 13.943°C. Similarly, with a t-value of 0 and a p-value of 1.00, the parameter, μ_{opt} (maximum specific growth rate at optimal temperature), was estimated to be 0.889 with a standard error of 1,290,000, indicating that it was not a reliable estimate because there were not enough data points

in the optimal temperature range. A comparison of the parameter estimates from the Cardinal model shows that all of the parameters have large confidence intervals and substantial standard errors, suggesting that the paucity of data points in the pertinent temperature ranges made it impossible to estimate these parameters with any degree of reliability. As a result, there is limited use of the Cardinal model to explain *Salmonella* growth in the temperature range under investigation, and care should be taken when interpreting these parameter estimations.

Discussion

Understanding the influence of temperature on the growth kinetics of *Salmonella* in leafy greens is critical for accurate microbial risk assessment and the development of science-based food safety controls. In this study, four widely used secondary models—Ratkowsky square-root (full and suboptimal), the Arrhenius-type (full and suboptimal), the Cardinal, and the Huang square-root models (full and suboptimal)—were evaluated and compared based on their statistical performance and biological interpretability when applied to literature-derived data describing *Salmonella* growth on leafy greens. Among the models tested, the suboptimal Arrhenius-type model yielded the lowest AIC value (-87.448) and highest R^2 (0.90), indicating the best overall fit to the data. Despite its superior empirical performance, the model's parameters lacked statistical significance and had wide confidence intervals, suggesting limited interpretability. This is likely due to insufficient high-temperature data or the empirical nature of the model, which prioritizes fit over biological meaning. The full Arrhenius-type model also yielded non-significant values for a , ΔG , T_{max} , and n , with wide confidence intervals. This reflects the model's limited capacity to capture the biological complexity of enzyme-mediated growth over broad temperatures. Our findings support Peleg & Corradini (2011), who reported that the Arrhenius model was not suitable for microbial growth because the variables measured during microbial growth are typically based on cell counts, which are not compatible with the concept of molar concentration used in chemical kinetics. In this context, both the definition and the verifiability of the assumed rate-limiting enzymatic reaction remain scientifically ambiguous. Furthermore, the authors concluded that the wide temperature range and the lack of justification for the logarithmic transformation of the "growth rate constant" render the application of the Arrhenius model to microbial growth and inactivation processes even more problematic (Peleg & Corradini, 2011). Likewise, the Cardinal model's estimates of T_{min} , T_{opt} , T_{max} , and μ_{opt} were all statistically unreliable, reinforcing how high standard errors often arise when data lack discriminatory power in temperature zones defining growth extremes.

By contrast, the Ratkowsky square-root model, although associated with a higher AIC (-79.558), produced highly statistically significant and precise parameter estimates. The T_{min} value (7.35°C) falls within the expected range for *Salmonella*, supporting the model's biological credibility in the suboptimal growth range. This result was in the range of the values reported in similar studies (Koseki & Isobe, 2005; Ndraha et al., 2022; Puerta-Gomez

et al., 2013; Tarlak et al., 2020; Veys et al., 2016). Our results aligned with past comparative analyses showing that model choice should be guided by data support and simplicity; more complex models may perform poorly without comprehensive coverage of the temperature-response curve (Peleg et al., 2012; Peleg & Corradini, 2011). Additionally, secondary models like this one work well for predicting outcomes when they accurately represent the temperature needs of pathogens; here, the suboptimal Ratkowsky model offers a reliable way to estimate *Salmonella* growth. The model's simplicity and robustness make it especially suitable for conservative risk assessments and regulatory applications where clarity and interpretability are prioritized (Baranyi et al., 2017; Ratkowsky et al., 1983).

This comparative study demonstrates that no single model is universally optimal; rather, model selection depends on the trade-offs between empirical fit and biological interpretability. For *Salmonella* in leafy greens, the Arrhenius-type model may be preferable for pure prediction tasks, whereas the Ratkowsky model offers a more interpretable and stable framework for risk assessment under suboptimal conditions. The results also highlight the limitations of using literature-derived data, particularly the lack of consistent high-temperature data points, which likely impacted the performance of models requiring estimates near or beyond the optimum growth range. Therefore, further research using experimentally derived, high-resolution growth data across the full temperature spectrum is needed to improve the robustness of secondary model fitting. Additionally, expanding the analysis to include other environmental factors such as pH and water activity, or incorporating machine learning approaches, may offer improved predictive performance in complex food matrices like leafy greens.

Conclusion

this study demonstrated that among the three models evaluated—the Ratkowsky square-root, Arrhenius-type, and Cardinal models—the sub-optimal Ratkowsky model most reliably describes *Salmonella* growth rate at temperatures below the optimum. The parameters a (0.02 h^{-1}) and T_{min} (7.35°C) were precisely estimated with narrow confidence intervals, while the full model's supra-optimal components (T_{max} , b) were poorly constrained due to insufficient high-temperature data. In contrast, both the Arrhenius-type and Cardinal models exhibited high uncertainty across all parameters, limiting their practical utility within the temperature range examined. These findings support the selection of simpler, empirically supported models whenever data lack full thermal coverage, aligning with best practices in predictive microbiology. Future research should focus on collecting richer high-temperature data to enable more comprehensive modeling of the supra-optimal growth decline.

Declarations

This study was presented at the IV. International Congress of the Turkish Journal of Agriculture - Food Science and Technology (Niğde, TURJAF 2025).

Ethical Approval Certificate

This study does not require ethical approval as it does not involve human participants or animal subjects.

Author Contribution Statement

Basri Omac: Data collection, investigation, formal analysis, project administration, conceptualization, methodology, writing the original draft, review and editing

Conflict of Interest

The authors declare no conflict of interest.

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