Assessment of Mathematical Models for Predicting  
*Staphylococcus aureus* Growth in Cooked Meat Products

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ABSTRACT

The growth of *Staphylococcus aureus* in commercially available vacuum-packaged cooked ham, turkey breast meat, and chicken breast meat stored at 2.3, 6.5, 10, 13.5, and 17.7°C was studied. Growth rates observed in these food products were compared with those predicted on the basis of various growth models found in the literature and with those generated by the Pathogen Modeling Program and the Food MicroModel software using graphical and mathematical analysis for performance evaluation. In general, the models studied overestimated the growth of *S. aureus*. The Dengremont and Membré model most closely matched the observed behavior of *S. aureus* in ham and chicken breast meat, with bias factors of 1.56 and 1.09, respectively. The Eifert et al. model accurately described the growth of *S. aureus* in turkey breast meat, with a bias factor of 1.51. The remaining models provided safe predictions of the growth rate of *S. aureus*, but with poor accuracy. Predictive microbiology models have an immediate practical application in improving microbial food safety and quality and are very useful decision support tools, but they should not be used as the sole determinant of product safety.

*Staphylococcus aureus* is a well-documented pathogenic microorganism and causes many foodborne diseases. Staphylococcal food poisoning occurs through the consumption of food containing a sufficient amount of one or more enterotoxins. These enterotoxins are generally synthesized either at the end of the exponential phase or during the stationary stage of a microorganism’s growth (40). Bergdoll (5) reported that *S. aureus* must attain a population of approximately 10⁵ CFU/g to produce toxin and cause illness. Incorrect storage temperatures and insufficiencies in the personal hygiene of food handlers have been reported to be the most important factors contributing to staphylococcal food poisoning (15).

Foods associated with the appearance of staphylococcal poisoning outbreaks include meat and cooked meat products, particularly ham (18, 38, 43); cream cakes; seafood; potato, chicken, tuna, and ham salads (5); and pre-prepared foods stored under inadequate refrigeration conditions after preparation (31).

The key to controlling *S. aureus* is an understanding of the factors that influence its growth in foods and the manipulation of those factors in order to limit potential risks. However, since food handlers are the primary source of *S. aureus* and since it is a fairly hardy species, this microorganism is likely to be introduced into, and grow in, a wide range of food products (6). Baird-Parker and Kilshy (1) concluded that the logical approach for determining the probable behavior of a foodborne pathogen is to use predictive models that estimate the microorganism’s response to the primary factors affecting its growth and survival. A number of mathematical models have been developed for use in assessing microbial food safety (6, 11, 20, 30, 37, 48, 50), but before they can be used in a practical situation, the applicability of these mathematical models to foods must be validated (46).

Given the wide range of potential food formulations and storage conditions, validated mathematical models could clearly become invaluable tools for rapidly and objectively assessing the relative safety of food products, although the validation of a mathematical model is one of the most crucial, and at the same time one of the most difficult, steps in the complete modeling cycle. Most predictive models of microbial growth are based on laboratory-scale experiments and are sometimes used under conditions that are very different from those of real food systems. Therefore, some difficulties are encountered in obtaining good models to make accurate predictions for actual food products, because not all of the factors that apply to food are considered in models. Deviations from predictions obtained with these models are sometimes encountered, but such deviations do not necessarily imply that a model is defective (28). For Gill (21), some variation is inevitable with complex foods such as meat and meat products if a model does not take into account all factors affecting growth. Many researchers have emphasized the need to validate models directly with foods such as meat and meat products (29, 42, 45–47).

To date, no standard model validation methods have been published (27). However, Ross (33) provided some performance indices for measuring the reliability of kinetic models; these indices were later modified by Baranyi et al. (2). As a result, in some cases it is no trivial practice to apply the models developed to real food products (44, 46).
The aim of this work was to assess the applicability of various predictive models of *S. aureus* growth found in the scientific literature to a food of particular interest, sliced cooked meat products.

**MATERIALS AND METHODS**

**Samples.** Three commercially available cooked meat products were used in this study: cooked ham with a natural NaCl level of 1.84%, an NaNO₂ residual level of 30 ppm, a water activity of 0.983, and an initial pH of 6.32; cooked turkey breast meat with a natural NaCl level of 2.4%, an NaNO₂ residual level of 29 ppm, a water activity of 0.971, and an initial pH of 6.22; and cooked chicken breast meat with a natural NaCl level of 1.76%, an NaNO₂ residual level of 39 ppm, a water activity of 0.971, and an initial pH of 6.31. Samples (25 g) of cooked meat products minced in a Moulinex mincer were inoculated with *S. aureus*. Samples were minced to ensure a more homogeneous distribution of *S. aureus* and to encourage its subsequent growth and recovery for microbiological analysis. Samples were vacuum-packaged with an Audionvac packer (Audion Elektro, B.V., Holland) in polypropylene plastic film (15 by 30 cm; Sacoliva Pape 150, Barcelona, Spain) with oxygen, carbon dioxide, and water vapor permeability values of 8 cm²/m²/24 h, 230 cm²/m²/24 h, and 2.0 g/m²/24 h, respectively.

The selected storage temperatures were 2.3, 6.5 (refrigeration), 10, 13.5 (moderate-abuse temperature), and 17.7°C (serious-abuse temperature). Five batches were made from each of the resulting samples and stored at these temperatures. Two samples of each type were kept aside for microbiological analysis on the day of packaging.

**Preparation of inoculum.** To determine with some degree of accuracy the number of cells injected into the samples, a calibration line was produced by taking three previous calibrations made with Bioscreen C (Labsystems, Finland) with *S. aureus* CECT 534 (Spanish Collection of Culture Types) at 600 nm under an optimal temperature of 37°C. For this purpose, double serial dilutions were carried out with brain heart infusion (Difco Laboratories, Detroit, Mich.) at different initial microorganism concentrations. At the same time, the inoculum was controlled by enumeration on plate count agar (CM325; Oxoid) and incubated at 37°C for 48 h.

The strain was grown separately in 50 ml of brain heart infusion (pH 7.0; no added NaCl) and subcultured on three successive days. The third subculture was grown for 18 h at 37°C until the stationary phase. The number of microorganisms present in the culture from the absorbance value was calculated with the calibration line described above. Subsequently, dilutions in physiological saline solution were performed to obtain 10⁵ CFU/g in the bags, and each sample was inoculated with 1 ml of the bacterial suspension.

**Microbiological analyses.** A direct plate count of *S. aureus* from decimal dilutions of the food in buffered peptone water (CM509; Oxoid) at 0.1% was carried out with Baird Parker agar (CM275; Oxoid), with the plates being incubated at 37°C for 48 h (25); for the lactic acid bacteria group, the count was performed with MRS agar (CM361; Oxoid), with the plates being incubated at 30°C for 48 h in an anaerobic atmosphere (16). Microbiological analysis was performed on days 0, 1, 2, 3, 6, 13, 20, 28, and 35 of storage at each of the five storage temperatures.

**Assessment of predictive growth models.** The *S. aureus* growth data obtained from cooked meat products were processed with the DMFit program, version 1.0 (J. Baranyi, Institute of Food Research, Norwich Research Park, UK), and fitted to the formula developed by Baranyi and Roberts (3) and to the modified equation of Gompertz (19). With the predictive growth data obtained from both formulas, an analysis of variance was performed to select the best fit to the experimental data observed. The following equation was used to estimate variance:

\[
\text{Variance} = \frac{\sum (Y_{obsp} - Y_{pred})^2}{\sum (Y_{obsp} - Y_{pobs})^2}
\]

where *Y* _obsp_ is the observed data, *Y* _pred_ is the predicted data, and *Y* _pobs_ is the average of the observed data.

Once the best data fit was selected, a comparison was made between the growth rates recorded for cooked meat products and those predicted by the models studied. The predictions used were those provided by the models shown in Table 1. The Pathogen Modeling Program (PMP), version 5.1, was developed at the U.S. Department of Agriculture by Dr. R. L. Buchanan and Dr. R. C. Whiting, and Food MicroModel (FMM), version 2.5, was developed in the UK with funding from the Ministry of Agriculture, Fisheries and Food by the Leatherhead Food Research Association (Leatherhead, UK).

In order to examine model predictions of kinetic parameters, the accuracy of growth rate prediction data can be assessed graphically or on the basis of mathematical and statistical indices. Observed growth rate values can be plotted against the predictions provided by the models studied. The resulting plot makes it easy to see which predictions would be unsafe in practice, as well as trends and any structural deviations.

Various mathematical and statistical indices can also be used to assess the performance of predictive growth models. One common index is the mean square error (MSE). The residual sum of squares divided by the number of datum points provides a measure of the remaining variability, which may derive from natural growth rate prediction models used in this study

<table>
<thead>
<tr>
<th>Model</th>
<th>Variables and ranges</th>
<th>Type of model</th>
<th>Strain</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ross and McMeekin (35)</td>
<td>T (5–35°C), a&lt;sub&gt;w&lt;/sub&gt; (0.997–0.848)</td>
<td>Square root</td>
<td><em>S. aureus</em> 3b</td>
</tr>
<tr>
<td>Dengremont and Membre (12)</td>
<td>T (10–37°C), pH (5–8), NaCl (0–10%)</td>
<td>Nonlinear</td>
<td>Strain C</td>
</tr>
<tr>
<td>Eifert et al. (15)</td>
<td>T (12–28°C), pH (5–7), NaCl (0.5–8.5%)</td>
<td>Response surface</td>
<td><em>S. aureus</em> 196E</td>
</tr>
<tr>
<td>Pathogen Modeling Program</td>
<td>T (12–42°C), pH (5.3–9), NaCl (0.5–16.5%), nitrite (0–150 ppm)</td>
<td>Polynomial (2nd order)</td>
<td><em>S. aureus</em> 196E</td>
</tr>
<tr>
<td>Food MicroModel</td>
<td>T (7.5–30°C), pH (4.2–7.2), NaCl (0–13.5%) a&lt;sub&gt;w&lt;/sub&gt; (0.907–1.000)</td>
<td>Polynomial (2nd order)</td>
<td>Mixed strain</td>
</tr>
</tbody>
</table>

*a* T, temperature; *a<sub>w</sub>* , water activity.
variability or from systematic errors. The lower the MSE, the more suitable the model for describing the data (40).

The Ross (33) indices, the bias factor (Bf) and the accuracy factor (Af), as modified by Baranyi et al. (2) were developed to measure the reliability of predictive models and to ensure an objective comparison of the performances of different models. When both indices display a value of 1, there is perfect agreement between observed and predicted values (line of equivalence). The Bf enables the researcher to determine whether, on average, observed values lie above or below the line of equivalence and by how much. It is also an indicator of the structural deviation of a model. A Bf of >1 indicates a “fail-safe” model: predicted growth rates exceed observed values and thus ensure a safety margin (33). The Af averages the distance from each point to the line of equivalence as a measure of the average proximity of predictions to observation. The larger the value of this index, the less accurate the average estimate. Thus, an Af of 2 indicates that the prediction differs from the observed value, on average, by a factor of 2. Ideally, a predictive model should ensure that $Af = Bf = 1$; usually, however, the accuracy factor will increase by 0.10 to 0.15 for each variable in the model (34).

Statistical analysis. Statgraphics, version 5 (Statistical Graphics Corporation), and Microsoft Excel 97 were used for analysis of statistical data, error deviation, and variance.

RESULTS AND DISCUSSION

Temperature has been singled out as the main factor in regulating the growth of *S. aureus* (9, 12), and, as expected, *S. aureus* was not able to grow at or below 6.5°C (41) but remained at population levels approximately equal to that of the original inoculum for the three cooked meat products studied until the end of the storage period (Fig. 1). *S. aureus* was also unable to grow on chicken samples stored at 10°C, and its level remained constant. Yang et al. (49) reported that no *S. aureus* growth was detected in egg products at 5°C and that *S. aureus* populations did not increase or decrease throughout the storage period. The possible survival of *S. aureus* is important from a safety standpoint, since any subsequent increase in temperature would allow *S. aureus* to grow.

Estimations of kinetic parameters (growth rate and lag phase duration) from predictive models of *S. aureus* were obtained for the remaining temperatures, 10, 13.5, and 17.7°C, for the three products studied. They were fitted to the Baranyi and Roberts (3) formula, which achieved a better fit than the Gompertz modified equation (19) after a variance analysis.

Figure 2 shows the log-transformed growth rate values observed and the values estimated by predictive models. Log transformation is the most suitable procedure because it results in a homogeneous error distribution, with the points being more evenly spread over a wider range (42). In general, observed growth rate values were lower than predicted values, so most models provided fail-safe estimates; nevertheless, some predictions lay below the line of equivalence and were thus considered unsafe (Fig. 2). Natural variability and additional factors affecting *S. aureus* growth but not included in the model design, such as the
presence of contaminating microorganisms, the addition of preservatives, and packaging in a modified atmosphere, may account for the lack of agreement between predicted and observed values (42).

Table 2 shows the growth values observed (GRobs) and the values predicted with the models studied (GRpred). Although the three meat products studied have similar matrices, S. aureus behaved differently in each of the three, as evidenced by the growth rate values. However, it can be seen that for the poultry products, temperatures of 13.5 and 17.7°C did not lead to significant differences in S. aureus growth rate values ($P > 0.05$).

The PMP program allows S. aureus growth predictions to be obtained for both aerobic and anaerobic conditions (inert N$_2$ atmosphere). Comparison of predictions generated under both conditions showed a higher growth rate for S. aureus in anaerobic conditions. Because it is advisable when dealing with pathogenic microorganisms to reflect the conditions that most favor growth in order to obtain the safest predictions, anaerobic conditions were selected for application of PMP predictions to meat products.

Table 3 shows mathematical and statistical comparisons of the models for the prediction of the growth of S. aureus on cooked meat products. The MSE comparison shows that the Dengremont and Membré (12) model and the Eifert et al. (15) model generally provided predictions that most closely match observed S. aureus growth data for the three products, while the values predicted by the FMM model were the farthest from observed values, as shown by higher MSE values.

Calculation of $B_f$ and $A_f$ provides an objective indication of model performance. As a whole, all models overestimated S. aureus growth for the three meat products; $B_f$ was $>1$, and thus estimates tended toward the fail-safe predictions (Fig. 2). This result was expected, since in most cases, rich liquid broth media were used to develop models, providing optimal growth conditions, and models based on data thus generated tend to give fail-safe predictions (42).

An exception to this general rule was seen for the growth rate estimates provided by the Dengremont and Membré (12) model for turkey breast meat, which were classified as “fail-dangerous” predictions ($B_f < 1$).

In general, two of the models applied to meat products showed good agreement between experimentally determined and predicted growth rate values, as expressed by lower $A_f$ and $B_f$ values. The Dengremont and Membré (12) model most closely predicted S. aureus growth in ham and chicken breast meat, while for turkey breast meat this mod-

### TABLE 2. Estimated (GRpred) and observed (GRobs) growth rates for *Staphylococcus aureus* in cooked meat products

<table>
<thead>
<tr>
<th>Model</th>
<th>Temperature (°C)</th>
<th>Ham GRobs (h$^{-1}$)</th>
<th>Ham GRpred (h$^{-1}$)</th>
<th>Turkey breast GRobs (h$^{-1}$)</th>
<th>Turkey breast GRpred (h$^{-1}$)</th>
<th>Chicken breast GRobs (h$^{-1}$)</th>
<th>Chicken breast GRpred (h$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ross and McMeekin (35)</td>
<td>10</td>
<td>0.0024</td>
<td>0.0096</td>
<td>0.0033</td>
<td>0.0086</td>
<td>NG</td>
<td>NG</td>
</tr>
<tr>
<td>Dengremont and Membre (12)</td>
<td>13.5</td>
<td>0.0057</td>
<td>0.0526</td>
<td>0.0259</td>
<td>0.0475</td>
<td>0.0119</td>
<td>0.0475</td>
</tr>
<tr>
<td></td>
<td>17.7</td>
<td>0.0171</td>
<td>0.1499</td>
<td>0.0279</td>
<td>0.1353</td>
<td>0.0167</td>
<td>0.1353</td>
</tr>
<tr>
<td>Eifert et al. (15)</td>
<td>13.5</td>
<td>0.0057</td>
<td>0.0071</td>
<td>0.0259</td>
<td>0.0068</td>
<td>0.0119</td>
<td>0.0071</td>
</tr>
<tr>
<td></td>
<td>17.7</td>
<td>0.0171</td>
<td>0.0334</td>
<td>0.0279</td>
<td>0.0321</td>
<td>0.0167</td>
<td>0.0333</td>
</tr>
<tr>
<td>Food MicroModel</td>
<td>10</td>
<td>0.0024</td>
<td>0.0310</td>
<td>0.0033</td>
<td>0.0280</td>
<td>NG</td>
<td>NG</td>
</tr>
<tr>
<td></td>
<td>13.5</td>
<td>0.0057</td>
<td>0.0710</td>
<td>0.0259</td>
<td>0.0660</td>
<td>0.0119</td>
<td>0.0710</td>
</tr>
<tr>
<td></td>
<td>17.7</td>
<td>0.0171</td>
<td>0.1660</td>
<td>0.0279</td>
<td>0.1560</td>
<td>0.0167</td>
<td>0.1660</td>
</tr>
<tr>
<td>Pathogen Modeling Program</td>
<td>13.5</td>
<td>0.0057</td>
<td>0.0557</td>
<td>0.0259</td>
<td>0.0528</td>
<td>0.0119</td>
<td>0.0540</td>
</tr>
<tr>
<td></td>
<td>17.7</td>
<td>0.0171</td>
<td>0.1158</td>
<td>0.0279</td>
<td>0.1115</td>
<td>0.0167</td>
<td>0.1115</td>
</tr>
</tbody>
</table>

*a* Nongrowth observed.

### TABLE 3. Evaluation of models predicting *Staphylococcus aureus* growth in cooked meat products according to various statistical characteristics

<table>
<thead>
<tr>
<th>Meat product</th>
<th>Index</th>
<th>Dengremont and Membre (12)</th>
<th>Eifert et al. (15)</th>
<th>Ross and McMeekin (35)</th>
<th>FMM</th>
<th>PMP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ham</td>
<td>MSE</td>
<td>0.00013</td>
<td>0.00379</td>
<td>0.00663</td>
<td>0.00908</td>
<td>0.00612</td>
</tr>
<tr>
<td></td>
<td>$A_f$</td>
<td>1.64</td>
<td>6.65</td>
<td>7.12</td>
<td>11.64</td>
<td>8.19</td>
</tr>
<tr>
<td></td>
<td>$B_f$</td>
<td>1.56</td>
<td>6.60</td>
<td>6.85</td>
<td>11.60</td>
<td>8.13</td>
</tr>
<tr>
<td>Turkey breast</td>
<td>MSE</td>
<td>0.00019</td>
<td>0.00087</td>
<td>0.00401</td>
<td>0.00621</td>
<td>0.00386</td>
</tr>
<tr>
<td></td>
<td>$A_f$</td>
<td>2.58</td>
<td>1.91</td>
<td>3.07</td>
<td>5.34</td>
<td>3.01</td>
</tr>
<tr>
<td></td>
<td>$B_f$</td>
<td>0.55</td>
<td>1.51</td>
<td>2.85</td>
<td>4.94</td>
<td>2.85</td>
</tr>
<tr>
<td>Chicken breast</td>
<td>MSE</td>
<td>0.00015</td>
<td>0.00367</td>
<td>0.00766</td>
<td>0.01289</td>
<td>0.00538</td>
</tr>
<tr>
<td></td>
<td>$A_f$</td>
<td>1.84</td>
<td>4.72</td>
<td>5.89</td>
<td>7.82</td>
<td>5.56</td>
</tr>
<tr>
<td></td>
<td>$B_f$</td>
<td>1.09</td>
<td>4.65</td>
<td>5.68</td>
<td>7.70</td>
<td>5.50</td>
</tr>
</tbody>
</table>
el showed less accuracy and also made fail-dangerous predictions. For this reason, the Eifert et al. (15) model, which yielded the most accurate result for turkey breast meat (Table 3), was chosen.

With regard to the results provided by other models, both the Ross and McMeekin (35) model and the PMP yielded very similar $B_f$ and $A_f$ values for turkey and chicken. The FMM provided the estimates that were the farthest from the observed values for all products tested, yielding the highest values for $B_f$, $A_f$, and MSE of all the models used.

Other authors have reported $A_f$ values ranging between 1.1 and 4.3 for different microorganisms. Values closer to 1 have been obtained in experiments using simple, homogeneous, sterile, and thus highly controlled foods; an $A_f$ value of 1.26 was reported for *S. aureus* by Ross (33), a value of 1.21 was reported for *Listeria monocytogenes* by Devlieghere et al. (13), and values of 1.1 to 1.4 were reported for pseudomonas by Neumeyer et al. (29). In contrast, accuracy decreases when nonsterile and complex-matrix foods are tested, with less agreement between predicted and observed values. Index values of 1.4 to 4.0 have been reported for fish products (10), and values of 1.4 to 4.3 have been reported for various food types (meat, fish, egg, milk, dairy products, cheese, and vegetables) for *L. monocytogenes* (42). For pseudomonas, reported values of $A_f$ range between 1.3 (29) and 1.46 for minced beef (2).

Similar findings have been reported for $B_f$ values: the values closest to 1 ($B_f = 0.968$) have been reported for *L. monocytogenes* in cooked, sterile meat products (13) from which contaminant microflora that might compete with the pathogen had been eliminated. The least accurate $B_f$ values have been found for foods from which competitive microflora have not been eliminated. $B_f$ values of between 1 and 3.9 have been reported for *L. monocytogenes* in seafood (10), and a value of 3.35 has been reported for pseudomonas in minced beef (2). Values as high as 5.2 have been reported for FMM predictions for naturally contaminated cold-smoked salmon (10). Dalgaard and Jørgensen (10) suggest that one reason for the failure of the models to predict the growth of *L. monocytogenes* in their study could be the growth of other microorganisms on the product. The so-called Jameson effect (39) refers to the suppression of the growth of all microorganisms on food when the total microbial population achieves maximum population density. Thus, the growth of a pathogenic microorganism is inhibited when faster-growing organisms reach maximum population density before it does (25). A similar effect has been reported for *S. aureus* in seafoods (35) and for *L. monocytogenes* in both meat products (23) and seafoods (10).

In vacuum-packaged cooked meat products, the dominant flora—which eventually causes spoilage of the food—is the lactic acid bacteria group (26, 36). In the present study, competitive microflora in the form of lactic acid bacteria reached maximum population density before *S. aureus* did (Fig. 3), impairing pathogen growth and thus testifying to the Jameson effect in the three meat products.

Lag phase values obtained with the FMM and the PMP were lower than observed values for both poultry products. At 13.5°C, a lag phase of 137.3 h was observed for turkey breast meat, while the PMP and the FMM predicted lag phases of 72.2 and 14.5 h, respectively. A lag phase of 151.3 h was observed for chicken breast meat, while the PMP and the FMM estimated lag phases of 62.7 and 13.9 h, respectively. At 17.7°C, a lag phase of 20.7 h was observed for turkey breast meat, while the PMP and the FMM predicted lag phases of 21.4 and 6 h, respectively. A lag phase of 40.2 h was observed for chicken breast meat, while the PMP and the FMM estimated lag phases of 18.9 and 5.3 h, respectively. Some of the lack of agreement observed can be explained by the fact that the lag phase partly depends on how the microorganism adapts to the new atmosphere and on its previous growth conditions (46). The predictions provided by these programs are safe and very similar when two products of very similar chemical compositions are tested. However, *S. aureus* displayed no lag phase in cooked ham. Various authors have reported the absence of a lag phase for a number of pathogenic microorganisms growing in foods, including *L. monocytogenes* in fresh green asparagus (7), *Aeromonas hydrophila* in veg-

![Figure 3](http://meridian.allenpress.com/jfp/article-pdf/65/4/659/1674557/0362-028x-65_4_659.pdf)
etable salads (17), *Escherichia coli* in pork (22), and *S. aureus* in egg products (49) and french fries (14).

It should be stressed that the lag phase in itself poses more prediction difficulties than the growth rate, since it depends both on the physical status of the inoculum and on growth conditions (32). Therefore, the lag phase predicted by the models should be interpreted with particular caution, and its inclusion in product safety assessments should be carefully considered. From a safety standpoint, it might be prudent to consider predictions without including the lag phase, although the significance of the lag phase in growth should not be underestimated, particularly at lower chilling temperatures. However, current models cannot predict lag accurately because they fail to take into account all of the conditions known to influence the lag phase. Moreover, current predictive modeling approaches cannot predict the effect of injury on the lag phase, and information concerning the effects of injury on the growth behavior of foodborne pathogens is required.

Cole et al. (8) suggested that validation with data drawn from the literature could be of some use but added that such data often reveal marked deficiencies. In the present study, certain difficulties were encountered when *S. aureus* growth models with a similar setup in scientific journals were sought in order to apply the growth data obtained for cooked meats products; practically none of the research studies located fulfilled this purpose. The study strain used here, for example, was not the one used in setting up the models, and certain behavioral differences are therefore apparent (4, 6). However, the differences recorded between microorganism growth in foods and that in culture media cannot be accounted for exclusively on the basis of inoculum size, since it has been demonstrated that size has no influence on *S. aureus* growth parameters (6).

**CONCLUSIONS**

This study employed various criteria for assessing model performance. Although $B_f$ and $A_f$ may be used to provide an indication of performance, graphical analysis of predicted and observed *S. aureus* growth in foods also enables the researcher to detect data trends and structural deviations.

Our results indicate that the predictive models studied provide fail-safe estimations of *S. aureus* growth in the three meat products tested and can therefore be applied in safety estimates for this type of food. However, only two models accurately reflected *S. aureus* growth in our products. Reasonable results for $MSE$, $A_p$, and $B_p$ were obtained compared with those of other studies. Predictive inaccuracy may be due to a number of food-related factors, such as the presence of spoilage microorganisms in competition with *S. aureus* (the Jameson effect), the possible presence of inhibitory substances produced by lactic bacteria (bacteriocins), the presence of nitrates, and packaging in an oxygen-free atmosphere; most of these factors are not included in the predictive models studied.

Users of microbial growth prediction models must be aware of the limitations of these models when evaluating performance. Although they afford a useful tool for assessing food safety, they should not yet be considered the only way to achieve this goal. Further research is required to develop models that reflect food storage conditions (e.g., vacuum-packaging). Models could also include factors such as the Jameson effect that result from the competition between microorganisms.

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