Predicting Growth Rate and Germination, Outgrowth, and Lag Phase (GOL) of the *Bacillus cereus* Group in Thermally Processed Ready-to-Eat Deli Meats

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Introduction

Food business operators producing ready-to-eat deli meats that are heat-treated in the final consumer package must manage the risk of germination and growth of surviving bacterial spores. For *Clostridium botulinum* in meat products, growth can be predicted using DMRI Predict; however, no equivalent predictive tool is currently available for the *Bacillus cereus* group in meat products. This study aimed to develop and validate a growth model for the *B. cereus* group in meat products, accounting for relevant intrinsic and extrinsic factors. The objective was to describe growth not only of *B. cereus* sensu stricto, but of species across the *B. cereus* group.

Methodology

87 deli meat challenge tests used for model development.

123 independent challenge tests used for external validation; 105 were usable for censoring-aware GOL evaluation.

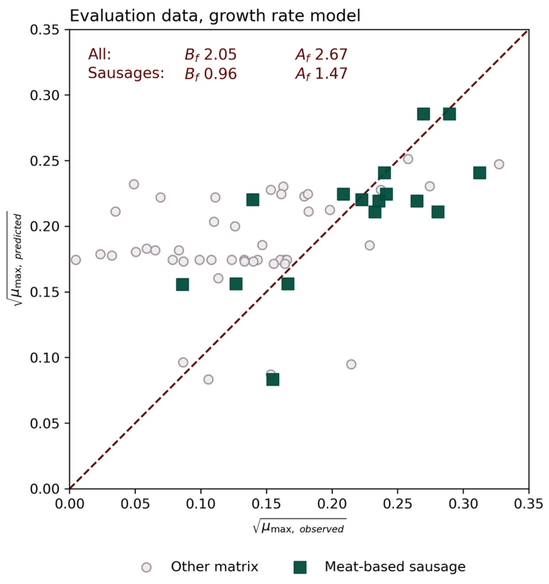
- Deli meat, ground meat, and compound meat-based food products.

Factors: temperature, pH, WPS, nitrite, organic acids, and packaging.

Outcomes: GOL duration and maximum specific growth rate.

Growth rate model

The growth-rate model used the updated psychrotolerant cardinal model of Maktabdar et al. (2025, Part 2) as its structural basis, including the low-temperature extension. Only the reference maximum specific growth rate, μopt, was recalibrated for the deli meat challenge tests; all other model parameters retained their published values. Calibration on 64 growth-positive training observations reduced μopt from the published dairy value of 2.67 h^{-1} to 1.587 h^{-1}. In grouped cross-validation, representing transfer to a new recipe within the same product matrix, the calibrated model achieved B_f = 0.99, A_f= 1.65, and an RMSE of 0.0257 h^{-1} for μmax. External validation showed that transfer was strongly product-matrix dependent: performance was acceptable for the meat-based sausage family (n=16, B_f = 0.96, A_f= 1.47) but substantially poorer when all food matrices were combined.



GOL model selection

Nine predeclared models were compared on 81 common training observations using cross-validation grouped by recipe. The full log-logistic AFT model ranked first by cross-validated log-likelihood and second by AICc (ΔAICc = 1.95) and was therefore selected. The model was subsequently refitted on all 87 training observations.

Prediction GOL by Accelerated Failure Time (AFT) model

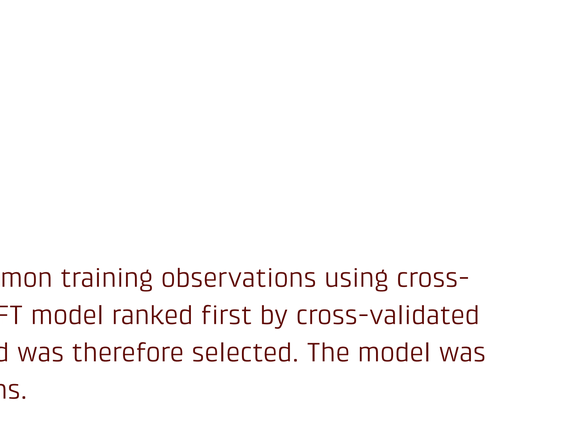
$$\begin{aligned} &ln(L) \\ &= 3.127 + \beta_T(T - T_{ref}) \\ &+ \beta_{pH}(pH - pH_{ref}) \\ &+ \beta_{WPS}(WPS - WPS_{ref}) + \beta_{Nitrite} \\ &\times Nitrite + \beta_{LACu} \times LAC_u + \beta_{AACu} \\ &\times AAC_u + \beta_{MAP} \times I_{MAP} \end{aligned}$$

$$P(T \le t) = \frac{(t/L)^{1/\sigma}}{1 + (t/L)^{1/\sigma}}$$

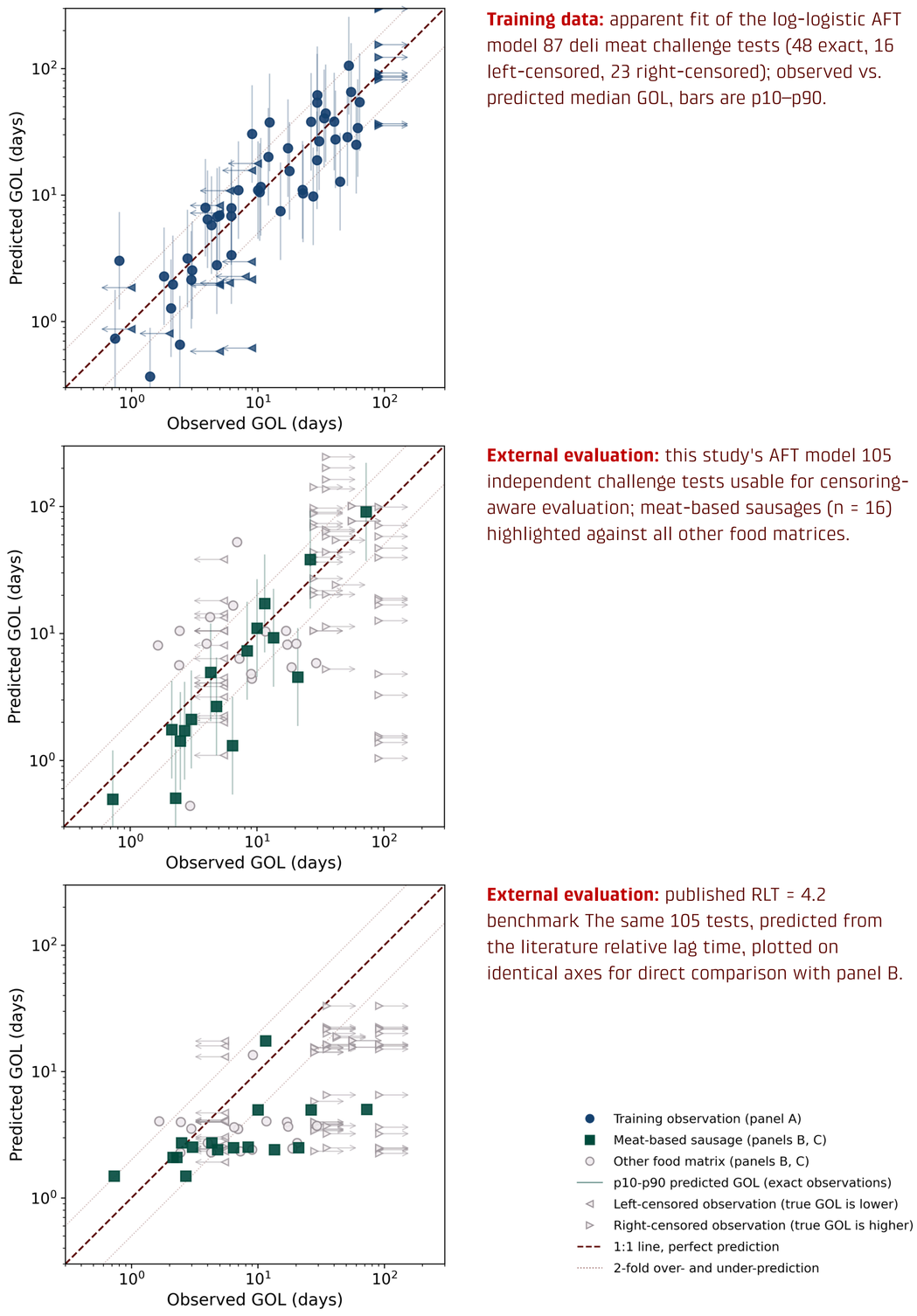
$$t = L \Rightarrow P(T \le L) = 0.5$$

L: Median GOL (h)
T: Temperature (°C)
WPS: Water-phase salt (%)
Nitrite: Ingoing nitrite (ppm)
LAC_u and AAC_u: Undissociated acids (mM)
1_{MAP}: 1 for MAP and 0 for vacuum

Predictor	Unit change	β	SE	Time ratio
Temperature	+1°C	−0.499	0.047	0.61
pH	+1 unit	0.594	0.408	1.81
WPS	+1 % point	0.740	0.111	2.10
Nitrite	+10 ppm	0.120	0.022	1.13
LACu	+1 mM	2.668	0.355	14.41
AACu	+1 mM	1.596	0.187	4.93
MAP or vacuum	MAP	1.244	0.190	3.47



Reference: 8°C · pH 6.2 · WPS 1.5% · 0 ppm nitrite · no organic acids · vacuum
Reference median GOL: 22.8 h
Distribution: log-logistic AFT, σ=0.404
pH and undissociated lactic acid are collinear by construction and should be interpreted jointly.



Training data: apparent fit of the log-logistic AFT model 87 deli meat challenge tests (48 exact, 16 left-censored, 23 right-censored); observed vs. predicted median GOL, bars are p10–p90.

External evaluation: this study's AFT model 105 independent challenge tests usable for censoring-aware evaluation; meat-based sausages (n = 16) highlighted against all other food matrices.

External evaluation: published RLT = 4.2 benchmark The same 105 tests, predicted from the literature relative lag time, plotted on identical axes for direct comparison with panel B.

Endpoint/model	Dataset	n^1	B_f	A_f	RMSE
Growth rate	Training, grouped out-of-fold	64	0.99	1.65	0.0257 h^{-1}
Growth rate	Validation, all matrices	61	2.05	2.67	0.0226 h^{-1}
Growth rate	Validation, meat-based sausages	16	0.96	1.47	0.0178 h^{-1}
GOL, AFT	Training, apparent fit	48	0.96	1.64	14.9 days
GOL, AFT	Validation, all matrices	33	0.83	2.21	11.4 days
GOL, AFT	Validation, meat-based sausages	16	0.67	1.75	7.19 days
GOL, RLT=4.2	Validation, all matrices	33	0.47	2.57	15.0 days
GOL, RLT=4.2	Validation, meat-based sausages	16	0.48	2.44	18.7 days

[1] Growth-rate metrics use growth-positive observations. GOL B_f, A_f, and RMSE use exact, uncensored GOL observations. The AFT model was fitted on all 87 training tests: 48 exact, 16 left-censored, and 23 right-censored. The external dataset contained 123 tests, of which 105 were usable for censoring-aware GOL evaluation and 33 had exact GOL estimates.

Bias-factor interpretation

Growth rate: B_f>1 means growth is predicted faster than observed.
GOL: B_f<1 means growth is predicted earlier than observed—the fail-safe direction

Conclusion and model performance

Both models transferred best within the meat-based sausage family. External growth-rate performance was B_f = 0.96 and A_f =1.47, while the GOL model achieved B_f = 0.67 and A_f =1.75, and an RMSE of 7.19 days. This substantially improved on the published RLT of 4.2. Performance was poorer across unrelated food matrices, demonstrating that model transfer is product-matrix dependent. The models therefore show potential for product development and risk assessment in thermally processed deli-meat sausages, while broader application requires further validation.

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Maktabdar M, Houmann RH, Scheel NH, Skytthe KB, Wemmenhove E, Gkogka E and Dalgaard P (2025). Evaluation and validation of extensive growth and growth boundary models for mesophilic and psychrotolerant Bacillus cereus in dairy products (Part 2). Front. Microbiol. 16:1553903. doi: 10.3389/fmicb.2025.1553903