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Published in:
10th International conference on predictive modelling in food

Publication date:
2017

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Buschhardt, T., Hansen, T. B., Bahl, M. I., Schaffner, D. W., & Aabo, S. (2017). Generic global regression models for growth prediction of Salmonella in ground pork and pork cuts. In *10th International conference on predictive modelling in food* [020] Cordoba, Spain.

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Generic global regression models for growth prediction of *Salmonella* in ground pork and pork cuts

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Introduction and Objectives

Models for the prediction of bacterial growth in fresh pork are primarily developed using two-step regression (i.e. primary models followed by secondary models). These models are also generally based on experiments in liquids or ground meat and neglect surface growth. It has been shown that one-step global regressions can result in more accurate models and that bacterial growth on intact surfaces can substantially differ from growth in liquid culture.

Material and Methods

We used a global-regression approach to develop predictive models for the growth of *Salmonella* for three pork matrices: on the surface of shoulder (neck) and hind part (ham), and in ground pork. We conducted five experimental trials and inoculated essentially sterile pork pieces with a *Salmonella* cocktail ($n = 192$). Inoculated meat was aerobically incubated at 4 °C, 7 °C, 12 °C, and 16 °C for 96 h. One part of obtained log-transformed cell counts was used for model development and another for model validation. The Ratkowsky square root model and the relative lag time (RLT) model were integrated into the logistic model with delay. Fitted parameter estimates were compared to investigate the effect of meat structure on bacterial growth and goodness-of-fit was evaluated by root mean squared errors (RMSE). We used the Acceptable Simulation Zone (ASZ) approach and cross-validation with model-independent data to investigate if generic predictive models could accurately describe microbial growth across all studied pork products and compared our models to already existing generic models.

Results

Our results indicated that the growth of *Salmonella* was affected by product characteristics such as pH and structure, but storage temperature was shown to be the only variable needed to predict growth independent of pH and structural differences. RMSE of 0.54 suggested acceptable goodness-of-fit for the *Salmonella* generic growth model. Model evaluations of the generic growth model showed that described growth responses on pork neck and in ground pork were highly accurate with 86 and 98% of all model-independent observations within the ASZ, respectively. Although growth descriptions showed less accuracy in the case of pork ham, a fail-safe model could still be developed. Model evaluation also showed that our model performed better than generic existing models.

Conclusions

We suggested that generic model with fewer variables might provide a more suitable approach to bacterial growth modeling in fresh pork if pH and the type of pork product are unknown. Our study provides a “ready-to-use” global regression model relevant for a wide range of time and temperature combinations and various fresh pork products. The model should be a useful tool to control growth of *Salmonella* in meat and set critical limits for temperature during production and storage of fresh pork.