



Predictive model for growth of *Bacillus cereus* during cooling of cooked rice

Vijay K. Juneja^{a,*}, Chase E. Golden^b, Abhinav Mishra^b, Mark A. Harrison^b, Tim Mohr^c, Meryl Silverman^d

^a U.S. Department of Agriculture, Agricultural Research Service, Eastern Regional Research Center, 600 East Mermaid Lane, Wyndmoor, PA 19038, United States of America

^b Department of Food Science & Technology, University of Georgia, Athens, GA 30602, United States of America

^c U.S. Department of Agriculture, Food Safety and Inspection Service, Office of Public Health Science, Science Staff, 530 Center Street, NE, Suite 401, Salem, OR 97301, United States of America

^d U.S. Department of Agriculture, Food Safety and Inspection Service, Office of Policy and Program Development/Risk, Innovations, and Management Staff, Washington, DC, United States of America

ARTICLE INFO

Keywords:

Predictive microbiology
Food safety
Baranyi model
Foodborne pathogens

ABSTRACT

Bacillus cereus is frequently implicated in foodborne outbreaks associated with the consumption of cooked rice. The main contributing factors leading to outbreaks is rice cooked in large quantities and subsequently, inadequately chilled or stored at room temperatures for a prolonged period of time prior to consumption. *Bacillus cereus* growth in cooked rice inoculated with approximately 2 log CFU/g of heat-shocked (80 °C/10 min) spores at several isothermal conditions (between 10 and 49 °C) was quantified. *B. cereus* populations were determined by plating on mannitol egg yolk polymyxin agar and incubating at 30 °C for 24 h. Primary growth models, namely Baranyi, Huang, modified Gompertz, and logistic models were fitted to growth data. Specific growth rates from all four primary models were used to fit the modified Ratkowsky square-root model with respect to temperature. All four primary models were well fitted by the modified Ratkowsky model (R^2 values from 0.90–0.99). Based on the goodness of fit secondary model statistics (R^2 , SSE, RMSE), the Baranyi model performed the best and was chosen for tertiary modeling. Acceptable prediction zone (APZ) analysis was performed for validation of the Baranyi model predictions during single rate exponential and biphasic linear cooling temperature profiles. For single rate cooling, 23 of the 24 predictions fell within the APZ (–1.0 to 0.5 log CFU/g). For biphasic linear cooling, 26 of the 28 predictions fell within the APZ. The developed dynamic model can be used to predict potential *B. cereus* growth from spores in cooked rice during chilling and thus, support the disposition of product subject to cooling deviations.

1. Introduction

Bacillus cereus, a spore-forming pathogen of public health significance for the last 40 years, is a common inhabitant of soil and may find its way into crops and hence into foods. The pathogen has been isolated from rice dishes, raw and pureed vegetables, dairy products, spices, food crops, and cooked, ready-to-eat foods (Eglezos et al., 2010; Fangio et al., 2010; Kramer and Gilbert, 1989; Pao et al., 2006; Rajkovic et al., 2005). While raw husked rice has been found to contain 2.5×10^1 CFU/g, raw unhusked rice can contain as high as 2.5×10^3 CFU/g of *Bacillus cereus* spores (Sarrias et al., 2003). In a survey conducted in retail foods, about 52.8% of the total 178 samples of raw rice were reported to be contaminated with spores of *B. cereus* (Ankolekar et al., 2009). In another survey, *B. cereus* was isolated from

54 of 136 samples of rice and their processed products (Jang et al., 2006). Thus, sufficient evidence exists to document that rice can be contaminated with spores of *B. cereus*.

B. cereus is an etiological agent of diarrheal as well as emetic foodborne illness syndromes. The pathogen is one of the main microorganisms, implicated in an estimated 63,400 episodes of foodborne illnesses annually in the United States (Scallan et al., 2011). Consumption of cooked rice is one of the main foods, frequently implicated in foodborne outbreaks with *B. cereus* and widely reported (Delbrassinne et al., 2015; Pao et al., 2006). The main contributing factors leading to outbreaks is rice cooked in large quantities in advance of a social event or a large gathering and inadequately chilled after cooking or stored at room temperatures for an extended period of time prior to consumption (Adams and Moss, 2000; Mossel et al., 1991).

* Corresponding author.

E-mail address: vijay.juneja@ars.usda.gov (V.K. Juneja).

<https://doi.org/10.1016/j.ijfoodmicro.2018.09.023>

Received 9 April 2018; Received in revised form 5 September 2018; Accepted 24 September 2018

Available online 26 September 2018

0168-1605/ Published by Elsevier B.V.

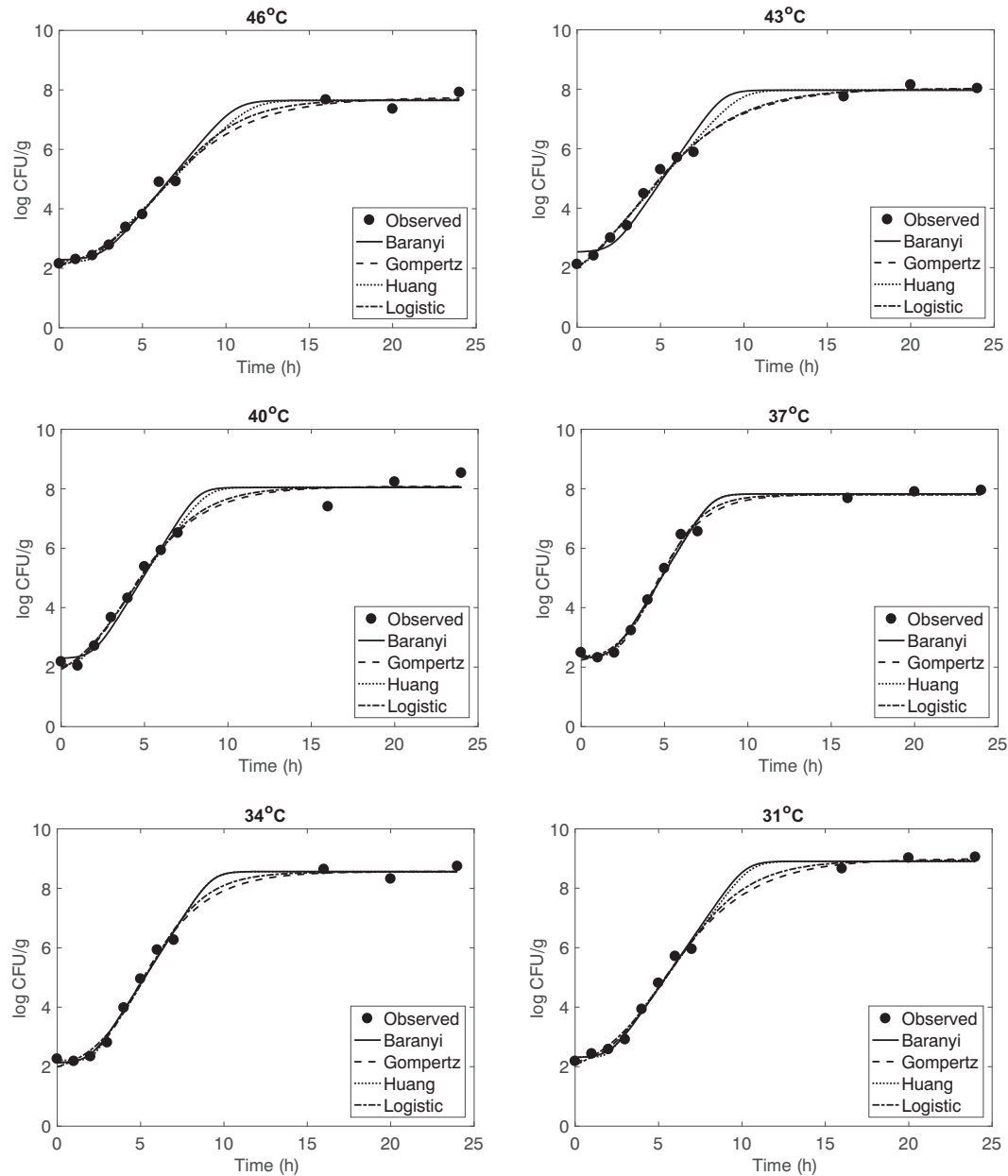


Fig. 1. Observed growth of *B. cereus* in cooked rice stored at different temperatures and fitted primary growth models. Each graph illustrates a representative trial for each temperature point.

Bryan et al. (1981) reported that the highest temperature achieved during cooking rice is 99 °C. While *B. cereus* vegetative cells are destroyed at this cooking temperature, spores are likely to survive since the decimal reduction time (D-value) at 100 °C ranged from 2.2–5.5 min to 80 min at 80 °C, depending on the strains of *B. cereus* (Montville et al., 2005). The heat activated spores can germinate, outgrow and multiply to potentially dangerous population levels (about 5–6 log CFU/g) or produce a heat-stable toxin (emetic toxin) in food (Little et al., 2002). After cooking rice, a public health hazard may occur because of inadequate rate and extent of cooling or storage at improper temperatures, such as storage at temperatures > 5 °C (41 °F) for > 4 h. Reheating precooked rice prior to consumption would not destroy the preformed toxin responsible for the emetic type of illness and may not sufficiently reduce the vegetative cell numbers to prevent diarrheal syndrome. Approximately 95% of the emetic syndrome outbreaks are primarily caused by the consumption of cooked or fried rice and is frequently reported in countries, such as Japan, where rice is a

staple food (Granum, 2005, 2007; Kramer and Gilbert, 1989).

Predictive microbial modeling programs such as the USDA Pathogen Modeling Program (PMP) and ComBase Predictor are extensively used by the regulatory agencies as well as the food industry to predict the behavior of pathogens in foods under conditions relevant to the food processing operations. While these user-friendly modeling tools include the cooling models to predict the relative growth of *Clostridium perfringens* or *Clostridium botulinum* from spores at temperatures applicable to the cooling of cooked foods, dynamic models for *B. cereus* are not currently available. Currently, there are only two growth models available for *B. cereus*, both of which have limitations in evaluating cooling deviations involving nonmeat components (e.g., rice, pasta, beans, etc.). These models are the ARS PMP 7.0/8.0 growth model for *B. cereus* and the ComBase Predictor growth model for *B. cereus*. The PMP 7.0/8.0 growth model for *B. cereus* has the following limitations to the model: Growth experiments conducted in broth culture not product; predictions based on static temperature conditions not dynamic

Download English Version:

<https://daneshyari.com/en/article/11016775>

Download Persian Version:

<https://daneshyari.com/article/11016775>

[Daneshyari.com](https://daneshyari.com)