Implementing a new dose-response model for estimating infection probability of *Campylobacter jejuni* based on the key events dose-response framework

Supplementary information

Hiroki Abe, Kohei Takeoka, Yuto Fuchisawa, Kento Koyama, Shigenobu Koseki*

Graduate School of Agricultural Science, Hokkaido University, Kita-9, Nishi-9, Kita-ku, Sapporo 060-8589, Japan

*Corresponding author: Phone/fax: +81 11 706 2552

E-mail address: koseki@bpe.agr.hokudai.ac.jp (S. Koseki)

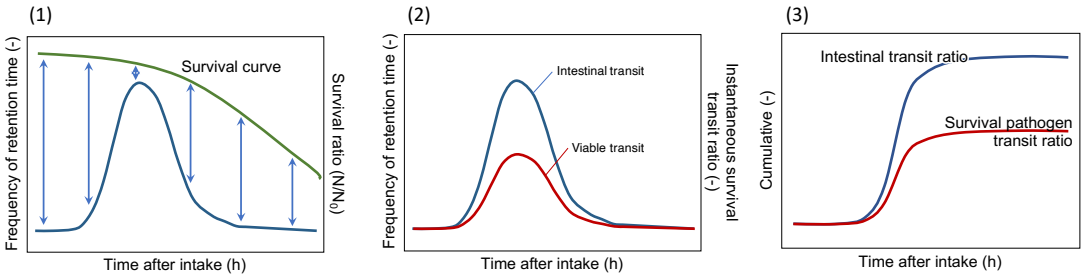

Figure S1. The scheme of the calculation for survival pathogen transit ratio from stomach to intestine (Eq. 4). (1): It is assumed that the intestinal transit rate of pathogen is equal to that of food. The survival ratio of the instantaneous pathogen transit corresponds to the instantaneous value of the survival curve. (2): Multiply the instantaneous values of survival curve and intestinal transit to calculate the instantaneous values of viable transit. (3): Integrating intestinal transit gives the ratio of all pathogens (dead or alive) that have transferred into an intestine. Similarly, the integral of viable transit represents the survival transit ratio of pathogens that have transferred into an intestine.

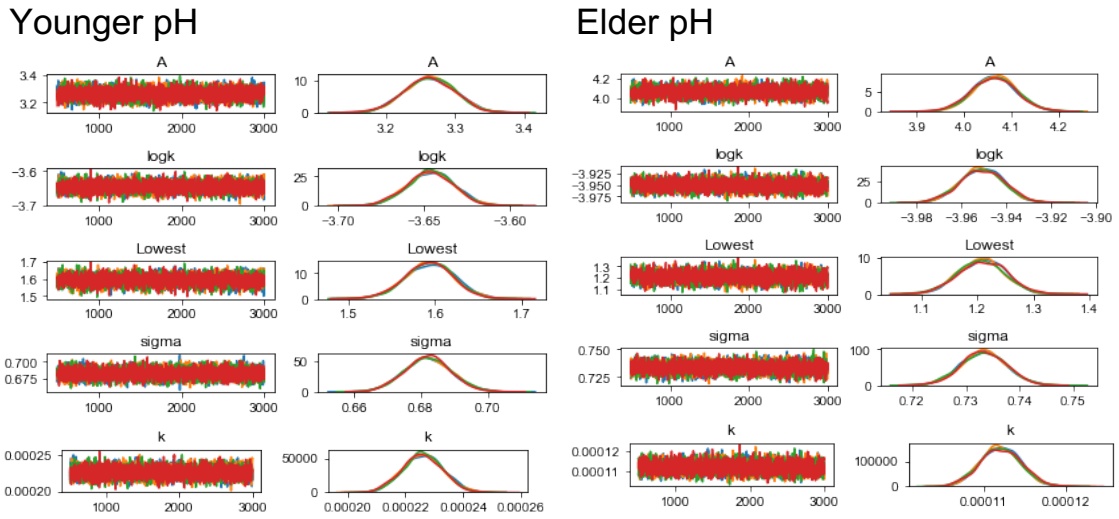

Figure S2. Trace-plots and posterior distributions for estimated parameters of younger and elderly people's pH change by Bayesian inference. Each color indicates each trace-plot and each distribution of the MCMC chain.

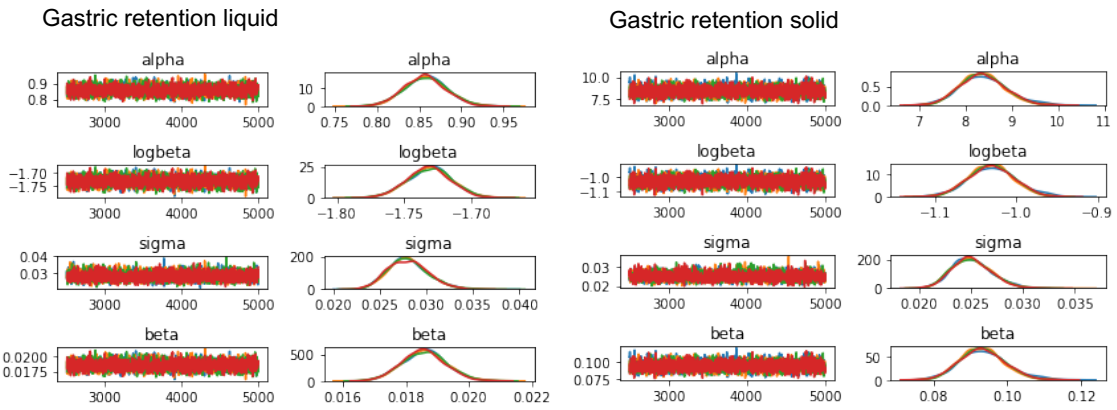

Figure S3. Trace-plots and posterior distributions for estimated parameters of gastric retention of liquid and solid by Bayesian inference. Each color indicates each trace-plot and each distribution of the MCMC chain.

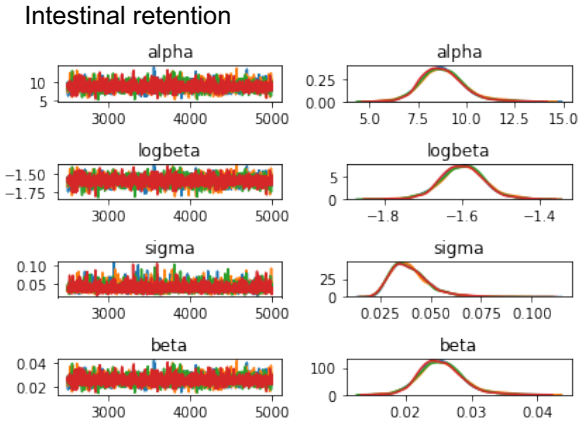

Figure S4. Trace-plots and posterior distributions for estimated parameters of gastric retention of liquid and solid by Bayesian inference. Each color indicates each trace-plot and each distribution of the MCMC chain.

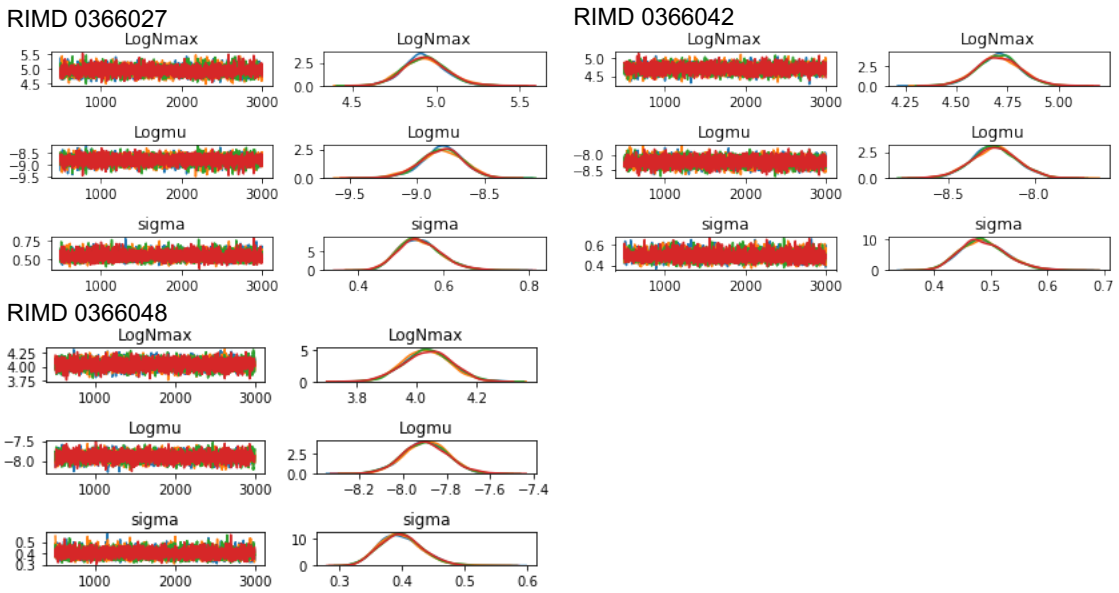

Figure S5. Trace-plots and posterior distributions for estimated parameters of the modified model from reported cell-invasion model (1)of *C. jejuni* (RIMD 0366027, 0366042 and 0366048) by Bayesian inference. Each color indicates each trace-plot and each distribution of the MCMC chain.

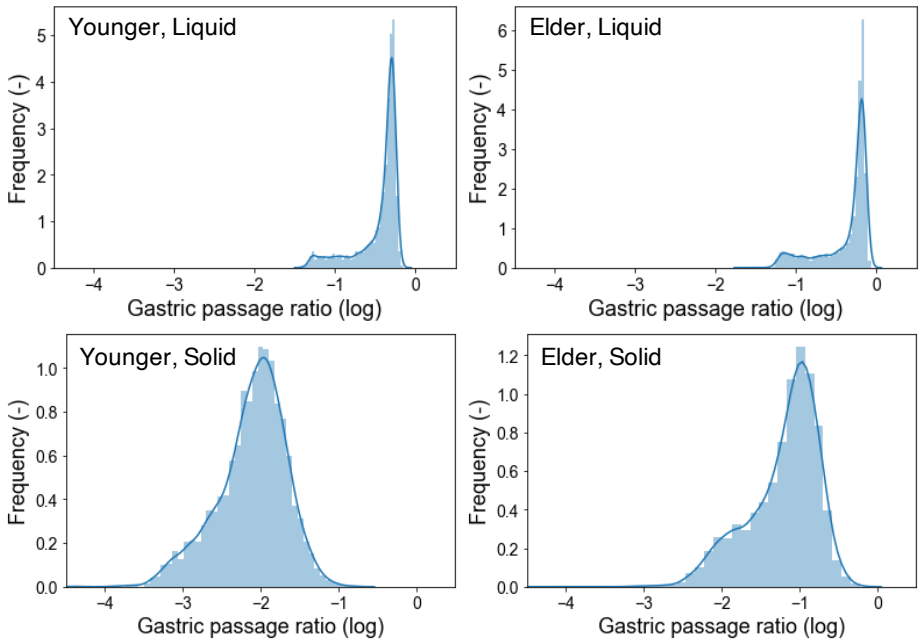

Figure S6. Histograms and kernel distributions (solid) of final survival transit ratio (12 hours after meal). Host age and food type were, from top left: Young-Liquid; Elderly-Liquid; Young-Solid and Elderly-Solid.

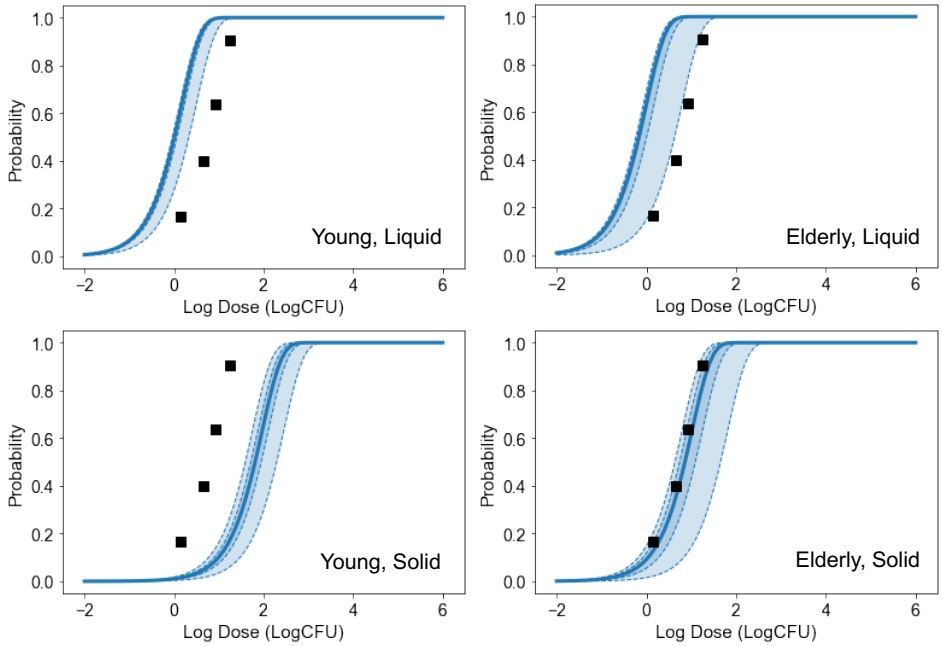

Figure S7. Cell invading probability (solid curve: median, dash curve and covered range: 60% and 95% prediction band) of *C. jejuni* (RIMD 0366027) under each condition (Same position as Fig. 7) & reported ill probability of milk outbreak against children (squares; Teunis et al., 2005 (2)).

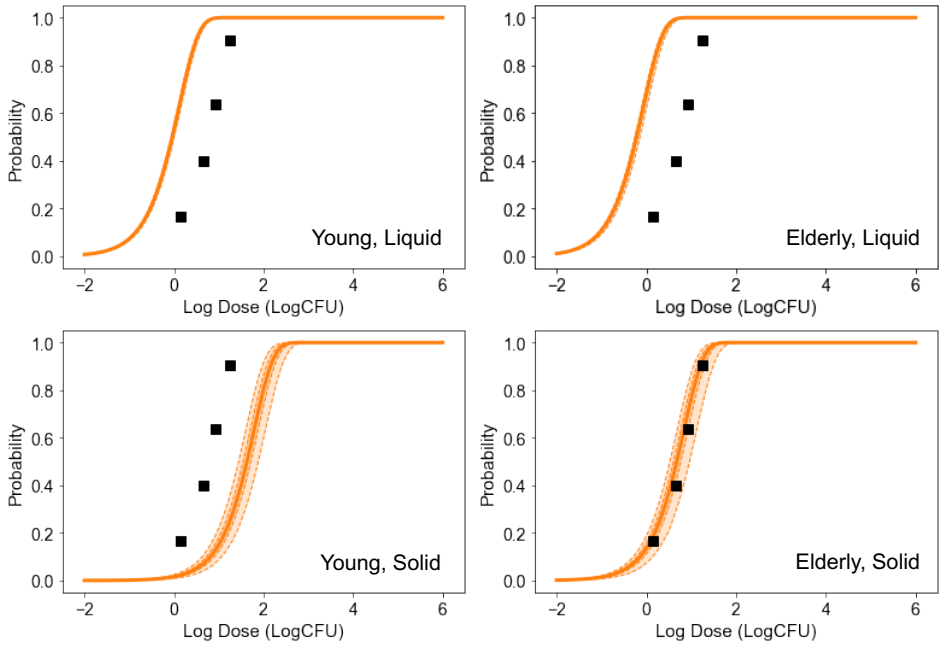

Figure S8. Cell invading probability (solid curve: median, dash curve and covered range: 60% and 95% prediction band) of *C. jejuni* (RIMD 0366042) under each condition (Same position as Fig. 7) & reported ill probability of milk outbreak against children (squares; Teunis et al., 2005 (2)).

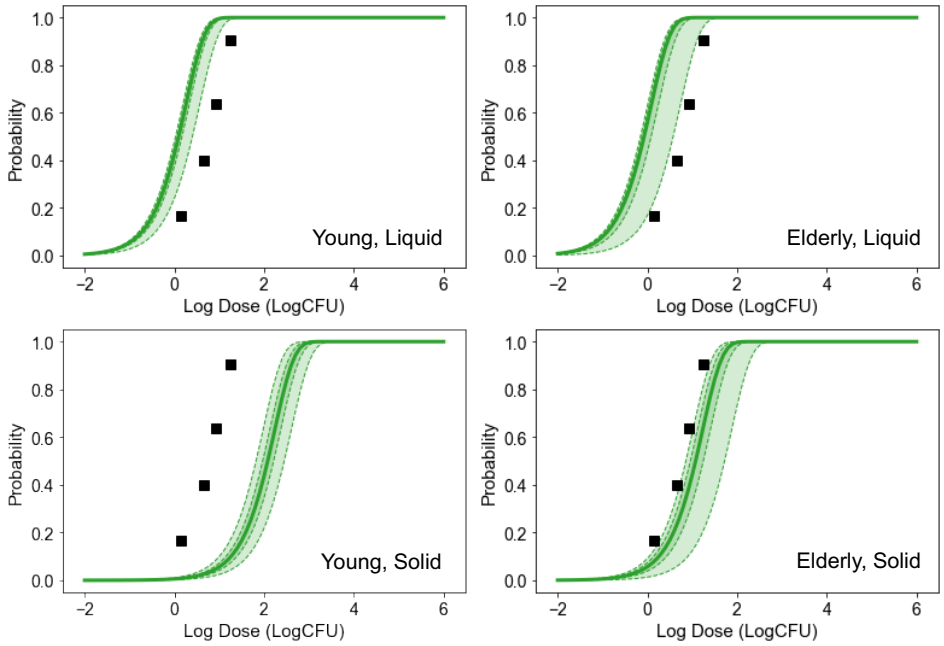

Figure S9. Cell invading probability (solid curve: median, dash curve and covered range: 60% and 95% prediction band) of *C. jejuni* (RIMD 0366048) under each condition (Same position as Fig. 7) & reported ill probability of milk outbreak against children (squares; Teunis et al., 2005 (2)).

1. **Abe H**, **Koyama K**, **Koseki S**. 2021. Modeling Invasion of *Campylobacter jejuni* into Human Small Intestinal Epithelial-Like Cells by Bayesian Inference. Appl Environ Microbiol **87**:687.

2. **Teunis P**, **van den Brandhof W**, **Nauta M**, **Wagenner J**, **van den Kerkhof H**, **van Pelt W**. 2005. A reconsideration of the *Campylobacter* dose–response relation. Epidemiology & Infection **133**:583–592.