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Letter to the Editor

Sencer Buzrul

On the use of Weibull model for isothermal and nonisothermal heat treatments

I read with much interest the recent article by Hassani *et al.* [1]. These authors provide important and valuable inactivation data for isothermal and non-isothermal heat treatments at three pH values (4.0, 5.5 and 7.4).

Investigation of the performance of different kinds of thermal kinetics models that accurately predicts heat inactivation for both isothermal and nonisothermal heat treatments is a topic of interest to microbiologists and food scientists. As acknowledged by Hassani *et al.* [1], Peleg and coworkers have been investigating aspects of this problem for over six years and their publications in this area can be considered state of the art, and also acknowledged by Hassani *et al.* [1], Mattick *et al.* [2] and Peleg *et al.* [3] accurately estimated survival curves *Salmonella typhimurium* and *Listeria monocytogenes* inactivation, respectively during non-isothermal heat treatments from their isothermal survival curves.

By using the same methodology, Hassani *et al.* [1] showed that estimations of survival curves during nonisothermal heat treatments (constantly rising heating rates, 0.5-9°C/min) obtained from heat resistance parameters of isothermal treatments did not adequately fit experimental values.

They fit the survival curves under isothermal conditions by Eq. (1) proposed by Peleg and Cole [4]:

$$\log_{10} S(t) = -b(T)t^{n(T)} \tag{1}$$

Correspondence: Sencer Buzrul, Food Engineering Department, Middle East Technical University, 06531 Ankara, Turkey
E-mail: sbuzrul@metu.edu.tr
Fax: +90-312-210-2767

where $S(t)$ is the survival ratio which is defined as the ratio between the number of survivors after an exposure time t, $N(t)$ and the initial number, N_0, *i. e.*, $S(t) = N(t)/N_0$. $b(T)$ and $n(T)$ are temperature dependent parameters of the model. If the temperature history or profile, $T(t)$, can be expressed algebraically, the theoretical survival curves under nonisothermal conditions can be estimated using the following differential equation based on Eq. (1) as described by Peleg and Penchina [5]:

$$\frac{d(\log_{10} S(t))}{dt} = -b[T(t)].n[T(t)] \cdot t^{*n[T(t)]-1} \tag{2}$$

with t^*, the time which corresponds to the momentary survival ratio:

$$t^* = \left(-\frac{\log_{10} S(t)}{b[T(t)]}\right)^{\frac{1}{n[T(t)]}} \tag{3}$$

Combining Eqs. (2) and (3) yields the differential equation:

$$\frac{d(\log_{10} S(t))}{dt} = -b[T(t)] \cdot n[(T(t)] \cdot \left(-\frac{\log_{10} S(t)}{b[T(t)]}\right)^{\frac{n[T(t)]-1}{n[T(t)]}} \tag{4}$$

As mentioned above, Hassani *et al.* [1] used Eq. (4) to estimate the inactivation of *S. aureus* during non-isothermal heat treatments; however, their results indicate that number of survivors higher than the estimated values obtained from Eq. (4). Therefore, they fitted the survival curves of nonisothermal heat treatments with another model proposed by Mafart *et al.* [6]:

$$\log_{10} S(t) = -\left(\frac{t}{\delta}\right)^{p} \tag{5}$$

where p is the equivalent of n in Eq. (1) and δ is the first decimal reduction time (units in min or s) *i.e.*, time needed to reduce the initial population, N_0 to $N_0/10$.

In fact, Eqs. (1) and (5) are the different expressions of the Weibull model (for more information about the Weibull model see van Boekel [7]) and without any calculation the goodness-of-fit of these two models would be the same (see Fig. 1 and Table 1). Moreover, both Equations are applicable to 'only' iso-conditions (isothermal, isobaric, isoconcentration, etc.) therefore fitting of Eq. (5) to nonisothermal survival curves is inadequate.

It is also possible to demonstrate the same methodology proposed by Peleg and Penchina [5] by using Eq. (5) instead of Eq. (1). In this case, instead of describing the parameter b in terms of temperature (where temperature is described in terms of time), the parameter δ would be described in

Table 1. Parameters ± 95% confidence intervals of Eqs. (1) and (5) fitted in Fig. 1, and regression coefficient (R^2), root mean square error (RMSE) values of each model.

pH	Eq. (1)		Eq. (5)		R^2	*RMSE*
	b	*n*	δ	*p*		
4	4.60 ± 0.61	0.80 ± 0.13	0.15 ± 0.03	0.80 ± 0.13	0.99	0.13
5.5	9.49 ± 1.40	0.79 ± 0.10	0.06 ± 0.009	0.79 ± 0.10	0.99	0.09
7.4	6.86 ± 1.10	0.54 ± 0.09	0.03 ± 0.009	0.54 ± 0.09	0.99	0.08

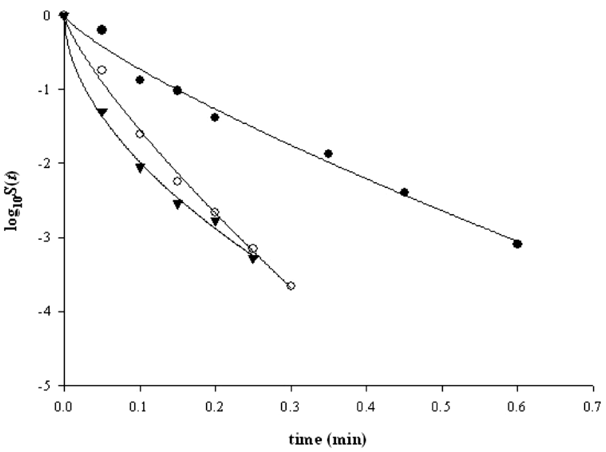

Figure 1. Inactivation data of Hassani *et al.* [1] (*S. aureus* heat treated at 64°C in TSB at pH 4.0 (●), 5.5 (○) and 7.4 (▼)). Survival curves were fitted with Eqs. (1) and (5).

terms of temperature. Thus, demonstration of Peleg's methodology [5] could have been also done with Mafart's equation [6]; most probably the same result would be obtained. Similarly, although it is not advisable as mentioned above, Eq. (1) could have been used instead of Eq. (5) to survival curves of nonisothermal treatments with a same degree of fit and with the same conclusions.

In order to show the results of fitting of these two forms of the Weibull model (Eqs. 1 and 5), the data of Hassani *et al.* [1] (Fig. 1) were digitized and the values of $\log_{10}S(t)$ and the time were determined graphically. Thereafter, the data were fitted with both models. Table 1 presents regression coefficient (R^2), root mean square error (*RMSE*) values and the parameters of the both models together with their corresponding confidence intervals. As expected both model has the same n and p values (also pointed out by Hassani *et al.* [1]) and same R^2 and *RMSE* values. Since n or p are the shape parameters *i.e.*, determine the shape of a survival curve both model produced the same degree of fit when they were applied to the data; however, the value of b and δ were different.

I would like to thank Hassani et al. [1] for the publication of these costly data.

References

[1] Hassani, M., Mañas, P., Condón, S., Pagán, R., Predicting heat inactivation of *Staphylococcus aureus* under nonisothermal treatments at different pH, *Mol. Nutr. Food Res.* 2006, *50*, 572–580.

[2] Mattick, K. L., Legan, J. D., Humphrey, T. J., Peleg, M., Calculating Salmonella inactivation in nonisothermal heat treatments from isothermal nonlinear survival curves, *J. Food Prot.* 2001, *64*, 606–613.

[3] Peleg, M., Penchina, C. M., Cole, M.B., Estimation of the survival curve of Listeria monocytogenes during nonisothermal heat treatments, *Food Res. Int.* 2001, *34*, 383–388.

[4] Peleg, M., Cole, M.B., Reinterpretation of microbial survival curves, *Crit. Rev. Food Sci. Nutr.* 1998, *38*, 353–380.

[5] Peleg, M., Penchina, C. M., Modeling microbial survival during exposure to a lethal agent with varying intensity, *Crit. Rev. Food Sci. Nutr.* 2000, *40*, 159–172.

[6] Mafart, P., Couvert, O., Gaillard, S., Leguerinel, I., On calculating sterility in thermal preservation methods: application of the Weibull frequency distribution model, *Int. J. Food Microbiol.* 2002, *72*, 107–113.

[7] van Boekel, M. A. J. S., On the use of the Weibull model to describe thermal inactivation of microbial vegetative cells, *Int. J. Food Microbiol.* 2002, *74*, 139–159.