Heat Transfer and Microbial Kinetics Modeling to Determine the Location of Microorganisms within Cucumber Fruit

F.R. MATTOS, O.O. FASINA, L.D. REINA, H.P FLEMING, F. BREIDT, JR., G.S. DAMASCENO, AND F.V. PASSOS

ABSTRACT: Microbiological and modeling (combined heat transfer and microbial kinetic equations [HTMK] model) approaches were used to determine the location of microorganisms within cucumber. The total number of aerobes found within/on cucumbers varied from 10^5 to 10^7 colony-forming units (CFU)/g. The highest and the least amount of microbiota were respectively found at the blossom end and middle part of the cucumbers and were within the 1st 6 mm of the cucumber surface. A comparison of the calculated thermal death time from the HTMK model with the values obtained from experimental data showed that total aerobic microorganisms were located within 0.65 mm of the fruit surface.

Keywords: heat transfer, thermal death kinetics, modeling, blanching

Introduction

The annual per capital consumption of fresh fruits and vegetables in the United States has increased by more than 13% over the past 2 decades. This increased demand has expanded greatly the geographic sources and distribution of fresh produce and has resulted in increases in amount and frequency of fresh produce–associated foodborne disease outbreaks in the United States in the past 30 y (Tauxe and others 1997).

Most of the contamination of fresh fruits and vegetables with pathogenic microorganisms (bacteria, viruses, and parasites) occurs while growing in fields or orchards or during harvesting, postharvest handling, and distribution. Bacteria are the greatest concerns in terms of serious illness and number of persons at risk of infection (Beuchat 1996). The amount of total aerobes typically found in fresh produce after harvest is about 10^5 to 10^6 colony-forming units (CFU)/g (Nguyen-the and Carlin 1994; Reina and others 1995).

Due to regulatory constraints, sodium hypochlorite is the only chemical sanitizer used to wash fresh produce to reduce their microbial load. Several studies have shown that microbial load reduction that can be obtained in fresh produce dipped in chlorinated water is usually less than 100-fold. Brackett (1987) showed that for Brussels sprouts a chlorine dip of 200 ppm reduced the population of *Listeria monocytogenes* by about 10^2 CFU/g. Chlorine treatment (2000 ppm) of cantaloupe cubes injected with a 5-serotype cocktail of *Salmonella* resulted in a less than 10^1 reduction in viable cells (Beuchat and Ryu 1997). Reina and others (1995) showed that chlorine dioxide in cucumber hydrocooling water was ineffective in reducing the microbial load of the cucumber fruit but was effective in reducing the load in the water itself. Other sanitizers such as organic acids, trisodium phosphate, and ozone, have been tried. None of these substances has been shown to eliminate more than 10^2 of microbes present in fresh produce at concentrations not detrimental to sensory quality (Annous and others 2001; Koseki and others 2001; Ukuku and Fett 2004).

Lund (1983) and Adams and others (1989) have attributed the failure of sanitizers to remove more of the microbiota present in fresh produce to the presence of hydrophobic pockets or folds in leaf surfaces, waxy cuticle, crevices, creases, and natural openings in fruits. The evidence for the presence of microorganisms within the tissue of fresh produce was provided by the study of Samish and others (1963). The authors carried out microbiological analyses on 10 fruits and vegetables that had been surface-sterilized. Bacteria were found within tomatoes, cucumbers, garden peas, and green peas. The authors reported their results in terms of the frequency of bacteria occurrence in the fruits. The number of bacteria within the fruit was, however, not quantified. Daeschel and others (1985) detected microorganisms within the mesocarp and skin sections, but not within the endocarp sections of cucumbers. There was no quantification of the dimensions of the sections and, therefore, their results may not be useful in the modeling of kinetics needed to inactivate the microbiota present in cucumbers.

Because surface-sanitizing has not been 100% effective on the microorganisms found in fresh produce, alternate means of removing the pathogens must be developed. A prerequisite to this is the determination of the location of microorganism within fresh produce. This was achieved by developing a heat transfer–microbial kinetic (HTMK) model and using the model to follow the rate of kill of microorganisms in cucumbers (used as model for fresh produce) during blanching. Despite the vast amount of research on heat transfer in processed foods and packages and corresponding experimental work on inactivation of pathogenic bacteria, very little published research is available that combines heat transfer and microbial kinetics. Bellara and others (1999) used the HTMK model to predict the inactivation of *Salmonella enterica* subsp. *typhimurium* and *Bacillus thermosphacta* in agar cylinders. Prediction results from the model were within a maximum of 3.6% from experimental data. The same approach was used by Vijayan and others (1997) to

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model heat transfer and the destruction of *Escherichia coli* O157:H7 during the cooking of hamburger patties. Simulation results showed that increasing grill temperature from 160 °C to 200 °C reduced heating time of the patties by 20 s when a 9-log reduction of the pathogenic bacteria is desired. However, the authors did not compare their predictions with experimental results.

The objective of this study was to determine the location of microorganisms in cucumber fruit using microbiological analysis and a combined heat transfer and microbial kinetics model.

Materials and Methods

The cucumbers used in this study were obtained from local processors and farmers and were free of obvious physical damage and disease. Before use, the cucumbers were washed in running water for 15 s. Physical properties (mass, diameter, length, and volume) of 20 cucumbers were measured. A digital vernier caliper (Digimatic, model nr CD-S6CP, Mitutoyo Co., Kawasaki, Japan) with 0.01-mm precision was used to measure the length and diameter of each cucumber, whereas an analytical balance (model LC 2200S, Sartorius, AG, Goettingen, Germany) was used to measure the mass of the cucumbers. The density of 20 cucumbers was calculated from the ratio of the mass of cucumbers to the volume. Cucumber volume was obtained by the fluid (water) displacement method of Mohsenin (1986). This involves measuring the mass of displaced water in a container when cucumber fruit of known mass was forced into the water. The volume of the cucumber fruit was obtained from the ratio of mass of displaced water to the density of water.

Size 3B (about 50-mm dia) cucumbers were used for this part of this study. To determine the distribution of microorganisms within different sections of cucumbers, 6 washed cucumbers were cut with a sterile knife into 3 equal pieces, stem end, middle part, and blossom end (Figure 1a). Each cut section was placed in a sterile blender jar and blended (Waring Blender Dynamic Products Co., New Hartford, Conn., U.S.A.) for 2 min at high speed with an equal amount (volume basis) of 0.1% peptone water. The blended sample was placed in a stomacher filter bag and processed at high speed for 2 min in a stomacher (Model 400, Spiral Biotech, Seward, U.K.). The samples were then enumerated for total aerobes and total spores as described subsequently.

A sterilized cork borer (37.80-mm dia) was used to remove the inner section of size 3B (about 50-mm dia) cucumbers (Figure 1b). The dimensions and weights of the cut sections were respectively measured with the vernier caliper and the analytical balance, as described previously.

Approximately 20 g of the internal part of the stem and blossom ends of the fruits was removed aseptically using a sterile spatula. The inner sections of the middle part, stem end, and blossom end were processed. The procedure for sample preparation for microbiological analysis of the outer part of the fruit was the same as the one used for the uncut sections of the fruit.

Blanching

To validate the HTMK model, 4 size 3A (about 50-mm dia) cucumbers were blanched in a circulated water bath set at 60 °C, 80 °C, or 90 °C. The time of blanching was estimated from the HTMK model based on 2-log (99.0%) reduction of vegetative cells present in cucumbers. This was based on preliminary results after blanching cucumbers at various temperatures for up to 40 min (see "Results and Discussion" section). After blanching, each cucumber was placed into a sterile blender jar and cooled using 0.1% cold peptone water. The cucumber was then blended at high speed for 2 min. Thereafter, approximately 200 mL of the sample was transferred to a stomacher filter bag and processed at high speed for 1 min in a stomacher (model 400, Spiral Biotech). Microbiological analyses were then carried out.

Enumeration of microorganisms

Total aerobic microbiota for cucumber samples was enumerated by using Plate Count Agar (PCA) agar plates (Difco Laboratories, Detroit, Mich., U.S.A.), following the procedure for standard plate count (Swanson and others 1992). *Enterobacteriaceae* were plated on VRBG agar (VRB agar, Difco, supplemented with 1% dextrose, Sigma Chemical Co., St. Louis, Mo., U.S.A.; Fleming and others 1992).

Bacterial cell counts for PCA and VRBG plates were determined using a spiral plate machine (Autoplate 4000, Spiral Biotech). The plates were incubated at 30 °C for 20 to 24 h. Petrifilm (3M) were used to determine the total aerobic plate count (Swanson and others 1992) and total *Enterobacteriaceae* were used for low cell numbers (less than 5×10^2 CFU/mL). Plates were incubated at 30 °C for 24 h. PCA and VRBG plates were counted using a Protos Colony Counter (Synoptics Ltd., Cambridge, England).

Mesophilic aerobic sporeformers (MAS) were grown on Tryptone Glucose Extract (TGE) (Difco), following the procedure for MAS with a slight modification (Stevenson and Segner 1992). TGE agar (25 mL) was placed in 50-mL, plastic, screw-cap tubes (6 tubes for each sample). Three additional tubes were prepared to serve as controls. Tubes were inoculated with 1 mL and 0.1 mL sample in triplicate. They were then agitated gently to disperse the sample throughout the medium. The tubes were transferred without delay to a circulating water bath (MGW Lauda RC20, Model B-2, Brinkmann Instruments, Inc., Wewstbury, NY) adjusted to 80 °C and held for 30 min. Cooling was done in tepid tap water, making sure that the temperature did not decrease to the point at which agar solidifies. Tubes were transferred to the 45 °C bath after the rapid cooling step and held there for a period not to exceed 10 min. The sample was poured into sterile petri plates (nr 0875713, Fisher Scientific, Pittsburgh, Pa., U.S.A.) and allowed to cool. Plates were incubated at 37 °C for 48 h.

Counts were made of surface and subsurface colonies. The average count of colonies on the set of 3 plates represented the num-

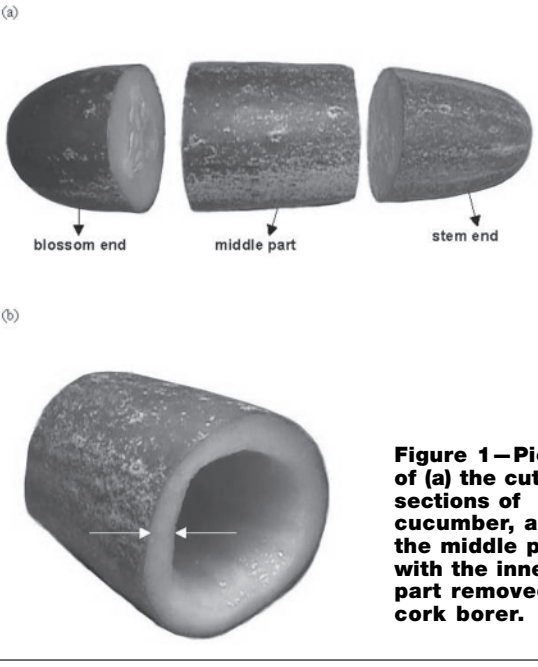

Figure 1—Picture of (a) the cut sections of cucumber, and (b) the middle part with the inner part removed by cork borer.

ber of aerobic mesophilic spores per gram. In the case of 0.1-mL samples, the number of spores per gram were multiplied by 10. The plates were counted manually.

Development of HTMK model

Heat transfer model. Cucumbers were approximated to be cylindrical in shape. Because several measurements of the length and diameter of cucumbers indicated an approximate length to diameter ratio of 3 to 1, a 2-dimensional (2-D) heat diffusion equation was used to describe the radial and axial flow of heat into the center of cucumbers during blanching in hot water as follows:

$$\rho c_p \frac{\partial T}{\partial t} = \frac{1}{r}\frac{\partial}{\partial r} kr \frac{\partial T}{\partial r} + k\frac{\partial^2 T}{\partial y^2} \quad (1)$$

Symbols are defined in the "Notation" section. The initial and boundary conditions to Eq. 1 are given by

$$T = To \qquad @\ t = 0 \quad (2)$$

$$\frac{\partial T}{\partial r} = 0 \qquad @\ t > 0;\ r = 0 \quad (3)$$

$$\frac{\partial T}{\partial y} = 0 \qquad @\ t > 0;\ y = 0 \quad (4)$$

$$-k\frac{\partial T}{\partial r} = h(T - T_\infty) \qquad @\ t > 0;\ r = R \quad (5)$$

$$-k\frac{\partial T}{\partial y} = h(T - T_\infty) \qquad @\ t > 0;\ y = L/2 \quad (6)$$

The above set of equations was used by Fasina and Fleming (2001) to describe the heat transfer characteristics of cucumbers during blanching. The authors showed from their study that mass transfer can be ignored during the blanching process and that Biot number (hR/k) is greater than 0.1.

Microbial kinetics model. When cucumbers are blanched, the lethality (measurement of the cumulative heat treatment effect on microbiota; Ramaswamy and Singh 1997) from the onset of the blanching process to time t at any location r within the fruit was modeled by the following equation:

$$F_{calc} = \sum_0^R \left[\int_0^t L_r\, dt \right] = \sum_0^R \left[\int_0^t 10^{\left(\frac{T_r - T_{ref}}{z}\right)} dt \right] \quad (7)$$

Numerical formulation and solution methodology

The heat transfer equations were numerically formulated in a finite difference method. Details of numerical formulation and solution methodology for Eq. 1 to 6 can be found in Fasina and Fleming (2001). The values of the thermo-physical properties of cucumbers used for HTMK simulation are given in Table 1 (Breidt and others 2000; Fasina and Fleming 2001).

Table 1—Values of parameters used in combined heat transfer–microbial kinetic (HTMK) simulation

Parameter	Symbol	Value
Density	ρ	980 kg/m^3
Thermal conductivity	k	0.62 W/m K
Specific heat	c_p	4.03 kJ/kg K
Heat transfer coefficient	h	1168 W/m^2 K
Reference temperature	Tref	52 °C
Decimal reduction time	D	4.5 min
Thermal resistance constant	z	7.8 °C

A flow chart of the solution methodology for the combined HTMK model is shown in Figure 2. At each stage of the iteration process (every 0.5 s), temperatures predicted at any location r and time from the heat transfer equations (Eq. 1 to 6) were incorporated into Eq. 7 to obtain F_{calc}. The location within the cucumber at which F_{expt} is numerically equal to F_{calc} is the deepest point that microorganisms can be found inside the fruit (Figure 2). F_{expt} is the experimental lethality obtained when the cucumbers were blanched at the temperature and time that were used as inputs to the heat transfer and microbial kinetics model. T_{expt} was calculated from the relation (Singh and Heldman 2001):

$$F_{expt} = D\left(\log \frac{N_o}{N}\right) \quad (8)$$

Results and Discussion

Physical properties

The average values of the measured physical properties of 200 size 3B cucumbers are given in Table 2. The length to diameter ratio was about 2.78. This is close to the value of 3.0 that we have observed in a previous study (Fasina and Fleming 2001). Coefficient of variation for all the parameters was less than 10.0%, thus indicating a small batch-to-batch variation for the physical attributes of the cucumbers.

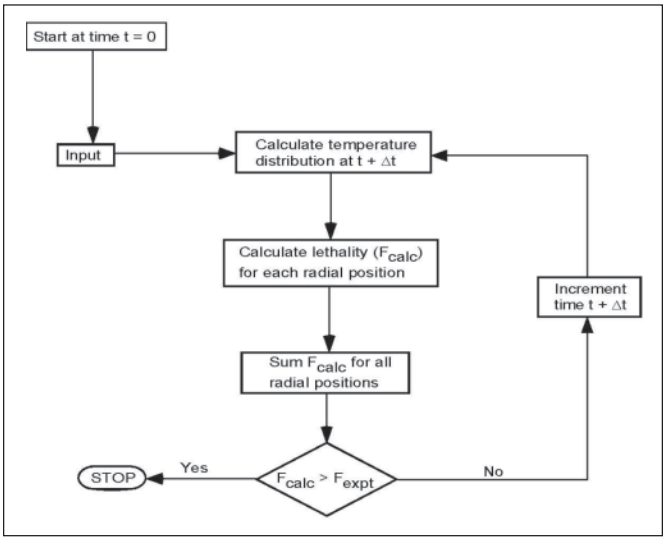

Figure 2—Flow chart for solving heat transfer–microbial kinetic (HTMK) model.

Microbial population within different sections of cucumbers

The total aerobes and total spores obtained at the different sections of cucumber are given in Table 3. The middle sections of cucumbers have the lowest microbial count. Analysis of variance using the GLM procedure (SAS Inst. 2002) indicated that the total number of aerobes for the sections were not significantly different at the 95% confidence interval. The total number of spores for the blossom section of the cucumber was, however, significantly higher than the spore count for the middle section. The results from this section of the study support the explanation of Samish and Dimant (1959) that microorganisms can enter through the blossom end of cucumbers, possibly at the time of abscission of the flower.

Distribution of microorganisms within cucumber

Microorganisms were not detected beyond approximately 6 mm from the surface of all the sizes of the cucumber (Table 3). The total aerobes found on/in the outer part of the cucumber were in the range of 10^6 to 10^7 CFU/g, whereas the number of spores was about 10^2 CFU/g. The results in Table 3 may indicate that, if bacteria enter cucumber through the stomata during gaseous exchange or during hydrocooling (Daeschel and Fleming 1981; Reina and others 1995), then the bacteria do not travel beyond 6 mm from the surface of the cucumber. To ensure the validity of the results presented in Table 3, the experiment was repeated on 60 (from 10 batches) size 3B cucumbers.

In the middle part of the 60 size 3B cucumbers, microorganisms could not be detected at distances greater than 5.0 mm (Table 4). The values of coefficient of variation of the experimental data indicate a high variation in the numbers of microorganisms present in the cucumbers (Table 5). Microorganisms were also not detected in the core samples taken from the stem and blossom ends of 24 cucumbers. This is despite the fact that preliminary results showed that the stem and blossom ends have higher microbial counts than the middle part of cucumbers.

Validation of heat transfer equations (Eq. 1 to 6)

A comparison of predicted temperatures from the heat transfer equations (Eq. 1 to 6) to experimental data for size 3B cucumbers blanched at 65 °C and 80 °C for 1000 s is shown in Figure 3. The details of experimental setup and data collection for blanching of the cucumbers have been reported in an earlier study (Fasina and Fleming 2001). Similar results were obtained for other sizes of cucumbers (25- to 45-mm dia) blanched at temperatures ranging from 50 °C to 95 °C. In all cases, the standard error (s.e.) of predicted values (Eq. 9) from experimental data were less than 4.5 °C.

$$s.e. = \sqrt{\frac{\sum_{t=1}^{1000}\left(T_t - \hat{T}_t\right)^2}{n-1}} \qquad (9)$$

Validation of the HTMK model

The number of microorganisms remaining in cucumbers after blanching at temperatures of 50 °C, 65 °C, and 80 °C for various times are given in Table 6. The difference in the numbers of total aerobes and the total spores for the unblanched samples is about 2 to 3 logs and represents the numbers of pure vegetative cells present in cucumbers. The rest of the total aerobes are the sporeformers and heat-resistant cells, as can be seen from the microbial cell count obtained after blanching for various times up to 40 min. After 40 min of blanching, predictions from the heat transfer model (Figure 4) indicate that the center of the cucumber (coldest point) would have been at a temperature of 70 °C or higher for more than 10 min. From the D and z values, this time/temperature combination is sufficient to kill all the vegetative cells present in cu-

Table 2—Measured physical properties of size 3B cucumbers

Parameter	Mean	c.v. (%)[a]
Mass (g)	230.84	9.16
Length (mm)	140.18	5.01
Diameter (mm)	50.27	3.45
Volume (mL)	236.49	9.38
Density (g/mL)	0.98	1.69

[a]Coefficient of variation.

Table 3—Distribution of microorganisms across sections of cucumber[a]

Section	Total aerobes (log CFU/g)	Total spores (log CFU/g)
Stem	6.30a	2.80a
Middle	6.07a	2.65a
Blossom	6.13a	3.02b

[a]Means with the same letter in each column are not significantly different at the 95% confidence level. CFU = colony-forming unit.

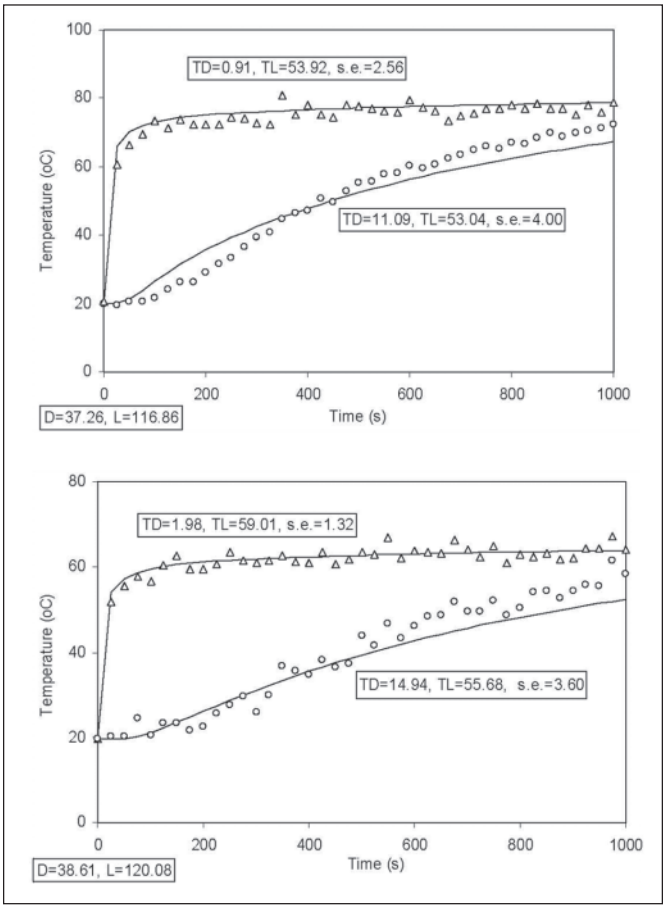

Figure 3—Experimental and predicted temperatures of cucumbers blanched at 60 °C and 80 °C. Symbols are experimental data, lines are predicted; TD and TL are the radial and axial locations, respectively, of thermocouple tip. D and L represent the diameter and length of whole cucumber. Dimensions of TD, TL, D and L are in millimeters and were measured from cucumber surface.

Table 4—Preliminary results on the distribution of microorganisms within cucumber[a]

Size	Cork borer dia (mm)	Depth (mm)	Total aerobes (log CFU/g)	Total *Enterobacteriaceae* (log CFU/g)	Total spores (log CFU/g)
Inner part					
1B	8.31	5.91	<1[b]	<1	<1
2B	8.31	14.17	<1	<1	<1
	17.34	9.35	<1	<1	<1
	23.75	6.45	<1	<1	<1
3B	8.31	20.09	<1	<1	<1
	17.34	15.28	<1	<1	<1
	23.75	12.34	<1	<1	<1
	37.80	4.89	<1	<1	<1
Outer part					
1B	8.31	5.91	7.15	6.39	2.51
2B	8.31	14.17	6.68	5.85	2.28
	17.34	9.35	6.30	5.81	2.52
	23.75	6.45	6.12	5.87	2.38
3B	8.31	20.09	6.54	6.16	1.73
	17.34	15.28	6.76	6.41	1.39
	23.75	12.34	6.55	6.49	1.81
	37.80	4.89	6.47	6.32	1.79

[a]See Figure 2 for a description of inner and outer parts. Numbers represent the average of 2 replicates. CFU = colony-forming units.
[b]Maximum level detectable by petri film plates.

Table 5—Distribution of microorganisms within size 3B cucumber[a]

Microbe type	Inner part (log CFU/g)	Outer part (log CFU/g)	c.v. for outer part (%)
Total aerobes	<10	5.00	10.67
Total *Enterobacteriaceae*	<10	3.95	17.52
Total spores	<10	2.41	16.09

[a]CFU = colony-forming units; c.v. = coefficient of variation.

Table 6—Effect of blanching time and temperature on cucumber microbiota[a]

Temperature (°C)	Time (min)	Total aerobes (log CFU/g)	Total spores (log CFU/g)
50	0	6.59	3.31
	10	4.53	3.13
	20	4.11	2.71
	40	3.10	2.16
65	0	6.66	3.21
	10	3.55	3.21
	20	3.38	3.00
	40	2.93	1.90
80	0	5.53	3.13
	20	3.61	2.47
	40	2.61	1.56

[a]Data points are the averages of 4 cucumber fruits. CFU = colony-forming units.

cumber. We believe that some of the spore-formers in the cucumber germinated into vegetative cells during the heating process, hence the reduction in total spore count as the heating time and temperature increased.

Table 7 shows that total aerobic count for size 3B cucumbers reduced by about 2 logs when the fruits were blanched at combinations of time and temperature (blanching time based on the HTMK model) needed to achieve a 2-log reduction. As expected, blanching did not significantly affect the total spore counts of the cucumbers except for samples blanched at 90 °C. From a practical standpoint, however, spore counts for the 90 °C process temperature may be considered to be similar to those of unblanched cucumbers because the difference in the log count of the 90 °C blanched and the unblanched cucumbers is less than 0.5 log.

Figure 5 shows a comparison of the predicted and experimental logarithmic reduction for total aerobes in size 3B cucumbers blanched at 60 °C, 80 °C, and 90 °C. The experimental results at each temperature represent the average for 24 cucumbers. The HTMK model gave a good prediction of the experimental data with average s.e. of 0.23. Furthermore, statistical testing at the 95% confidence interval using analysis of variance procedure (SAS Inst. 2002) indicated that the predicted values are not significantly different from the experimental values.

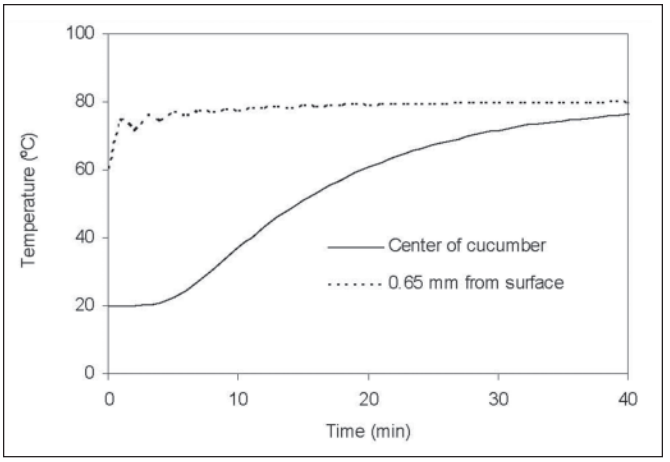

Figure 4—Temperature profile at the center and 0.65 mm from surface of cucumbers blanched at 80 °C for 40 min.

Location of microorganisms within cucumber

Using the condition that F_{expt} should be numerically equal to F_{calc}, the HTMK model predicted that the total aerobic microbiota in cucumbers are located between the surface and a critical depth of 0.65 mm from the surface. This critical depth of 0.65 mm was the same irrespective of blanching temperature/time used for experimentation and for simulation. Figure 6 shows the predicted total lethality of the cucumber with heating time at the blanching temperatures of 60 °C, 80 °C, and 90 °C. As expected, increasing

blanching temperature reduced the time required for F_{calc} to approach F_{expt} (9.0 min).

Further analysis of the temperature simulation results showed that the critical depth occurred where the temperature is about 54 °C for the different combinations of blanching temperature and time (Figure 7). We could not provide a reason for this because there is no theoretical basis for the heat transfer results to be unified with the microbial kinetics results.

Conclusions

Total aerobes (10^5 to 10^7), total *Enterobacteriacae* (approximately 10^4), and spores (approximately 10^2) are found in cucumbers. The total aerobes for the stem, middle, and blossom sections of the cucumbers were not significantly different. For all sizes, analysis showed that microorganisms are located between the surface and a distance of 6 mm from fruit surface. When a combined heat transfer and microbial kinetics (HTMK) modeling approach was applied, predicted and experimental results showed that microorganisms are located between the surface and a critical depth of 0.65 mm. The location of the critical depth was found to correspond to the intersection of the temperature profiles when cucumbers were blanched at various temperatures. It can be concluded from this study that treatments used to the reduce microbial load in cucumber fruits must penetrate to a depth of 0.65 mm to be effective. Disinfectant solutions such as chlorine-based compounds may not be able to penetrate the outer layer of the fruit and inactivate subsurface microorganisms. To kill subsurface bacteria, heat, radiation, or other treatments capable of penetrating beneath the surface of cucumbers or similar fruit may be required.

Table 7—Microbiota of cucumbers blanched to achieve 2-log reduction[a]

Temperature (°C)	Time (s)	Total aerobes (log CFU/g)	Total spores (log CFU/g)
Unblanched	—	5.60a	2.67a
60	112.5	3.66b	2.76ab
80	12.5	3.61b	2.54a
90	6.5	3.28b	2.98b

[a]Data points are the averages of 4 cucumber fruits. Averages in each column with different letters are significantly different ($P < 0.05$). CFU = colony-forming units.

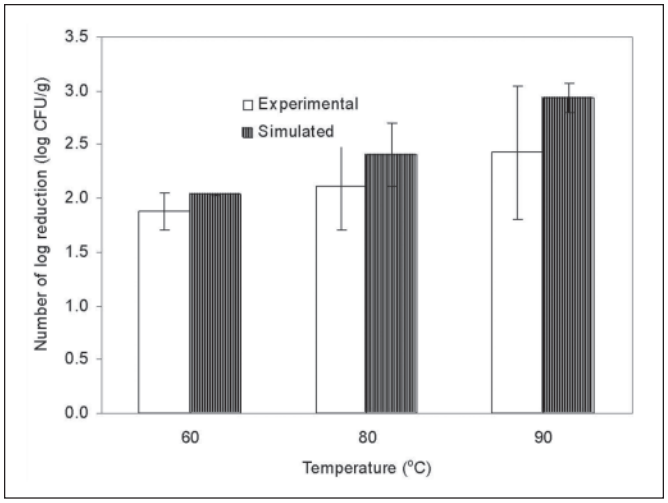

Figure 5—Experimental and predicted log reduction in total aerobic count of cucumbers blanched at temperatures of 60 °C, 80 °C, and 90 °C.

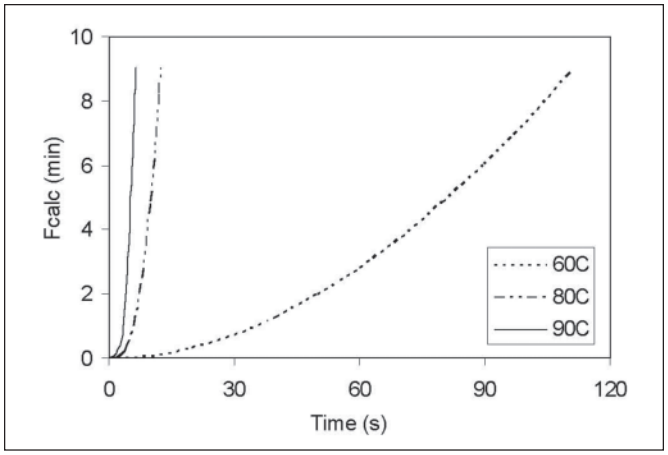

Figure 6—Change in lethality during blanching at temperatures of 60 °C, 80 °C, and 90 °C.

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Notation

c_P = specific heat (J/kg K)
D = decimal reduction time (s)
F_{calc} = calculated lethality (s)
F_{expt} = experimentally obtained lethality (s)
h = heat transfer coefficient (W/m^2 K)
k = thermal conductivity (W/m K)

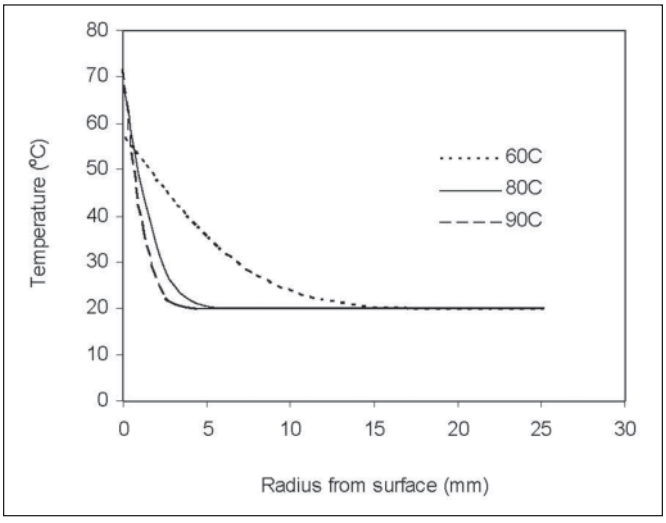

Figure 7—Predicted temperature in the cucumber fruit when blanched to achieve 2-log reduction in total aerobes at temperatures of 60 °C, 80 °C, and 90 °C.

L = cucumber length (m)
L_r = lethal rate
N = desired number of total aerobic microorganism
N_o = initial number of total aerobic microorganism
R = cucumber radius (m)
r = radial distance (m)
T = temperature (°C)
t = time (s)
T∞= blanching water temperature (°C)
T_{ref} = reference temperature (52 °C)
y = axial distance (m)
z = thermal resistance constant (°C)

Greek letters

π = density (kg/m^3)

References

Adams MR, Hartley AD, Cox LJ. 1989. Factors affecting the efficacy of washing procedures used in the production of prepared salads. Food Microbiol 6:69–77.

Annous BA, Sapers GM, Mattrazzo AM, Riordan DCR. 2001. Efficacy of washing with a commercial flatbed brush washer, using conventional and experimental agents, in reducing populations of *Escherichia coli* on artificially inoculated apples. J Food Prot 64:159–63.

Bellara S, Fryer PJ, McFarlane CM, Thomas CR, Hocking PM, Mackey BM. 1999. Visualization and modeling of the thermal inactivation of bacteria in a model food. Appl Environ Microbiol 65:3095–9.

Beuchat LR. 1996. Pathogenic microorganism associated with food produce. J Food Prot 59:204–16.

Beuchat LR, Ryu J. 1997. Produce handling and processing practices. Emerg Infect Dis 3:459–65.

Brackett RE. 1987. Antimicrobial effect of chlorine on *Listeria monocytogenes*. J Food Prot 50:999–1003.

Breidt F, Hayes JS, Fleming HP. 2000. Reduction of microbiota on whole pickling cucumbers by blanching. J Food Sci 65:1354–8.

Daeschel MA, Fleming HP. 1981. Entrance and growth of lactic acid bacteria in gas-exchanged brined cucumbers. Appl Environ Microbiol 42:1111–8.

Daeschel MA, Fleming HP, Potts EA. 1985. Compartmentalization of lactic acid bacteria and yeasts in the fermentation of brined cucumbers. Food Microbiol 2:77–84.

Fasina OO, Fleming HP. 2001. Heat transfer characteristics of cucumbers during blanching. J Food Eng 47:203–10.

Fleming HP, McFeeters RF, Daeschel MA. 1992. Fermented and acidified vegetables. In: Vanderzant C, Splittstoesser DL, editors. Compendium of methods for the microbiological examination of foods. Washington, D.C.: American Public Health. p 929-52.

Koseki S, Yoshida K, Isobe S, Itoh K. 2001. Decontamination of lettuce using acidic electrolyzed water. J Food Prot 74:652–8.

Lund BM. 1983. Bacterial spoilage. In: Dennis C, editor. Postharvest pathology of fruits and vegetables. London: Academic Press. p. 219-57.

Mohsenin NN. 1986. Physical properties of plant and animal materials: structure, physical characteristics and mechanical properties. New York: Gordon and Breach Science.

Nguyen-the C, Carlin F. 1994. The microbiology of minimally processed fresh fruits and vegetables. Crit Rev Food Sci Nutr 34:371–401.

Ramaswamy HS, Singh RP. 1997. Sterilization process engineering. In: Valentas KJ, Rotsetin E, Singh RP, editors. Handbook of food engineering practice. Boca Raton, Fla.:CRC Press. p 37–70.

Reina D, Fleming HP, Humphries EG. 1995. Microbiological control of cucumber during hydrocooling water with chlorine dioxide. J Food Prot 58:541–6.

Samish Z, Dimant D. 1959. Bacterial population in fresh, healthy cucumbers. Food Manuf 34:17–20.

Samish Z, Etinger-Tulczynka R, Bick M. 1963. The microbiota within the tissue of fruits and vegetables. J Food Sci 28:259–66.

SAS Inst. 2002. SAS users' guide. 6th ed. Cary, N.C.: SAS Inst.

Singh RP, Heldman DR. 2001. Introduction to food engineering. 3rd ed. New York: Academic Press. 659 p.

Stevenson KE, Segner WP. 1992. Mesophilic aerobic sporeformers. In: Vanderzant C, Splittstoesser DF, editors. Compendium of methods for the microbiological examination of foods. Washington, D.C.: American Public Health Assn. p 211-9.

Swanson KMJ, Busta FF, Peterson EH, Johnson MG. 1992. Colony count methods. In: Vandezant C, Splittstoesser DF, editors. Compendium of methods for the microbiological examination of foods. Washington, D.C.: American Public Health Assn. p 62-82.

Tauxe R, Kruse H, Hedberg C, Potter M, Madden J, Wachsumuth K. 1997. Microbial hazards and emerging issues associated with produce. A preliminary report to the Natl. Advisory Committee on microbiological criteria for foods. J Food Prot 60:1400–8.

Ukuku DO, Fett WF. 2004. Method of applying sanitizers and sample preparation affects recovery of native microbiota and Salmonella on whole cantaloupe surfaces. J Food Prot 67:999–1004.

Vijayan J, Pan Z, Singh RP. 1997. Modeling heat transfer and destruction of *E. coli* 0157:H7 during cooking of hamburger patties. In: Jowitt R, editor. Engineering and food. 7th Intl. Congress on Engineering and Food. 1997 April 30 - May 10; Sheffield, U.K.: Academic Press. p K45–8.