Food Sci. Biotechnol. Vol. 18, No. 5, pp. 1243 ~ 1252 (2009)

Food Science and Biotechnology

Development of Convenient Software for Online Shelf-life Decisions for Korean Prepared Side Dishes Based on Microbial Spoilage

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Abstract User-friendly software was developed to determine the shelf-life of perishable Korean seasoned side dishes in real time based on growth models of spoilage and pathogenic microorganisms. In the program algorithm, the primary spoilage and fastest-growing pathogenic organisms are selected according to the product characteristics, and their growth is simulated based on the previously monitored or recorded temperature history. To predict the growth of spoilage organisms with confidence limits, kinetic models for aerobic bacteria or molds/yeasts from published works are used. Growth models of pathogenic bacteria were obtained from the literature or derived with regression of their growth rate data estimated from established software packages. These models are also used to check whether the risk of pathogenic bacterial growth exceeds that of food spoilage organisms. Many example simulations showed that the shelf-lives of the examined foods are predominantly limited by the growth of spoilage organism rather than by pathogenic bacterial growth.

Keywords: shelf-life determination, food spoilage, food safety, temperature history, real-time monitoring

Introduction

Microbial deterioration is usually the principal concern in the quality and safety of Korean prepared side dishes, and primarily limits their shelf-life (1,2). Even when the foods are stored and distributed under chilled conditions, psychrotrophic spoilage organisms and pathogenic microorganisms can proliferate and cause spoilage and/or compromise food safety. Therefore, proper shelf-life control and management are very important to ensure their quality and safety. However, the shelf-life of prepared foods is usually defined as a fixed period at a specified temperature and does not take into account temperature variations through the food supply chain (3-5). Time-temperature integrators or indicators overcome this limitation on rigid shelf-life control and are sometimes used to provide a real sense of the food quality in response to the temperatures to which the food has been exposed (6). Recently, the real-time monitoring of food temperatures has been made possible by advanced technology, such as radiofrequency identification (RFID) tags and the relevant sensors (7). The integration of this technology with a microbial spoilage model may allow the prediction of the online quality of prepared foods that are exposed to dynamic environmental conditions.

Although the growth of pathogenic organisms must be avoided or limited to below a certain critical limit to ensure food safety, spoilage organisms must also be controlled through proper shelf-life management in order for food quality to be assured. Therefore, predicting the growth of both spoilage and pathogenic organisms on a real-time basis is expected to be useful in the development of shelf-life control systems based on the foods' microbial status. Kinetic growth models have been established for many pathogenic organisms from their experimental growth data in synthetic microbial media, and are available in several databases (8). There have been extensively reported kinetics on specific spoilage organisms (SSO) like *Pseudomonas* spp., *Photobacterium phosphoreum*, and *Shewanella putrefaciens* for perishable foods such as fish and vegetables, and they were constructed as software to predict the product shelf-life, which is very useful for improvement in stock rotation and quality assurance (9-11). However, these models cannot be applied for Korean seasoned side dishes due to their different nature and characteristics. Even with limited extent, some simplified models on the growth of spoilage organisms on Korean side dishes have also been reported in the literature (1,12-14). All these growth models can potentially be combined into a real-time shelf-life decision system, allowing the effects of temperature fluctuations to be considered (15).

Therefore, this study aimed to develop an easy-to-use shelf-life decision system in the form of software applicable to the dynamic chilled distribution of Korean prepared side dishes.

Materials and Methods

Scheme of program The overall algorithm for the real-time shelf-life decision presented in Fig. 1 was applied to Korean side dishes which are usually chill-stored and distributed in food chain and service. Property data is read or input for a specific food item of interest, and then used for screening the spoilage and pathogenic organisms able to grow there. Their growth is simulated or estimated to determine the shelf-life for expected or experienced temperature conditions by using the appropriate growth models.

Korean side dishes Twenty-one Korean prepared side dishes were investigated in this work. Their product characteristics were taken from the literature (16) or

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Received May 22, 2009; Revised July 28, 2009;
Accepted July 30, 2009

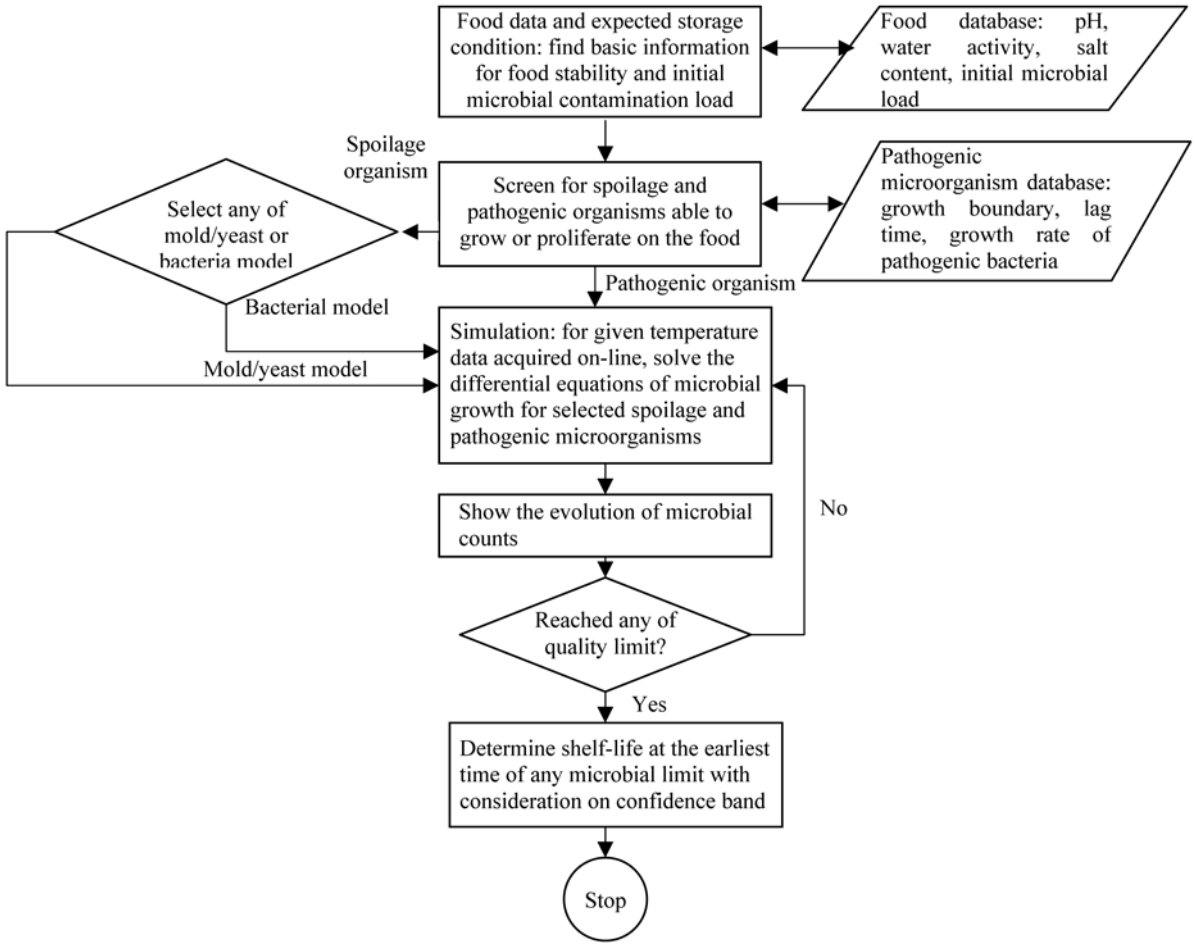

Fig. 1. Algorithm for online shelf-life decisions based on changes in microbial food status.

measured directly in this study (Table 1). The database also contains data for the usual range of aerobic bacteria and molds/yeasts. When a specific food is considered for shelf-life determination, the product variables are examined to narrow the potential group of spoilage and/or pathogenic microorganisms of the food, as was demonstrated by Wijtzes *et al*. (5).

Selecting microorganisms for shelf-life determination A concise database of pathogenic bacteria and their kinetic growth models was constructed as a pool from which the organisms able to grow on a particular food are selected (Table 2 and 3). Any pathogenic organism is defined by its growth parameters of tolerable pH, water activity, and temperature. The growth boundaries were taken from Forsythe (17), Shapton and Shapton (18), and Leistner and Gould (19). Table 2 also contains the usual ranges of pathogenic bacterial contamination levels on typical Korean foods, which were collected from the literature (20-25): those foods on which pathogenic bacterial contamination levels are reported, are mostly non-heat preserved foods such as salads, meats, poultry, sandwich, *gimbap* (rice rolled in dried laver), *sashimi* (sliced raw fish), and frozen processed meats. Due to the limited data on pathogenic bacterial contamination, adopting or assuming those levels in Table 2 for Korean side dishes may cause some exaggeration but will give an inference as preliminary estimate. When the reports only presented the number (p) of positive samples in n samples with volume V, the mean level of contamination ($\overline{N}_o$) in cells/g was estimated using the following equation (26):

$$\overline{N}_o = -\frac{1}{V}\ln\left(\frac{n-p}{n}\right) \quad (1)$$

Kinetic information is required to estimate the progress of pathogenic bacterial growth. Therefore, the lag time and growth rate were formulated as mathematical functions of pH, water activity, temperature, and/or NaCl content derived from the literature (27-31) or the responses from the software Combase Predictor (32). The kinetic equations for pathogenic bacterial growth used in this study are given in Table 3.

From the expected storage and distribution temperature, lag time, and specific growth were calculated for all the pathogenic bacteria whose growth boundary regions are tolerated by the food's compositional property. The time (t_p) for each species to reach its critical limit was calculated to identify the most relevant organism:

$$t_p = t_{lag} + \frac{\ln(N_c/N_o)}{\mu} \quad (2)$$

where t_{lag} is the lag time (days) obtained as L_t at a given temperature in Table 3; μ is the specific growth rate (inverse of the time required for the microbial count to

Table 1. Database of Korean side dishes with their physical properties and initial microbial contamination levels

Food	Water activity	pH	NaCl content (%)	Initial contamination[1)] (log CFU/g)	
				Aerobic bacteria	Molds/ yeasts
Braised black beans	0.85	5.86	2.39	3.56±0.05	2.88±0.33
Braised dried anchovies	0.73	6.52	2.97	3.52±0.01	1.72±0.16
Braised dried pollack	0.88	6.47	1.85	5.91±0.01	0.86±0.43
Braised kidney beans	0.81	6.21	1.15	3.00±0.03	2.11±0.23
Braised lotus root cuts	0.88	4.79	1.49	0.51±0.17	0.50±0.06
Braised sesame leaves	0.93	5.16	4.93	4.92±0.05	2.91±0.63
Braised shrimp with pumpkin seeds	0.77	7.65	0.99	3.80±0.01	1.80±0.19
Pan-fried meat patties	0.95	6.68	1.19	3.86±0.06	0.83±0.14
Parched dry anchovies with green peppers	0.82	6.42	4.08	3.34±0.03	0.00±0.00
Parched dry anchovies with hot pepper paste	0.71	6.31	2.83	5.68±0.03	3.65±0.15
Parched shrimp	0.82	6.21	2.43	4.93±0.05	2.62±0.03
Seasoned balloon flowers	0.95	5.67	2.13	2.46±1.02	1.81±1.07
Seasoned bracken	0.94	5.82	2.60	3.32±0.07	0.00±0.00
Seasoned burdock	0.95	5.93	1.33	4.28±0.04	3.70±0.06
Seasoned green pumpkin	0.95	6.46	2.67	3.41±0.11	1.62±0.21
Seasoned parched peanuts	0.72	5.85	1.89	2.92±0.09	2.27±0.15
Seasoned sea lettuce	0.94	4.43	1.64	4.23±0.05	2.60±0.08
Seasoned sea tangles	0.94	5.89	1.49	5.05±0.12	2.56±0.06
Seasoned soybean sprouts	0.94	6.42	1.73	3.77±0.02	1.65±0.15
Seasoned garlic stalks	0.92	5.60	1.72	5.59±0.02	2.89±0.04
Seasoned rape leaves	0.95	6.62	1.07	4.71±0.03	1.68±0.08

[1)]Values for initial contamination are mean±SD.

Table 2. Boundaries of pathogenic bacterial growth and their contamination levels on some Korean foods

Microorganism	Growth boundary			Common contamination level (cells/g)	Critical limit (cells/g)
	pH	Water activity	Temperature (°C)		
Bacillus cereus	4.9-7.4	0.93-1	5-34	0.0056	10^5
Clostridium perfringens	4.5-8.0	0.96-1	7-52	0.0047	10^5
Escherichia coli	4.4-7.0	0.95-1	7-30	0.0010	10^2
Listeria monocytogenes	4.3-7.5	0.92-1	1-35	0.0017	10^2
Staphylococcus aureus	4.0-7.1	0.86-1	7-30	0.0016	10^5
Yersinia enterocolitica	4.4-7.1	0.96-1	0-30	0.0016	5×10^3

increase e (2.718) fold, 1/day); N_o is the initial level of microbial contamination in cells/g or colony forming units (CFU/g) and N_c is the critical limit of microbial density (cells/g or CFU/g).

The organism with the shortest t_p (i.e., the fastest growing organism, reaching its limit most rapidly) is selected for growth simulation under real dynamic temperature conditions, which is then compared with that of the spoilage organism relevant specifically for the food.

Because various microorganisms can be involved in food spoilage, different kinds of spoilage microbial flora were included: molds/yeasts on acidic (pH<5.0) and/or low water activity (Aw<0.88) foods, aerobic bacteria on vegetable products with high pH and water activity, and aerobic bacteria on meat products with high pH and water activity. This simplified treatment is based on the assumption that many Korean side dishes have similar microbial spoilage characteristics (1) and their spoilage can be represented by one of these 3 typical groups. The criteria used to choose molds/yeasts or bacteria as the spoilage organisms were arbitrarily based on the general dependence of microbial growth on pH and water activity and the authors' experience with the storage of Korean side dishes. Furthermore only limited information on microbial spoilage kinetics has been published so far. With the accumulation of more kinetic food spoilage data relevant for Korean side dishes, other additional groups of specific spoilage organisms can be integrated to the above microbial groups. Kinetic equations for microbial spoilage taken from the literature (12-14) are given in Table 4, together with the criteria for selecting spoilage bacterial groups (see Equation 5-8 below for the spoilage model).

Model of microbial growth on foods under fluctuating temperatures To take into account the temperature effect on the lag time duration (t_{lag}) of the pathogenic bacteria in dynamic temperature conditions, the contribution of each time increment to the lag phase period (L_t) (corresponding

Table 3. Growth kinetics of pathogenic bacteria

Organism	Functions[1)] for lag time and specific growth rate	Source
Bacillus cereus	L_t=(exp(21.462-0.388 T-4.222 pH+0.5817 NaCl+0.0043 T^2+0.303 pH^2-0.1902889 $NaCl^2$+0.0299425 T NaCl))/24 μ=exp(–20.251+0.411 T+3.743 pH–0.0034 T^2–0.2220 pH^2+0.00000603 $NaCl^2$–0.0203 T pH–0.000058 T NaCl–0.00066 pH NaCl)×24	Olmez and Aran (27)
Clostridium perfringens	$L_t=10^{(-0.033\,lT+1.8)}/24$ μ=[0.075(T-7.71)(1-exp(0.023(T-63.27)))]^2×24	Smith-Simpson and Shaffner (29)
Escherichia coli	L_t=(exp(13.5304-0.2544 T-2.0912 pH+0.37NaCl-0.00449 T pH+0.00528 T NaCl-0.0329 pH NaCl+0.00342 T^2+0.1648 pH^2+0.00402 $NaCl^2$)-(1/exp(-11.9212+0.2407 T+1.8524 pH-0.657 NaCl+0.000938 T pH-0.00125 T NaCl+0.0386 pH NaCl-0.000295 T^2-0.1373 pH^2+0.0489 $NaCl^2$))/24 μ=ln(10)(exp(-11.9212+0.2407 T+1.8524 pH-0.657 NaCl+0.000938 T pH-0.00125 T NaCl+0.0386 pH NaCl-0.000295 T^2-0.1373 pH^2+0.0489 $NaCl^2$)×6.34/e)×24	Buchanan *et al.* (28)
Listeria monocytogenes	L_t=3.09×ln(2)/μ μ=1.016×24×[(T-45.5)(T+2.7)^2/((37+2.7)×((37+2.7)(T-37)-(37-45.5)×(37-2.7-2T)))] ×[(Aw-1)(Aw-0.91)^2/((0.997-0.91)×((0.997-0.91)×(Aw-0.997)-(0.997-1)×(0.997+0.91–2Aw)))]×[(pH-9.61)(pH-4.55)/((7.1-4.55)×(pH-7.1)-(7.1-9.61)×(4.55-pH))]	Augustin and Carlier (31)
Staphylococcus aureus	L_t=1/(exp(788.06-184.72/T+730.73/T^2-1626.1 Aw+834.01 Aw^2+2.439 pH-0.161 pH^2) /24) μ=exp(-4137.1-102.17/T+8327.5 Aw–4226.1 Aw^2+10.97 pH-0.750 pH^2)×24	Zurera-Cosano *et al.* (30)
Yersinia enterocolitica	L_t=(1630.422–42.276 T+0.064 T^2–320.374 pH+3.886 pH^2–510.155 Aw–955.635 Aw^2 +0.581 T pH+37.058 T Aw+270.214 pH Aw)/24 μ=(103.367–0.356 T+0.00007 T^2–0.167 pH–0.013 pH^2–209.306 Aw+105.510 Aw^2 +0.002 T pH+0.360 T Aw+0.315 pH Aw)×24	Combase (32)

[1)]T, temperature (°C); NaCl, salt content (%); Aw, water activity (decimal).

to the current temperature T) is calculated according to the formula in Table 3, and then integrated through time until the summation reaches 1 using the following equation:

$$\int_0^{t_{lag}} \frac{dt}{L_t(T)} = 1 \quad (3)$$

The time at which the integrated value reaches 1 is defined as the end of the lag phase, after which exponential growth starts. This kind of calculation to obtain the duration of the lag phase under dynamic temperatures has been used by other researchers (33-35).

The exponential phase growth of the pathogenic bacteria after lag phase can be simulated simply according to the differential equation:

$$\frac{dN}{dt} = \mu(T)N \quad (4)$$

where N is the microbial number (cells/g or CFU/g) at time t. Note that L_t and μ in Eq. 3 and 4 both depend on temperature.

The growth of spoilage organisms under fluctuating temperature conditions is simulated using the growth model described by the differential equations proposed by Baranyi and Roberts (36):

$$\frac{dq}{dt} = \mu_{max}(T)q \quad (5)$$

$$\frac{dN}{dt} = \mu_{max}(T)\left(\frac{q}{1+q}\right)\left(1-\frac{N}{N_{max}}\right)N \quad (6)$$

where q is the normalized concentration of an unknown substance critically required for cell growth, representing the physiological state of the cell population at time t; μ_{max} is the maximum specific growth rate (1/day); and N_{max} is the maximum cell density (cells/g).

With the model parameters given in Table 4, changes in spoilage microbial counts under fluctuating temperatures can be simulated according to the method of Lee *et al.* (13). The length of the lag phase is determined using Eq. 2, with contributions from each time increment as a function of the temperature-dependent initial q (q_o) and m_{max}:

$$\frac{1}{L_t(T)} = \frac{\mu_{max}(T)}{\ln(1+1/q_o(T))} \quad (7)$$

After the lag time (t_{lag}) is determined for an assumed constant microbial density, q_o is adjusted to an average value, as described by the following equation:

$$\log q_o = \frac{\int_0^{t_{lag}} \log q_o(T)dt}{t_{lag}} \quad (8)$$

where q_o value is understood to be the temperature-dependent relative readiness for adaptation for growth, being tuned for start-up of microbial count increase in the next exponential growth phase (13).

During the exponential phase, log N at time t is obtained by the numerical solution of differential Eq. 5 and 6, starting from log N_o at the end of the lag phase, with the incorporation of temperature-dependent functions for μ_{max} and/or N_{max}. The confidence interval for the predicted microbial count is calculated by applying the 95% confidence limit values for the model parameters (Table 4) and the initial microbial density reported or measured (37). The range of the initial contamination is assumed to be the mean±1.96 standard deviation (SD).

Table 4. Growth models for spoilage organisms depending on food type

Organism	Parameter	Equation with coefficients
Bacteria on vegetable dishes with pH≥5.0 and Aw≥0.88	**log q_o**	
	Regression curve	log q_o= –3.7468–0.2554 T+0.1152 T^2
	2.5% percentile curve	log q_o= –4.8787–0.0275 T+0.0794 T^2
	97.5% percentile curve	log q_o= –3.4693+0.1392 T+0.1103 T^2
	$\mu_{max}^{1/2}$	
	Regression line	$\mu_{max}^{1/2}$=1.5607+0.0541 T
	2.5% percentile line	$\mu_{max}^{1/2}$=1.4094+0.0556 T
	97.5% percentile line	$\mu_{max}^{1/2}$=1.6294+0.0504 T
	log N_{max}	
	Regression line	log N_{max}=7.7985+0.1726 T
	2.5% percentile line	log N_{max}=7.7573+0.1697 T
	97.5% percentile line	log N_{max}=7.8356+0.1777 T
Bacteria on meat dishes with pH≥5.0 and Aw≥0.88	**log q_o**	
	Regression line	log q_o= –4.2894+0.3100 T
	2.5% percentile line	log q_o= –5.1081+0.3152 T
	97.5% percentile line	log q_o= –3.8357+0.3770 T
	$\mu_{max}^{1/2}$	
	Regression line	$\mu_{max}^{1/2}$=0.9402+0.0545 T
	2.5% percentile line	$\mu_{max}^{1/2}$=0.8813+0.0508 T
	97.5% percentile line	$\mu_{max}^{1/2}$=1.0064+0.0574 T
	log N_{max}	
	Average	log N_{max}=8.978
	2.5% percentile line	log N_{max}=8.855
	97.5% percentile line	log N_{max}=9.111
Molds/yeasts on acid (pH<5.0) and/or low Aw (Aw<0.88) foods	**log q_o**	
	Regression line	log q_o= –1.8634+0.4952 T
	2.5% percentile line	log q_o= –2.4269+0.4976 T
	97.5% percentile line	log q_o= –1.2131+0.4690 T
	$\mu_{max}^{1/2}$	
	Regression line	$\mu_{max}^{1/2}$= 0.5990+0.0564 T
	2.5% percentile line	$\mu_{max}^{1/2}$= 0.5798+0.0554 T
	97.5% percentile line	$\mu_{max}^{1/2}$= 0.6184+0.0577 T
	log N_{max}	
	Average	log N_{max}=7.698
	2.5% percentile line	log N_{max}=7.445
	97.5% percentile line	log N_{max}=7.928

Results and Discussion

User interface The logical procedure described above was coded in Excel VBA and interfaced with the user for data input and the output of the results. Food properties affecting shelf-life were to be input and progress of microbial spoilage was designed to be given as output.

According to the scheme shown in Fig. 1, the task of online shelf-life presentation starts with the input or selection of the prepared food item and its expected storage or distribution temperature, as shown in Fig. 2. If the data for physical properties such as pH and water activity and the initial contamination density are specifically available for the food selected, they are entered. If there is no such information available, those from the food database are used to select the most relevant pathogenic organism and the most relevant spoilage organism, based on the principle described above. The preliminary shelf-life can be estimated based on both the growth of the pathogenic species (Eq. 2) and the growth of the spoilage organism (Eq. 5 and 6) predicted for the assumed temperature (Fig. 3). The output of calculation based on common criteria of 10^7 aerobic bacterial cells/g or 10^4 mold/yeast cells/g showed that the shelf-lives of the Korean prepared foods examined in this study, under constant chilled storage temperatures (1-15°C), were predominantly determined by the growth of the spoilage organism, and not by the growth of the pathogenic bacterium except for the pan-fried meat patties at higher temperature of 15°C (Table 5), where both shelf-lives according to spoilage and pathogenic organisms are almost equal (2.46 vs. 2.24 days). This generally suggests that shelf-life determination based on spoilage organism growth is safe under chilled conditions of 0-10°C. It is also inferred that temperature abuse combined

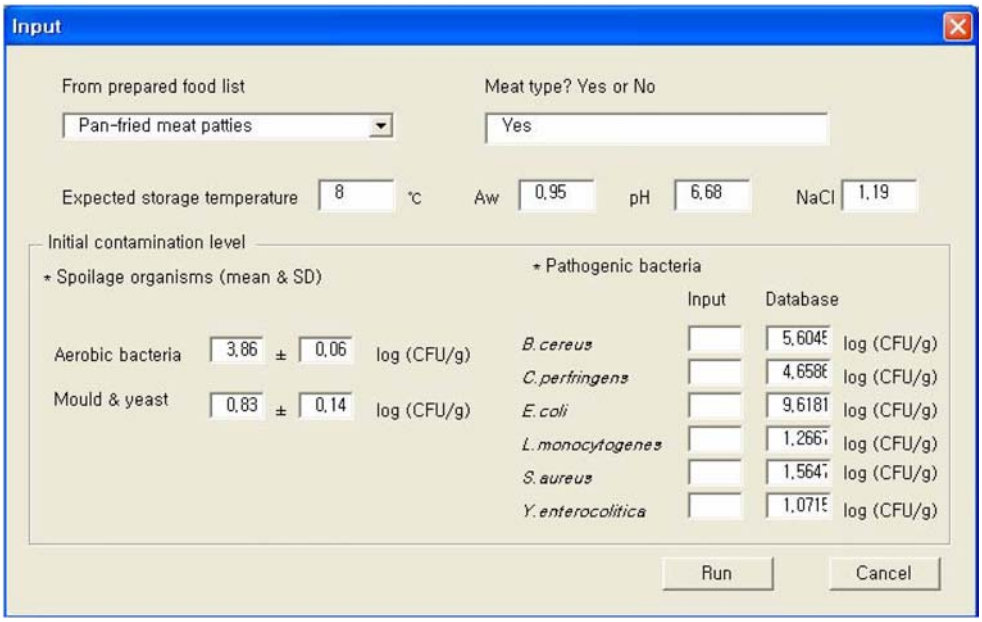

Fig. 2. Input window for food properties and expected storage temperature.

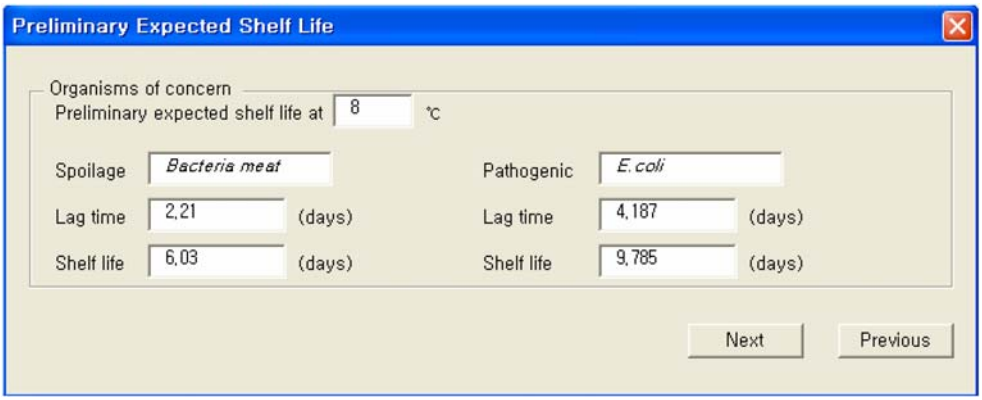

Fig. 3. Output for preliminary estimation of the shelf-life based on the expected storage temperature.

with some higher contamination of pathogenic bacteria may bring about earlier arrival to critical limit of pathogenic bacterial growth than to that of spoilage organism growth, which may be risky in usual food storage and distribution. However, it is noted that Table 5 contains some degree of underestimation of pathogenic bacterial shelf-life due to use of the contamination level data on the non-heat preserved foods. The importance of maintaining chilled temperature conditions in shelf-life control and management is still emphasized.

The temperature data throughout the supply chain are assumed to be acquired instantaneously or saved onto a data storage device in the display cabinet or food package with the appropriate sensing and data-transmitting tools. When a package device, such as an RFID tag, contains the temperature history of the product throughout the distribution channel, it can be downloaded at an appropriate check-out point to calculate the resultant microbial food status. From the time-temperature history obtained, a series of temperature data in short-term increments is supplied to compute the simulated microbial growth. A similar format for the temperature data management has been reported by Alfaro *et al*. (11) when predicting microbial and sensory qualities of fresh turbot fish in shelf-life determination. Examples of temperature histories in this study are given in Fig. 4-6.

Simulation of the growth of spoilage and pathogenic microorganisms under fluctuating temperature conditions With the available temperature history data, the progress of microbial quality changes can be estimated from the solutions of differential Eq. 4-6. With the known temperature history data, the microbial quality of the food at any time can be presented on the screen of a computer or other device. For the spoilage organism, the upper and lower bounds can also be provided in addition to an average estimate, whereas the prediction of pathogenic bacterial growth is given as a mean value (Fig. 4-6). The reasoning is that the shelf-life of the food is terminated when either the spoilage organism or pathogenic bacteria count reaches the respective critical limit. Furthermore, when real food supply chain is simulated for a food package over a sufficiently long period, the quality limit at

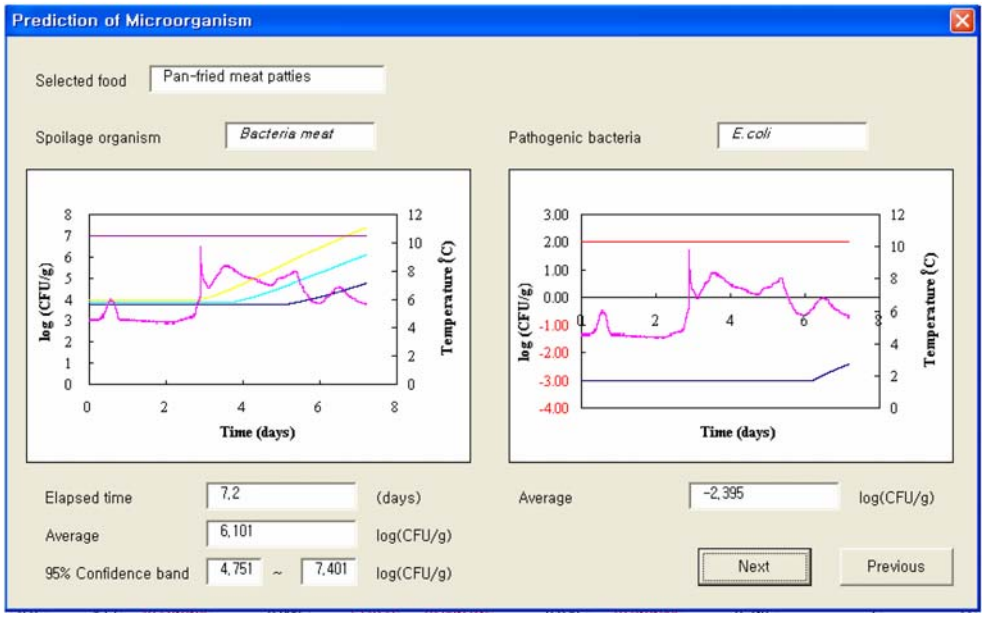

Fig. 4. An example output for the simulation of microbial quality changes in pan-fried meat patties exposed to dynamic temperature conditions. The fluctuating horizontal lines in both panels show the temperature history, and the smoothly increasing curves represent the microbial growth (mean and 95% confidence interval values for the spoilage organism and the mean estimate for the pathogenic bacterium). Horizontal dotted lines are the critical limits (7.0 and 2.0 in log N for aerobic bacteria and *Listeria monocytogenes*, respectively).

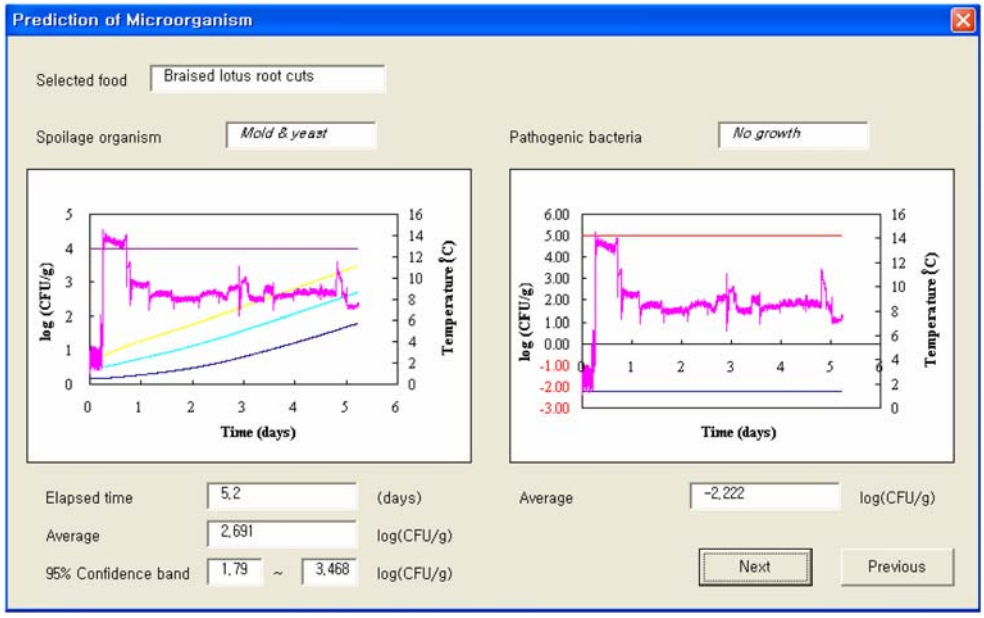

Fig. 5. An example output for the simulation of microbial quality changes in braised lotus root cuts exposed to dynamic temperature conditions. The fluctuating horizontal lines in both panels show the temperature history, and the smoothly increasing curves in the left panel represent the microbial growth of molds/yeasts (mean and 95% confidence interval values). Horizontal dotted line in left panel is the critical limit for mold/yeast count (4.0 in log N).

the end of shelf-life would be reached and then exceeded further, so that the output gives the shelf-life estimate based on the growth of the spoilage organism or the pathogenic bacterium (Fig. 6). As same in Table 5 of constant temperature conditions, many simulations for dynamic temperature conditions also gave the results that the shelf-lives of the Korean prepared foods were restricted by the growth of the spoilage organism. As shown in Fig. 5, there was no growth of any of the pathogenic bacteria examined on the braised lotus root cuts because of their low pH and Aw (Table 1 and 2). It is encouraging that shelf-life limits of the Korean prepared side dishes even with exaggerated contamination levels are reached earlier by spoilage organism growth than by pathogenic bacteria.

It needs to be mentioned that this software can be a useful tool to give prediction on microbial quality on real

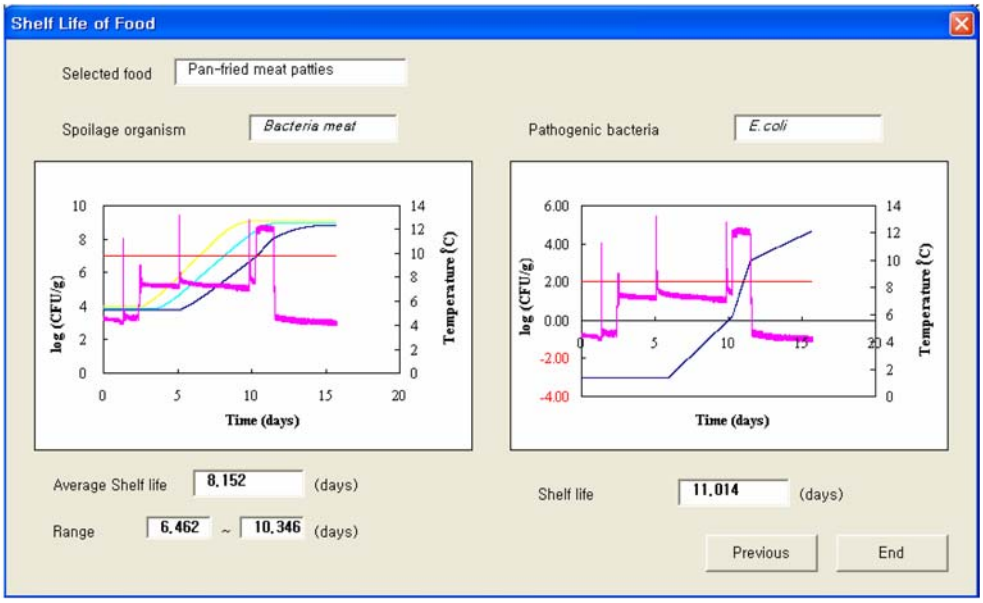

Fig. 6. An output window showing the shelf-life estimate for food (pan-fried meat patties) that has experienced the food supply chain for a sufficient period of time. The fluctuating horizontal lines in both panels show the temperature history, and the smoothly increasing curves represent the microbial growth (mean and 95% confidence interval values for the spoilage organism and the mean estimate for the pathogenic bacterium). Horizontal dotted lines are the critical limits (7.0 and 2.0 in log N for aerobic bacteria and *L. monocytogenes*, respectively).

time basis. At the same time, it should be admitted that the software was developed based on limited information. Only limited models verified for specific food categories are currently available for microbial spoilage on Korean side dishes. Accumulation and establishment of microbial spoilage model on wide range foods are required for improving the reliability and usefulness of this software. Moreover, there is data paucity of contamination levels or probabilities of pathogenic bacteria on the Korean side dishes. Even though software output is better to be confirmed eventually by experimental data, it would be very difficult or may be impossible to run experiments of microbial spoilage test and inoculated pack test for wide range of foods with realistic probability of pathogenic bacterial contamination. Just as a small confirmation of the proposed method by a literature data (38), braised kidney

Table 5. Some examples of shelf-life estimates for typical foods and storage temperatures

Commodity	Temperature (°C)	Shelf-life estimate based on spoilage organism (day)	Shelf-life estimate based on pathogenic organism (day)	Concerned pathogenic organism with fastest growth
Pan-fried meat patties	1	16.57	188.36	*L. monocytogenes*
	5	9.21	39.83	*B. cereus*
	10	4.55	6.26	*E. coli*
	15	2.46	2.24	*E. coli*
Seasoned soybean sprouts	1	6.28	350.64	*L. monocytogenes*
	5	3.69	51.72	*B. cereus*
	10	1.68	16.76	*B. cereus*
	15	1.32	6.57	*B. cereus*
Braised kidney beans[1)]	1	28.87		No growth
	5	12.15 (10.6)		No growth
	10	6.81 (9.7)		No growth
	15	4.41 (5.5)		No growth
Seasoned green pumpkin	1	6.60	195.65	*L. monocytogenes*
	5	3.94	45.73	*L. monocytogenes*
	10	1.87	8.83	*E. coli*
	15	1.47	3.28	*E. coli*

[1)]Shelf-life of braised kidney beans was estimated based on the time for the mold count to increase from 0 to 4.0 in log (CFU/g), which was compared with Lee *et al.* (38). The numbers in brackets are experimental data of Lee *et al.* (38).

beans of known contamination level of molds/yeasts were shown to have the estimated shelf-lives comparable to the real ones under constant temperatures (Table 5).

In conclusion, computer software was developed to estimate the microbial quality of Korean seasoned side dishes on a real-time basis. This software provides a useful tool in controlling the shelf-life of prepared food products in dynamic temperature environments, ensuring their quality and safety. The shelf-lives of Korean seasoned side dishes examined were mostly limited by the growth of spoilage organisms rather than by the growth of pathogenic bacteria. However, it needs to be mentioned that this work has been conducted based on the limited information on spoilage organism growth and microbial contamination data on Korean prepared foods, and thus could be reinforced further by building more extensive database of food properties and microbial spoilage kinetics for the wider and versatile applications. Still the logical scheme of this tool is a valid and useful starting point for the robust version.

Acknowledgments

This work was supported by Korea Science and Engineering Foundation (Project # R01-2005-000-10235-0).

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