A Decision Support System for Prediction of the Microbial Spoilage in Foods

MARCEL H. ZWIETERING*, TACO WIJTZES, JACORA C. DE WIT, and KLAAS VAN'T RIET

Department of Food Science, Agricultural University Wageningen, P.O. Box 8129, 6700 EV Wageningen, The Netherlands

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ABSTRACT

A method was developed to combine qualitative and quantitative information to predict possible growth of microorganisms in foods. The pH, water activity, temperature, and oxygen availability of foods are coupled to the growth characteristics of microorganisms. Therefore, a database with characteristics of foods and a database of kinetic parameters of microorganisms were built. In the first database, a tree structure based on physical similarity was built, for the case that information about the characteristics of a particular food is unknown. By comparing with similar products at the same level of the tree or the level above, the product information can be estimated. A method is developed to make an estimation of the microbial growth kinetics on the basis of models. This is done by introducing a growth factor, which can be calculated on the basis of readily available data from literature. Since all the information can be altered, the system can give better predictions when more and more accurate information is added.

Food quality

Food quality can be defined as the sum of the characteristics of a food that determines the satisfaction of the consumer and compliance to legal standards. Thus, food quality is a combination of numerous factors, such as organoleptic properties (e.g., texture, flavor, color), nutritional value (e.g., caloric content, fatty acid composition), and safety conditions (e.g., microbial number, toxins, hormones). Some of these factors (e.g., microbial numbers) can be quantified relatively easily, others (e.g., flavor) are very difficult to assess quantitatively. Food quality thus cannot be quantified in every detail, and overall quantification depends strongly on the priority of the different aspects determining the quality. To determine the total food quality, quality indicators are needed and must be weighed, depending on the product, trends, producer, and market.

Food quality is gaining more and more interest for a number of reasons. The food market deals in most cases with satiation; therefore, quality becomes more important than quantity. There are new quality attributes which are highly appreciated by the modern consumer (in contrast to traditional quality demands). Consumers show an increasing interest in convenience foods with the appearance and taste of fresh products and food quality aspects such as flavor and (assumed) health aspects (e.g., nutrition, fatty acid quantity and composition, energy content, salt concentration, additives, such as preservatives).

Prediction of the kinetics of possible quality loss is important for the following reasons. Consumers are willing to pay a higher price for quality. The manufacturer wants to produce constant quality products at the lowest costs. Many products have a limited shelf life. Production and storage conditions affect quality very strongly; therefore, production and distribution are often critical. From the past there are many dried, salted, frozen, sterilized products, while nowadays chilled and intermediate-moisture foods are becoming more important. The shelf life of a product should match the distribution regime: daily delivery for perishable products such as fresh milk, bread, fresh vegetables, and fresh meat, or less frequently as for salads, margarine, etc. Distribution routes have become longer, and therefore, there is a need for an increase in shelf life. In some areas there is a rather rapid product development (changes in product formulation). Consequently, it will be very useful to make an estimation of the shelf life during product development. Formulation of products may be different in different countries or regions, because of legal requirements or regional food preferences. Therefore, it would be useful to know the effects of different compositions on the shelf life, so that each formulation does not require a laborious shelf-life test.

New techniques are being developed to meet these quality demands, such as new technologies (e.g., microwave, ultrahigh temperature processes, modified atmosphere packaging, irradiation), and new strategies (e.g., logistics, and modeling).

Quality loss

Quality loss can be a result of microbial, chemical, enzymatic, or physical reactions. Different factors influence quality loss, such as the composition of the product, and the processing and storage conditions. Deterioration reactions may occur when the physical variables of the product are within the range of the specific reaction. For quantification of the reaction rate, the kinetics of the reaction should be known. This can be done by models that include the range in which spoilage can occur and the physical variables of the product. As soon as good models are available and
values for the physical variables are estimated, the rate of spoilage processes can be predicted. The resulting quantitative estimation can be compared with quality parameters.

A considerable amount of research has been conducted on the deterioration of food (e.g., 2,10). This research yielded a large amount of quantitative data. Also, much qualitative information is available. Yet, for a quantitative prediction of the quality of a given food product, there are often not enough data, or the data show too large a measuring error to be used. It is difficult to combine a broad range of information, from qualitative to quantitative. However, it will be very useful to combine all this information in a structured manner, to predict product quality in the best possible way.

The objective of this work is to develop a system in which quantitative data can be combined in a structured manner with qualitative data, information, and models. Such a system would be a useful tool in product development, predicting possible spoilage and estimating the kinetics of possible deterioration. As soon as more data, information, or new models are gathered, this can be added, resulting in more valuable predictions.

**SYSTEM STRUCTURE**

The system

A system was developed that determines the possible growth of microorganisms on a certain food product. Numerous factors can influence growth. From the most important factors, pH, water activity (a_,) temperature (T), and oxygen availability are taken into account. These physical properties of the product are compared with the properties of the microorganisms (Fig. 1). The physical variables of various foods are collected in a database (database 1) as are the growth data of microbes (database 2). The data for each microorganism are matched with the physical variables of the food product, by simply determining if the physical variables of the product are within the growth limits of that microorganism (“pattern matching”). For these organisms, an estimate of the growth rate is calculated on the basis of the value of the physical variables. The estimation of growth is carried out by using models that describe growth over the range of physical variables.

**Table 1. An example of the information stored in the product database.**

<table>
<thead>
<tr>
<th>Name</th>
<th>Yogurt</th>
</tr>
</thead>
<tbody>
<tr>
<td>Identification code</td>
<td>S.A.B.A.C</td>
</tr>
<tr>
<td>Temperature (T)</td>
<td>5</td>
</tr>
<tr>
<td>pH</td>
<td>4.2</td>
</tr>
<tr>
<td>a_</td>
<td>0.990</td>
</tr>
<tr>
<td>Oxygen availability</td>
<td>no oxygen</td>
</tr>
</tbody>
</table>

The number of food products is more or less infinite and, as may be expected, not all the physical variables of all different foods are known. Therefore, the database is structured in such a way that the products are ordered with respect to their physical properties, so that foods that are gathered together are closely related (Fig. 2). The classification system proposed by Jowitt (4) based on the physical properties of foods is therefore used. In such a way, missing information, even when a product is absent, can be substituted with knowledge from comparable products.

**Figure 1. Structure of the system.**

The list of organisms that may spoil the product is sorted by growth rate. This list can be altered by applying rules to diminish the number of organisms in the list or to improve the value of the predictions. Some of these rules are dependent on the product, some on the properties of organisms, and some are of general application. In this way the final list of organisms is obtained, which is now based on physical variables of the product, growth parameters of microorganisms, models, and qualitative reasoning.

It should be noted that spoilage of a product will only occur if an organism is present and able to grow in that product. Until now, it is assumed that all organisms can be present everywhere. This can result in predictions of growth of organisms that are unlikely to be present in such a product. Therefore, knowledge of the presence of organisms on certain products can be included in the information base. Another possibility is that the usual microflora of products is included in the food database. However, organisms that up to now have not caused problems in a product are often not known to be present in a product. If the composition or processing of such a product is changed, these organisms may start to cause problems. Therefore, it is assumed that all organisms can be present everywhere.

**Food database**

Database 1 (Fig. 1) contains the physical variables as shown in Table 1 of different foods. The physical variables are known only for a limited number of products. The remainder contains name and identification code (I.D.). The I.D. of a product determines the position of the product in the classification tree (Fig. 2). The first letter (S) stands for food, addition of the second for the first subdivision of food (dairy (S.A), bakery (S.D), vegetables (S.F), meat (S.H), etc.). These groups of products are divided by addition of the third letter of the I.D., etc.
Organism database

A database is built for microorganisms, to contain the information as given in Table 2. The database contains the name of the organism and the growth ranges of the physical variables: oxygen requirement, the minimum and maximum pH, $a_w$, and temperature. Additionally, the optimum growth rate and the optimum values of pH and temperature are stored to be used in kinetic models. Furthermore, the Gram staining, type, and spore-forming abilities are stored to be used for further selection procedures (qualitative reasoning) or future use. The possibility exists to alter all information.

Table 2. An example of the information stored in the organism database.

<table>
<thead>
<tr>
<th>Genus</th>
<th>Pseudomonas</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
<td>putida</td>
</tr>
<tr>
<td>Oxygen necessity</td>
<td>aerobic</td>
</tr>
<tr>
<td>Type (bacterium, yeast, mold)</td>
<td>bacterium</td>
</tr>
<tr>
<td>Gram stain (only for bacteria)</td>
<td>negative</td>
</tr>
<tr>
<td>Spore forming</td>
<td>no</td>
</tr>
<tr>
<td>$T$: min max opt</td>
<td>8 -43 30</td>
</tr>
<tr>
<td>pH: min max opt</td>
<td>4.7 -8.5 7.8</td>
</tr>
<tr>
<td>$a_w$: min max opt=max</td>
<td>0.96 -1000</td>
</tr>
<tr>
<td>Optimum growth rate (h$^{-1}$)</td>
<td>1</td>
</tr>
</tbody>
</table>

Selection of organisms that can grow on a particular product

As soon as the physical variables of a product are known, a matching is carried out with the organisms database. All the organisms that can grow on that product on the basis of the physical variables are found by "pattern matching". First, the total list of organisms is reduced to those organisms that can grow at the pH of the product, then at the temperature of the product, and then at the $a_w$ of the product. Lastly, the effect of the availability of oxygen is included. The procedure results in a list of organisms which can grow in a certain product with particular physical variables.

Kinetic models

To estimate the growth rate of organisms at suboptimum conditions for $T$, $a_w$, and pH, models have to be used. The growth rate can be estimated using models relating growth at the actual value of a variable to the optimum value and the limits. Each variable that is not at the optimum value can reduce the growth rate. Therefore, a method to combine these effects must be established. This is done by introducing a growth factor:

$$\gamma = \frac{\mu}{\mu_{opt}}$$

with

$\mu$: the actual growth rate (h$^{-1}$).

$\mu_{opt}$: the growth rate (h$^{-1}$) at optimum conditions.

$\gamma$: the actual growth factor.

This growth factor is equal to 1 at optimum conditions and between 0 and 1 for all other conditions. Others have shown that the inhibitory effect of temperature and $a_w$ and the effect of temperature and pH can be multiplied ($1.6$). It is assumed therefor that the growth factor can be calculated by multiplying all $\gamma(x)$ values, with $\gamma(x)$ defined for each of the variables separately, independent of the value of the other variables:

$$\gamma = \gamma(T) \cdot \gamma(pH) \cdot \gamma(a_w) \cdot \gamma(O_2)$$ (2)

If all variables are at optimum conditions, the growth rate is equal to $\mu_{opt}$. If one of the variables is below the minimum or above the maximum value, this results in one of the $\gamma$s to be zero, resulting in a growth rate of zero.

Each $\gamma(x)$ factor can be determined from the database data, in combination with a model for that variable. In the microorganism database, the minimum, optimum, and maximum temperatures for growth of different organisms can be found. If these data are known, the parameter $c$ of the Ratkowsky equation (9) can be calculated:

$$\mu = (b \cdot (T - T_{min}) \cdot \exp[c(T - T_{max})])^2$$ (3)

with

$T$: actual temperature (°C)

$b, c, T_{min}, T_{max}$: Ratkowsky parameters.

If $c$ is known, the growth factor $\gamma(T)$ for each temperature value can be evaluated with:

$$\gamma(T) = \frac{\mu}{\mu_{opt}} = \left(\frac{(T - T_{min}) \cdot \exp[c(T - T_{max})]}{(T_{opt} - T_{min}) \cdot \exp[c(T_{opt} - T_{max})]}\right)^2$$ (4)

The value of $c$ can be calculated from the known $T_{min}$, $T_{max}$, and $T_{opt}$ as follows. The derivative of equation 3 can be calculated as:

$$\frac{d\mu}{dT} = b \cdot (1 - \exp[c(T - T_{max})]) \cdot c \cdot (T_{opt} - T_{min}) \cdot \exp[c(T - T_{min})]$$ (5)

At $T = T_{opt}$, this derivative is zero. Since $b$ cannot equal zero and $T_{opt}$ cannot equal $T_{min}$ or $T_{max}$, the first part of the equation cannot equal zero. Therefore, the second part of the equation must be zero:

$$1 - \exp[c(T_{opt} - T_{max})] \cdot c \cdot (T_{opt} - T_{min}) \cdot \exp[c(T_{opt} - T_{max})] = 0$$ (6)

This can be rewritten as:

$$1 - c(T_{opt} - T_{min}) \cdot \exp[c(T_{opt} - T_{max})] = 0$$ (7)

c can be calculated iteratively from this equation, to be used in equation 4.

The same procedure is carried out for the pH. The same formula from Ratkowsky (9) is used, only $T$ is substituted for pH:

$$\mu = (f(pH - pH_{min}) \cdot \exp[g(pH - pH_{max})])^2$$ (8)

with

$f, g, pH_{min}, pH_{max}$: Ratkowsky parameters.

$pH$: actual pH

If all variables are at optimum conditions, the growth rate is equal to $\mu_{opt}$. If one of the variables is below the minimum or above the maximum value, this results in one of the $\gamma$s to be zero, resulting in a growth rate of zero.

Each $\gamma(x)$ factor can be determined from the database data, in combination with a model for that variable. In the microorganism database, the minimum, optimum, and maximum temperatures for growth of different organisms can be found. If these data are known, the parameter $c$ of the Ratkowsky equation (9) can be calculated:

$$\gamma = \frac{\mu}{\mu_{opt}} = \left(\frac{(pH - pH_{min}) \cdot \exp[g(pH - pH_{max})]}{(pH_{opt} - pH_{min}) \cdot \exp[g(pH_{opt} - pH_{max})]}\right)^2$$ (9)

with $g$ to be calculated from:
1 - (g pH_{sp} - g pH_{min} + 1) \cdot \exp[\gamma (pH_{sp} - pH_{min})] = 0 \quad (10)

McMeekin et al. (6) show that the growth rate is linear with \(a_w\) at suboptimum water activity levels. For the water activity therefore, a linear relation is assumed:

\[
\gamma (a_w) = \frac{a_w - a_{w, min}}{1 - a_{w, min}} \quad (11)
\]

with

\[
a_{w, min}: \text{minimum water activity}
\]

\[
a_w: \text{actual water activity}
\]

Oxygen availability is used as a selection parameter (\(\gamma (O_2) = 0\) or 1, Table 3). For oxygen availability, this segmentation model is used, since for most microorganisms the growth kinetics as a function of the oxygen availability are not known. The same is true for the oxygen concentration in products. If models and model parameters are known, this can be altered, since the segmentation model as shown in Table 3 is a very rigorous one.

**TABLE 3. The effect of the availability of oxygen on \(\gamma (O_2)\).**

<table>
<thead>
<tr>
<th>Organism</th>
<th>Aerobic</th>
<th>Facultative anaerobic</th>
<th>Anaerobic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Product with oxygen</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Product with very little oxygen</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Product with no oxygen</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

The combination model selected and used here is not yet thoroughly validated. However, it can be used to make kinetic predictions, although the numerical value is indeed a prediction only. Yet, a good estimate is made about the growth rate. Whenever more knowledge is present for models describing the effect of the variables used here, these models can be incorporated. It should be noted that there are no correlation effects assumed between \(T, a_w, pH,\) and \(O_2\).

There are many more variables determining the growth rate of microorganisms, such as preservatives (sorbic and benzoic acid, alcohol, nitrite). These compounds will often be present in specific products, such as alcohol in alcoholic beverages and nitrite in meat products. The effect of these compounds can be incorporated by applying knowledge rules. This method is better than the use of kinetic models, since at present models and model parameters are not well established for these compounds.

Only if all information is present can exact predictions be made. This is an impossible situation; therefore, every result will always be an approximation.

**Addition of qualitative reasoning**

Information can be added to the system to decrease the number of possible organisms that can cause problems. Four types of rules are implemented in the system (Table 4); i) relationship between microorganisms and product characteristics (example: In high moisture food and low acid products molds and yeasts will be overgrown by bacteria if the temperature is below 35°C); ii) interaction among microorganisms (example: Antagonists of *Salmonella* spp.; Lactic acid bacteria); iii) interaction among microorganisms in combination with the product (example: On meat if either *Pseudomonas* spp., *Moraxella* spp., or *Acinetobacter* spp. is present, all three are likely to be present (7)); iv) general rules (example: If pasteurization is carried out, only thermoduric organisms will survive).

Before these rules are applied, the user is asked if this rule is applicable, since they can be too stringent sometimes.

**RESULTS AND DISCUSSION**

The program was developed using TURBO-Pascal 5.0 (Borland). No expert system shells are used, because a shell that exactly fulfills our needs could not be found. Furthermore, programming in a second generation language has the advantage that all necessary procedures can be programmed. Then the problem does not need to be fitted into the possibilities of a shell.

The system is started entering the name of a food. The program then searches database 1 for the name of that food, or foods, with a very similar name. Within this list of names, a final selection can be made for the food of interest. The physical variables of this product are displayed when present in the database. If the physical variables of the product are not known, comparable products (if any) are given (Fig. 2). An estimation of the physical variables can be obtained by a selection from this list.

With the physical variables of the food, a matching is carried out with the organisms database. The organisms
that can grow on that product considering the physical variables (pH, T, a_w, and oxygen availability) are determined on basis of the growth ranges of the organisms by "pattern matching". This results in a list of microorganisms that can cause spoilage together with the growth factor (eq. 2). Now rules can be applied to diminish the number of organisms in the list or to improve the value of the predictions. The knowledge rules that are implemented are given in Table 4.

In total, 845 products are collected in database 1 at present. For 153 of these products, this database contains information as given in Table 1.

In total, 20 gram-negative bacteria, 19 gram-positive bacteria, 10 yeast species, and 9 molds are incorporated in database 2 at present. If the optimum growth rate of organisms is not known, for bacteria 1 h⁻¹, for yeasts 0.5 h⁻¹, and for molds 0.1 h⁻¹ is assumed.

Open structure

The parameters of the organisms, the physical variables of the products, and the qualitative rules can be altered and expanded. It should be noted, however, that the value of the system is dependent mainly on the quality of the data that are stored. Therefore, changes in the databases can only be made by authorized users.

Output

Two lists of possible spoilage organisms are generated. The first list contains the possible spoilage organisms, based on physical variables. The second list contains the knowledge rules that are applied and the list of spoilage organisms that are likely to spoil the product, after the knowledge rules are applied. As output, not only the final list should be considered, the first list also contains valuable information. (For example, if pasteurization is carried out, the final list will give no thermosensitive organisms. However, if the product is contaminated after pasteurization, the thermosensitive organisms can be of interest).

The possibility exists to remove certain groups of organisms (gram positive, gram negative, all nonspore-forming organisms, molds, and yeasts). This can be valuable for instance if a product is pasteurized (e.g., remove all nonspore-forming organisms).

Example for milk

In the following part, an example for milk stored at refrigeration temperature is given.

Selection of organisms

During storage of milk, a temperature of 5°C can be achieved. The atmosphere is aerobic. In the components database, the following data can be found for milk: pH = 6.6; a_w = 0.993. In the organism database, the data of all database, the following data can be found for milk: pH = 6.6; a_w = 0.993. In the organism database, the data of all organisms are examined. For instance, for Pseudomonas the data are given in Table 2. Combining this information results in the deduction that Pseudomonas can grow in milk stored at 5°C. If this is carried out for all organisms, the system comes up with 11 bacteria, 6 molds, and 6 yeast species (Table 5). All bacteria are reported to grow in milk at 5°C by Gilmour and Rowe (3).

<table>
<thead>
<tr>
<th>TABLE 5. Prediction of the microorganisms that can grow in milk stored at 5°C (alphabetized).</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lit.</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
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<tr>
<td></td>
</tr>
</tbody>
</table>

Yeasts

<table>
<thead>
<tr>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Rodotorula spp.</td>
</tr>
<tr>
<td>Candida spp. (macedoniensis)</td>
</tr>
<tr>
<td>Debaryomyces spp. (hanseniti)</td>
</tr>
<tr>
<td>Hansenula spp. (anamala)</td>
</tr>
<tr>
<td>Pichia spp. (membranaefaciens)</td>
</tr>
<tr>
<td>Torulopsis spp. (psychrophilica) + Torulopsis candida</td>
</tr>
</tbody>
</table>

Molds

<table>
<thead>
<tr>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Aspergillus spp.</td>
</tr>
<tr>
<td>Botrytis spp.</td>
</tr>
<tr>
<td>Cladosporium spp.</td>
</tr>
<tr>
<td>Geotrichum candidum (o. lactis)</td>
</tr>
<tr>
<td>Mucor spp.</td>
</tr>
<tr>
<td>Penicillium spp.</td>
</tr>
</tbody>
</table>

' = Microorganisms able to grow in milk at 5°C given by (3).

If this exercise was done for skim milk, it may have appeared that the database did not have the physical variables for skim milk. The system would then have searched for a product that is physically comparable to skim milk, which would have been milk (Fig. 2).

Kinetic estimation

For all organisms that can grow on milk, the growth factor will be calculated (eq. 2). This will be done as an example for Pseudomonas.

For the temperature, equation 7 can be used, using the kinetic data of Pseudomonas (Table 2), resulting in:

\[ 1 - (38c + 1) \cdot \exp(-13c) = 0 \quad (12) \]

This equation can be solved iteratively and results in \( c = 0.143 \). With equation 4, the \( \gamma(T) \) can be calculated at every temperature.

\[ \gamma(T) = \left( \frac{1}{38[1 - \exp[0.143(T - 43)]]} \right)^2 \cdot \left( \frac{T + 8[1 - \exp[0.143(T - 43)]]}{32.08} \right)^2 \quad (13) \]

For the pH, equation 10 can be used resulting in:

\[ 1 - (3.1 g + 1) \cdot \exp[g(-0.7)] = 0 \quad (14) \]
This equation can be solved iteratively and results in $g = 3.55$. With equation 9, the $\gamma(pH)$ can be calculated.

$$
\gamma(pH) = \frac{(pH-4.7)(1-\exp[3.55(pH-8.5)])^2}{3.1(1-\exp[3.55(0.7)])} \cdot \frac{(pH-4.7)(1-\exp[3.55(pH-8.5)])^3}{2.842}
$$

(15)

For the $a_v$, equation 11 can be used resulting in:

$$
\gamma(a_v) = \frac{a_v - 0.96}{0.04}
$$

(16)

For milk, the following growth factors are calculated:

- For $T = 5$, $\gamma(T) = 0.163$;
- For $pH = 6.6$, $\gamma(pH) = 0.446$; and
- For $a_v = 0.993$, $\gamma(a_v) = 0.83$.

$$
\gamma = \gamma(T) \cdot \gamma(pH) \cdot \gamma(a_v) = 0.060
$$

(17)

$$
\mu_{opt} = 1 \text{ h}^{-1}
$$

Now the growth rate can be estimated with equation 1.

$$
\mu = \gamma \cdot \mu_{opt} = 0.060
$$

(18)

**Addition of qualitative reasoning**

In the reasoning, the knowledge about the heat treatment of the milk can be added to the system. If no pasteurization is used, we have to deal with the natural contamination of milk. The bacteria will grow much faster than the yeasts and the molds (because milk has a very high water activity and a neutral pH). An estimation of the growth rate can be made on the basis of models, describing the effect of the physical variables on the growth rate. In the example given above, the conditions in milk are not optimum for *Pseudomonas*; therefore, the growth rate will be smaller than the optimum growth rate. It is assumed that the fastest growing organisms will cause problems (10% rule). If this knowledge is used, the system comes up with four species (Table 6), including *Pseudomonas* and *Enterobacter* which are reported to be main spoilers of milk (3,5,8). The kinetic predictions are not yet very precise.

**TABLE 6. Microorganisms that are predicted to cause spoilage in milk stored at 5°C.**

<table>
<thead>
<tr>
<th>Species</th>
<th>Growth rate (h^{-1})</th>
<th>Literature value</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Enterobacter</em></td>
<td>0.322</td>
<td>0.075 (5)</td>
</tr>
<tr>
<td><em>Proteus</em></td>
<td>0.134</td>
<td></td>
</tr>
<tr>
<td><em>Pseudomonas</em></td>
<td>0.060</td>
<td>0.18 (8)</td>
</tr>
<tr>
<td><em>Brochothrix</em></td>
<td>0.057</td>
<td></td>
</tr>
</tbody>
</table>

If a pasteurization is carried out, only the thermoduric organisms will survive. This results in 1 bacterium (*Bacillus*), 6 yeasts, and 6 molds. As the spores of yeasts and molds are less likely to grow out very fast, it can be concluded that the bacterium *Bacillus* will be the main spoiler. Of course, the product may be contaminated after the heat treatment; therefore, the information that is produced before the effects of the heat treatment is of importance. It must be stressed that all the information, from the beginning to the end, must be studied, as it is always a result of a number of models, i.e., simplification.

**Possible expansion of the system**

A great deal of information is present on quality loss processes in foods, depending on composition, process variables, and kinetics. It could be useful to develop a system in which this information is combined. The system can be expanded by including chemical, enzymatic, and physical spoilage in the same manner as described. In this way, effects of a large number of changes in the product or process can be evaluated. This can be done for instance for the addition of onions to a salad dressing (microbial, enzymatic, physical). The effect of chemical and microbial spoilage when a heat treatment is carried out at a higher temperature can be evaluated, as can the effect of storage in a modified atmosphere (if the effects of gases are known). For new product development, the possible spoilage reactions, the order of magnitude of these reactions, the approximate shelf life, and distribution temperature can be evaluated. By using more or less complicated models and kinetic parameters, predictions can be made of these deterioration reactions.

**CONCLUSIONS**

A system was developed which shows a promising potential for product development and shelf-life prediction. Quantitative and qualitative information and predictive models can be combined to predict possible spoilage reactions, with an estimate of their kinetics, on the basis of models. To that purpose, a database was built and filled with physical variables of foods, as was a database with organisms with their growth limits for the same physical variables. A combined model was built to be able to make a kinetic estimation, on basis of the data in the databases. Furthermore, an information base was built which can be used to add qualitative information concerning products and microorganisms. The system combines all this information. Since it is impossible to collect quantitative data for all possible deterioration reactions on different products, a prediction is made on the basis of the data and knowledge collected in the system until now.

The program can help to determine possible spoilage organisms. It can estimate the change in growth rates of organisms, when the physical properties are changed. It should be noted that the program does not give an exact, complete list of all possible spoilage organisms, since it is based on limited information. The more information that is combined and added to the program, the better the predictions will be.

**REFERENCES**


