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A decision support system for the prediction of microbial food safety and food quality

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Abstract

The development of a method to predict microbial food safety and quality is described. The manufacture of a food from its ingredients is simulated, using a recipe. Food engineering heuristics are combined with models developed in predictive microbiology. Parameter values of ingredients of foods, such as water activity and pH, and models for microbial growth and decay are used for the prediction of the kinetics of microorganisms generally found in ingredients. The values of these parameters are collected in databases. If required information is lacking, methods are described for making reliable guesses of the parameters. Food quality can be calculated as a function of fluctuating temperature in time. Several food distribution chains can be simulated in order to assess the influence of distribution chains on food quality. The described methods were implemented into a computerised decision support system that can be used in food production, product development and training. In the future it may be possible to apply specific expert knowledge in production and development of foods to improve the quality of prediction. © 1998 Elsevier Science B.V.

Keywords: Decision support system; Food safety; Food quality; Simulation; Predictive microbiology; Food technology

1. Introduction

Food quality is the result of numerous factors such as physical, biochemical and microbiological characteristics. Rejection of a food on the basis of quality, is the result of decay in the widest sense of the word. Presence or growth of microorganisms often are major problems related to the quality of foods. Presence and growth of microorganisms are also important factors for food safety. Other factors that play a role in the determination of food safety and food quality are, for instance, the presence of chemicals or food foreign substances such as glass fragments. Decreased quality may have a large impact on credibility of food manufacturers and costs of food products (Jay, 1992; McMeekin et al., 1993; Shapton and Shapton, 1991).

At the moment standard procedures are in use that assess and control possible deviations from safety standards. These procedures, such as Good Manufac-

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turing Practice (GMP) and the HACCP approach, are well known in food production. These procedures will be implemented more and more into food production, resulting in a better understanding of processes and connected possible problems or hazards (ICMSF, 1988; Jay, 1992; Shapton and Shapton, 1991). However, in practice it proves very hard to actually control all possible hazards.

In predictive microbiology, the change in numbers of microorganisms in time can be estimated, given for example the pH, temperature, or water activity of a food. The models that are developed in predictive microbiology can be used to calculate microbial numbers given a specific food composition, a food manufacturing line, or a food distribution chain. In combination with the above mentioned procedures, predictive microbiology gives improved, quantitative insight into the food properties and processes that are of importance to the safety and quality of foods (McMeekin et al., 1993; Zwietering et al., 1992).

The development of a computerised decision support system that simulates composition, production and distribution of foods is described in this paper. The computer system uses both mathematical models and expert knowledge of food technologists for the determination of the microbial numbers in foods. The decision support system can be used to find microorganisms that grow in a specific food and the extent to which growth takes place. The quality and safety of foods under production or distribution can therefore be predicted. The described system uses databases of an earlier developed system by Zwietering et al. (1992). This system, however calculates, the effect of processing and distribution and is able to determine shelf life of foods thus being the first step in a microbiological risk assessment procedure. The microbiological safety and quality of newly designed foods can be assessed without performing costly and time consuming challenge tests for each product formulation. Unfeasible new product formulations can be omitted from challenge and shelf life tests. The microbiological implication of small deviations in set points of processing equipment and product formulation can also be calculated. The results can help with the acquisition of improved insight in the processes that are of importance to the safety and quality of foods. Apart from some background in predictive microbiology, the layout and the workings of the decision support system are described and examples will be given.

2. Microbial growth

For the prediction of food quality, usually, lag time and exponential growth phase play the most important role. Foods are usually spoiled if numbers of microorganisms become larger than 10^7 cells per gram product, which is generally lower than the maximum possible level achievable in products. Furthermore, for pathogenic microorganisms safe numbers are generally far lower. Specific growth rate and lag time of microorganisms depend on the value of the environmental conditions (mainly temperature, pH, water activity and amount of oxygen).

Mathematical models have been developed that relate specific growth rate and lag time to the environmental conditions. In earlier research, the effect of pH on the growth parameters of microorganisms was quantified (Wijtzes et al., 1993, 1995) as well as the effects of several other environmental conditions (Ratkowsky et al., 1983; McMeekin et al., 1993). Several mathematical equations were developed to describe the effect of these environmental conditions. Under optimal pH conditions ($pH = pH_{opt}$), specific growth rate will be maximal (μ_{opt}). For several microorganisms, the values for pH_{min}, pH_{max}, pH_{opt} and μ_{opt} can be found in literature. A dimensionless growth rate γ can be used to describe the relative effect of each controlling factor (Zwietering et al., 1992):

$$\mu = \gamma \times \mu_{opt} \tag{1}$$

so that

$$\gamma(pH) = \frac{\mu(pH)}{\mu(pH_{opt})} = \frac{b(pH - pH_{min})\{1 - \exp[c(pH - pH_{max})]\}}{\mu_{opt}} \tag{2}$$

If the value for pH_{opt} is known, c can be determined iteratively. After the value of c is determined, the b value can be derived, since under optimal conditions, ($pH = pH_{opt}$), γ has to equal unity, by definition.

The effect of multiple environmental conditions on specific growth rate has been investigated by several researchers (Ratkowsky et al., 1983; McMeekin et al., 1993; Wijtzes et al., 1993, 1995). It proved that separated effects of, for instance, temperature and

water activity or temperature and pH on specific growth rate could be multiplied. In dimensionless growth rate, γ(total) this can be represented as:

$$\gamma(\text{total}) = \gamma(T)\gamma(\text{pH})\gamma(a_w)\gamma(O_2) \quad (3)$$

In the case a value for μ_{opt} for a specific organism is unknown, the order of magnitude can be estimated for individual microorganisms. For bacteria the value of μ_{opt} is set to 2 h^{-1}, yeasts 0.75 h^{-1}, and moulds 0.25 h^{-1}.

The concept of dimensionless growth rates can also be used for the estimation of lag time (λ) since research proves that lag time is roughly inversely proportional to specific growth rate (Adair et al., 1989; Zwietering et al., 1991). Eq. (4) relates actual lag time (λ) to lag time under optimal environmental conditions (λ_{opt}) and to the environmental conditions [γ(total)]. If values for λ_{opt} are not known for individual microorganisms, these values are set to 1 h for bacteria under optimal conditions, 5 h for yeasts and 10 h for moulds.

$$\lambda = \frac{\lambda_{opt}}{\gamma(\text{total})} \quad (4)$$

3. Food design support system

A computerised food decision support system is described which simulates the production of foods (Food Design Support System, FDSS). The simulation takes place in different steps as shown in Fig. 1.

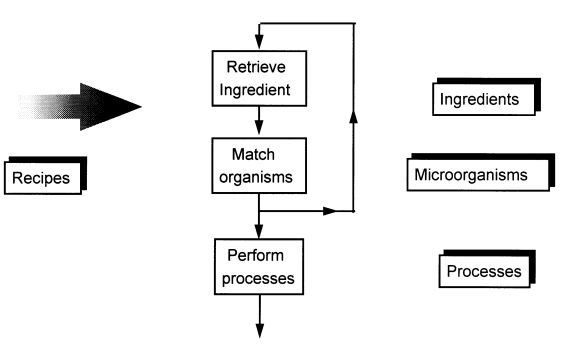

Fig. 1. Food design support system (FDSS), program flow.

3.1. Recipe

The composition of foods starts with the definition of a recipe. The recipe database consists of records (single entities) with descriptions of recipes. A recipe is a description of ingredients and preparation methods for the simulation of the preparation of a food product, equivalent to recipes in a cook book. After a recipe is found, the production of the food is simulated.

3.2. Ingredients

The characteristics of ingredients are present in the ingredient database as described earlier by Zwietering et al. (1992). In the ingredient database, physical and chemical characteristics of food ingredients are stored. An ingredient is defined as a (part of a) food having a homogeneous physical and chemical composition on the scale of microorganisms. The acidity range (pH), water activity range (a_w), temperature range (T) and amount of oxygen (O_2) of an ingredient were obtained from literature. An example of a record from the ingredient data base is given in Table 1. Since there are large numbers of ingredients and the required values for the environmental conditions are not always known, the ingredients are grouped on the basis of their origin and physical composition. This grouping technique results in an inverse tree structure. At the top, a general ingredient can be found and going further into the branches of the tree structure, more and more specific ingredients can be identified. An excerpt of the tree structure is shown in Fig. 2.

On the basis of the described tree structure, ingredient information can be inherited through hierarchical inference. If information is required for specific ingredients of which the values are not readily available in the database, the tree structure is presented to the user to find related food ingredients of which the characteristics are known. Information

Table 1
Example record from the ingredient characteristics database

Semi-skimmed milk		Minimum	Maximum
Temperature (°C)	7	4	7
pH	6.2	6.1	6.5
Water activity	0.98	0.98	0.99
Aerobicity	Aerobic		

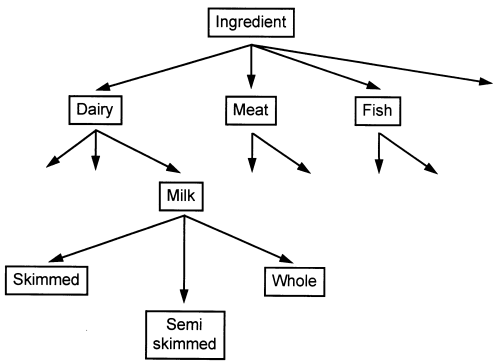

Fig. 2. Hierarchical ingredient database.

can therefore be deduced from less detailed levels in the tree structure. It is not possible to be complete, but specific information can be entered when needed or available.

3.3. Microorganisms

After values of physical and biochemical characteristics of ingredients are found, this information is coupled with kinetic parameters of microorganisms. In the microorganism database, properties of individual microorganisms are stored. For each microorganism, growth ranges with respect to environmental conditions such as temperature, water activity and pH were obtained from literature and stored. Moreover, of each organism in the database, the type (yeast, bacterium or mould), Gram-stain, spore forming capacity, decimal reduction times, *z*-values and pathogenicity are stored. An example record of the microorganism database is given in Table 2. In total, the database consists of 57 different microorganisms that are of importance to food spoilage and food safety. Individual models relating growth characteristics of microorganisms to environmental conditions, can be entered into this database. Microorganisms are only included in the database if the growth ranges with respect to temperature, pH, water activity and oxygen are known. If more or better information becomes available on microorganisms kinetics and characteristics, the database of the system can easily be extended.

Coupling ingredients and microorganisms is a two-step operation. The program first determines which microorganisms can grow on the ingredient.

Table 2
Example record from the microorganism database

Lactobacillus curvatus			
Gram positive bacterium			
Fac. anaerobic			
No spores			
Not pathogenic			
Growth ranges			
	Minimum	Optimum	Maximum
Temperature (°C)	−3.00	35.00	42.00
pH	4.29	6.88	9.28
a_w	0.947		1.0
Growth kinetics parameters			
μ_{opt}	1.2 h^{-1}		
λ_{opt}	1.0 h		
Thermal death kinetics parameters			
D-value	3.3 min at 61°C		
z-value	6°C at 61°C		
Water activity kinetics parameter			
a_w resistance	Moderate		
Cut-off numbers			
Spoilage level	$1 \cdot 10^7$ cfu per ml		

This is done by an earlier described pattern match procedure (Zwietering et al., 1992). This first step is carried out for all known environmental characteristics of an ingredient except temperature. The second step uses experts' knowledge on incidence of microorganisms on known food ingredients. Both methods are described below.

3.3.1. Pattern matching

Growth of microorganisms can only take place between, for instance, minimum pH and maximum pH. If the value of a controlling environmental parameter (pH, a_w) of an ingredient lies between the boundary values for a microorganism, it is able to grow on the ingredient. An example is given in Fig. 3.

The selection on oxygen tolerance also takes place in this stage. For this selection no explicit mathematical models are available, so an expert model is applied in the form of a truth table. Facultatively anaerobic microorganisms can grow under any oxygen concentration. Anaerobic microorganisms can only grow under purely anaerobic conditions whereas aerobic microorganisms only grow under conditions where enough oxygen is present. If the food contains a small amount of oxygen, it contains too much oxygen for anaerobic microorganisms and too little air for aerobic microorganisms. Table 3 translates this description in $\gamma(O_2)$ values.

The selection of microorganisms in the pattern match phase involves the calculation of γ as function of pH, water activity and amount of oxygen, only. If γ has a non-zero value after calculation, the organism is supposed to be able to grow in the product. The selection on temperature does not take place at this stage because temperature may fluctuate in later stages of food production.

3.3.2. Incidence of microorganisms

In the second step of finding the microorganisms that are present on an ingredient, expert knowledge on incidence of microorganisms in ingredients can be used. For several ingredients, knowledge exists on the possible incidence of microorganisms on specific ingredients (such as spore forming microorganisms occurring frequently on herbs and spices). This knowledge can be used to fine-tune the list of selected growing microorganisms.

Because of the large numbers of ingredients, this knowledge cannot be available for all existing ingredients. Information on incidence of microorganisms is also stored in the earlier described tree structure. Through hierarchical inference this information becomes available for most ingredients. If, for parts of the tree structure, no information on incidence of microorganisms is available at all, it is assumed that Beijerinck's rule applies. This rule implies that all microorganisms can be found everywhere and the environmental conditions determine incidence of microorganisms. This rule is implemented as the earlier described pattern match procedure. The most appropriate method can be chosen for any situation. If required, both methods can be tried for their outcome after processing.

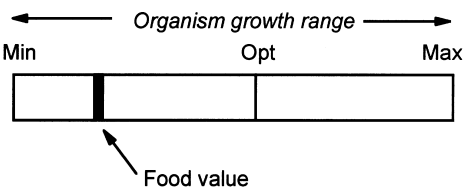

Fig. 3. Combining ingredient information with microbial growth ranges.

3.4. Processes

In this system the concept of performing processes to a number of ingredients is developed further, the next step in the simulation of the production of a food (Fig. 1). The preparation of foods always requires processing steps such as mixing, heating, stirring etc. Processes are methods to alter or combine ingredients. Results of processes usually are altered physical, chemical and microbiological properties of the processed products. In this system, processes are built up of several so-called unit operations. Each unit operation has its own specific impact on the ingredients to which they are applied and to the microorganisms that undergo a unit operation. Unit operations can be combined to result into one overall process. Several unit operations are worked out in the following sections.

3.4.1. Temperature related unit operations

Temperature has a large impact on growth characteristics of microorganisms. In this system it is assumed that between the minimum and maximum temperature for growth of a microorganism, the

Table 3
Truth table for the calculation of $\gamma(O_2)$

$\gamma(O_2)$	Ingredient		
	No O_2	Small amount of O_2	O_2 present
Anaerobic organism	1	0	0
Fac. anaerobic organism	1	1	1
Aerobic organism	0	0	1

organism grows with the maximum specific growth rate at that temperature.

If temperature becomes larger than the maximum growth temperature, microorganisms start dying. First-order inactivation kinetics is used to calculate the decrease in microbial numbers. Generally, D values and z values are found in microbiological literature (Jay, 1992). These values are calculated into the Arrhenius parameters E_a and k_∞. Different temperature time relations can be applied to result in, for instance, sterilisation, freezing, pasteurisation, appertisation or cooling.

3.4.2. Water activity related unit operations

Drying foods is also a well known method of preventing microbial decay. Here, drying is defined as a modification of the amount of water in a product. Microorganisms are assumed to be not directly affected by altering the amount of water, but by changing the relative water pressure, water activity (a_w). A microorganism starts growing if the water activity of a product is higher than the minimum water activity ($a_{w,min}$) for its growth. Below $a_{w,min}$, microorganisms may be inactivated.

Inactivation of microorganisms as a result of drying consists of two distinct phenomena, dehydration inactivation (fast) and inactivation during storage (slow), so called decay. Decay starts to play an important role after a microorganism was kept at low water activities for 24 h or more (Linders et al., 1994). Since it is assumed that production processes usually last for shorter periods of time, this type of inactivation does not play an immediate role in this stage of the production of foods. Dehydration inactivation, however, plays an immediate role in the determination of microbial numbers. The number of surviving microorganisms is defined by means of a residual activity (A_{res}). The resulting number of microorganisms [N_t (cfu/ml)] after a drying step can be calculated as (Linders et al., 1994):

$$N_t = N_0 A_{res} \quad (5)$$

where N_0 (cfu/ml) is the number of microorganisms before drying.

Some microorganisms are known to have a high resistance to drying, such as spores from spore forming bacteria, spores from moulds and yeasts, which results in a high residual number after drying. Other microorganisms have very low residual activities (Linders et al., 1994). Residual activity of microorganisms as a function of water activity is shown in Fig. 4 for three types of microorganisms. Each type of organism has a different resistance to drying. If for specific microorganisms, no data are available on resistance to drying, it is assumed that the resistance to water activity is moderate. All default settings and models can be changed if more or better information becomes available.

3.4.3. Acidity related unit operations

Acids can be used to modify pH values of food products, consequently, this affects the growth rate

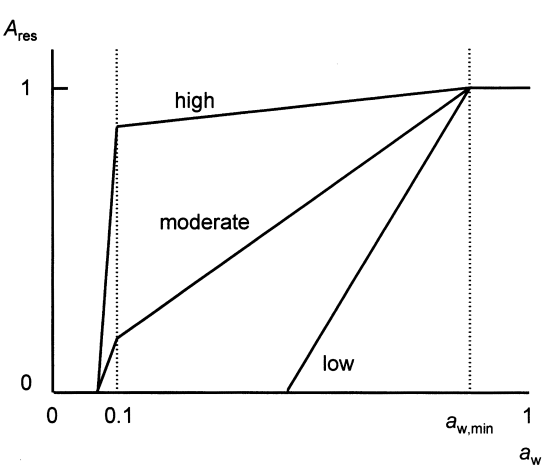

Fig. 4. Residual activities of three different types of microorganisms as functions of water activity (a_w).

of microorganisms. Eq. (6) was developed to describe the effect of pH and temperature on growth rate of *Lactobacillus curvatus*, a known spoilage organism (Wijtzes et al., 1995).

$$\mu_m = b(T - T_{min})^2(pH - pH_{min})(pH - pH_{max}) \quad (6)$$

This response is generalised for all microorganisms. However, it is highly unlikely that all microorganisms have an optimum pH that lies exactly in the middle of pH_{min} and pH_{max}, therefore asymmetrical curves have also been implemented (Wijtzes et al., 1993). The default type of curve used is asymmetrical, but Eq. (6) can be selected as well. If environmental pH becomes smaller than pH_{min} or higher than pH_{max}, numbers of microorganisms decrease. The kinetics of the decrease of microorganisms in these regions is approximated by a simple line through (pH_{opt}, μ_{opt}) and (pH_{min}, 0) or (pH_{max}, 0). Improved models for death kinetics as a result of pH can be implemented, whenever available.

3.4.4. Mixing unit operation

Mixing is defined as combining two or more ingredients. Mass averaged numbers of microorganisms of all involved ingredients are summed. Mass averaged temperature, pH and water activity are chosen as estimates of the resulting physical parameters. The amount of oxygen is approximated in the form of a truth table. Better models for mixing food ingredients are needed, but since these are not available, these simple models are implemented. Approximations such as these, do not have a large impact on the calculation of the quality of foods since, in later stages of the simulation of foods, more precise information can be used for calculation.

3.4.5. Combining unit operations

A process consists of one or more, earlier described, unit operations. As a result of a unit operation, temperature, water activity and pH may change in time. Process time is divided in smaller time slots where unit operations can be combined. A pasteurisation process would, for instance, consist of three unit operations, heating up to the required temperature, keep at the required temperature for a certain time and then cool down.

For calculation, time slots are divided into even smaller time steps in which the conditions are assumed to be constant. The size of these time steps depends on the resulting increase or decrease of the changing environmental variable (temperature, pH and a_w). In a time step, temperature is allowed to change by a maximum value of 0.5°C, pH is allowed to change 0.05 pH point, and water activity is allowed to change 0.005 unit. These default settings can be altered if more precise calculations are required. If unit operations are combined, the largest number of calculated time steps is used for the calculation of growth and decay.

In each small time step, the value of γ for each of the environmental parameters is calculated for a microorganism. Negative γ values override positive values, since microbial decay cannot take place at the same time as microbial growth. To assume worst case, lag time effects are not taken into account while processing foods. It is assumed that microorganisms start growing as soon as favourable environmental conditions for growth are reached. Numbers of microorganisms are calculated on the basis of immediate exponential growth or exponential decay.

4. Distribution chains

Changes in microbial numbers during distribution are calculated during various stages of product distribution. Scenarios are relationships between temperature and time after production of foods. The initial values of the environmental conditions of a food product are calculated by the food design program in the previous step. During distribution, pH, water activity and amount of oxygen are assumed to remain constant. Different scenarios can be entered such as deep cooling, or temperature abuse. A typical temperature time relation is shown in Fig. 5.

While calculating through a distribution scenario, microbial numbers may increase in one step, and remain constant in another. For each step in the scenario, the distribution chain program performs the final step of the pattern match procedure. Temperature is matched with the kinetic temperature parameters of each microorganism. If a certain organism cannot grow at the current temperature, the number

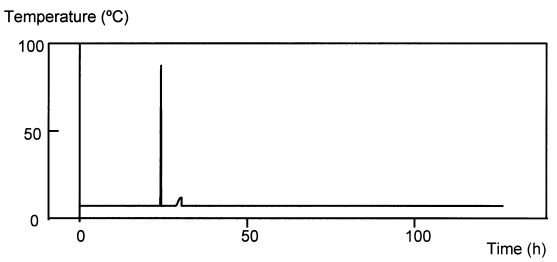

Fig. 5. Example of a temperature–time relation for the processing and distribution of milk.

remains constant until a favourable temperature for growth of this organism is reached.

Numbers of microorganisms in time, can be calculated if the values for lag time, growth rate and the asymptote are known at the prevailing values for the environmental conditions. For calculation a time delayed exponential growth model with asymptotic cut-off value is used (Eq. (7)). Temperature is not constant, therefore, numbers of microorganisms under changing temperature conditions have to be calculated. The length of the lag phase (λ) and the microbial growth rate (μ) are calculated by means of the γ concept, at small time steps i. The size of these time steps is determined as described in combining unit operations. Lag time is only calculated if a microorganism has experienced stressful environmental conditions, where numbers of microorganisms decrease, such as drying, low pH or high temperature conditions. The time step at which a temperature applies ($t_i - t_{i-1}$) is compared with the lag time at these conditions. n is the number of time steps needed to reach the end of the lag phase. As soon as enough time has passed for a microorganism to complete its entire lag time ($\Phi = 1$), exponential growth starts at a specific growth rate (μ) that belongs to the environmental conditions at time t_i. If $\Phi = 1$ is reached within a time step ($t_i - t_{i-1}$), the remaining time for exponential growth is calculated.

$$\text{While} \quad \Phi \le 1 \Rightarrow \Phi = \sum_{i=1}^{n} \frac{(t_i - t_{i-1})}{\lambda_i} \text{ and } N_i = N_0$$

$$\text{If} \quad \Phi > 1 \Rightarrow \ln(N_i) = \ln(N_{i-1}) + \mu_i (t_i - t_{i-1})$$

$$\text{If} \quad N_i \ge A \Rightarrow N_i = A \qquad (7)$$

5. Examples

In this section two examples are described, one of the production and distribution of packaged pasteurised whole milk from raw milk, and storage of the product in refrigerated sale cabinets. Another example is the production of a dried, extruded food product, spaghetti.

5.1. Milk production

Dairy products such as milk, butter, cream and cheese are all susceptible to microbial spoilage because of their chemical composition. Milk is an excellent growth medium for most common spoilage microorganisms, including yeasts and moulds. Raw, non-pasteurised milk contains varying numbers of microorganisms. The characteristics of raw milk are looked up in the ingredient database where the values for the parameters under aerobic atmospheric conditions are found to be pH = 6.6 and $a_w = 0.993$.

After milking, raw milk is put at refrigeration temperatures (5–7°C) until it is collected and brought to the dairy company (Table 4). The simulation of three production and distribution schemes starts at this point. Scheme 1 describes a dairy company, keeping storage temperatures low and performing V-HTST (very high temperature, short time) pasteurisation (0.01 s at 100°C). Scheme 2 represents a dairy company that applies higher storage temperatures and lower pasteurisation temperatures. The HTST pasteurisation (1 s at 89°C) is a well known method for decreasing numbers of microorganisms in milk (Jay, 1992). Scheme 3 is equal to scheme 1 except for a HTST pasteurisation instead of V-HTST.

Table 4
Production and distribution schemes for the production of pasteurised whole milk

	Scheme 1	Scheme 2	Scheme 3
Collection	5°C for 24 h	7°C for 24 h	5°C for 24 h
Pasteurisation	100°C for 0.01 s	89°C for 1 s	89°C for 1 s
Distribution			
Factory	5°C for 4 h	7°C for 4 h	5°C for 4 h
Truck	7°C for 2 h	12°C for 2 h	7°C for 2 h
Shop/home	7°C for 96 h	7°C for 96 h	7°C for 96 h

Table 5
Result of three processing schemes for pasteurised whole milk

Processing	Stage of production	Organisms	Log_{10} (Nos.)/ml
Scheme 1	After collection	>20 species	<5
	After pasteurisation	*Bacillus* spp.	−3.2
Scheme 2	After collection	>20 species	>6
	After pasteurisation	*Bacillus* spp.	−0.2
Scheme 3	After collection	>20 species	<5
	After pasteurisation	*Bacillus* spp.	−2.9

The pattern match procedure of microorganisms to the characteristics of raw milk results in a large list of bacteria, moulds and yeasts. Expert knowledge from literature is applied to roughly estimate initial numbers of microorganisms, where worst case is assumed in all scenarios. The total microbial count roughly equals 10^5 cfu/ml. No other expert knowledge is applied for removing non-applicable microorganisms. After performing the processing as described the main microorganisms and numbers are listed in Table 5.

The described distribution chain causes an increase in numbers of microorganisms (Table 6). Reference criteria are used for the determination of shelf life, here shelf life is defined as the time until a level of 10^3 cfu/ml *Bacillus* spp. (Jay, 1992) is reached after the product is unloaded from the truck. In Table 6 the calculated shelf life of the product is also given at refrigeration temperatures (7°C).

The decision support system calculates that the pasteurisation step in scheme 1 reduces the total microbial count from 10^5/ml to a number below 1/ml. In this system, the *Bacillus* spp. is represented by three species, *Bacillus cereus* (pathogenic), *B. subtilis* and *B. licheniformis*. During pasteurisation, a slight increase in *B. subtilis* can be observed. Numbers of *B. cereus* and *B. licheniformis* decrease. After processing, the calculated count of *Bacillus* spp. equals $7 \cdot 10^{-4}$ cfu/ml; so on average about one *Bacillus* can be found in 1.5 l of pasteurised milk. *B. subtilis* has some species that can grow at low temperatures. In this case worst case increase of *B. subtilis* is calculated which results in a final number of 30/ml.

In scheme 2 the milk was collected at a higher temperature of 7°C. Microbial growth can be observed at this temperature, therefore microbial numbers increase slightly in the collection phase. The product is not spoiled yet, but requires an extensive decrease in microbial numbers. A slightly milder pasteurisation step is applied to the product which results in a larger number of *Bacillus* spp. present after pasteurisation. Since the distribution chain runs at temperatures of 7°C and 12°C, *B. subtilis* grows throughout the entire distribution chain which results in 10^3 cfu/ml. The calculated shelf life then changes to five days.

In scheme 3 a lower pasteurisation temperature results in a shelf life of six days, which is the regular reported shelf life of milk on milk cartons. These excersises show that both a low temperature during distribution and a high temperature for pasteurisation are very important factors influencing the shelf life of the product. In practice however, also spoilage

Table 6
Result of three distribution schemes for pasteurised milk

Distribution	Organisms	^{10}Log (Nos./ml)	Calculated shelf life of product at 7°C
Scheme 1	*Bacillus* spp.	1.5	7 days
Scheme 2	*Bacillus* spp.	3.0	5 days
Scheme 3	*Bacillus* spp.	2.0	6 days

organisms are found in milk, such as *Pseudomonas* spp. (Jay, 1992). These organisms are removed from the milk during pasteurisation, so presumably, these organisms are reintroduced after pasteurisation (e.g., during filling of milk cartons). The system can also be used to simulate the introduction of spoilage organisms after pasteurisation. This, however, requires knowledge on recontamination, which is not yet incorporated in the current system.

5.2. Spaghetti production

Spaghetti is an exceptionally dry product ($a_w = 0.7$) and not very susceptible to microbial spoilage. However, the individual ingredients of spaghetti, eggs and flour, are known to cause microbial problems in products. Flour is also a very dry ingredient, but, as a result of the milling process, contains large numbers of spore forming bacteria, enterobacteriaceae, moulds, and microorganisms that are usually found in the environment such as faecal streptococci (Jay, 1992). This knowledge cannot be derived from performing matching of microorganisms, but results from adding additional knowledge stored in the ingredient tree structure. Eggs are also known to bring along microorganisms. The other ingredients of which the product is composed are water and salt.

The production process is a two step operation, extrusion and drying. The extrusion process is a combination of mixing, temperature and water activity unit operations. The final water activity of the extruded spaghetti half product is approximately 0.75, the pH of the product approximates 7 and the product can be stored at room temperature (25°C). The extrusion process lowers water activity slightly, and results in a mild pasteurisation step (2 min at 70°C). The product is then dried in an aseptic drying tunnel at an initial temperature of 50°C. In the drying tunnel, temperature drops to a value of 25°C. The entire process lasts 10 h, in this time water activity drops to 0.7. This example is worked out here to see whether the microorganisms present in the final product are pathogenic and may cause harm when present in a wet product such as prepared spaghetti. Since non of the microorganisms present in spaghetti are likely to grow because of the low water activity, a distribution chain is not simulated.

According to the data stored, the number of microorganisms present on flour is the same as the amount of microorganisms present on grain, which equals about 10^6/g. The same holds for the amount of moulds present, which is recorded as 10^5/g and the amount of yeasts present is approximately 10^4/g. It is assumed that the numbers are equally distributed over all microorganisms present. As an example: 15 different mould species are recorded; the amount of moulds per gram equals 10^5/g, therefore each species inherits about $7 \cdot 10^3$ moulds/g. In Table 7 the influence of the extrusion step on the amount of microorganisms present is shown, as well as the influence of the drying step.

The extrusion process reduces the number of microorganisms present from 10^6/g to 15/g. The tunnel drying process reduces the number of microorganisms slightly, and alters the water activity of the product so that non of the remaining microorganisms can grow. A stable product with very low numbers of pathogenic microorganisms (*Clostridium* spp., *Bacillus* spp. and *Salmonella* spp.) (Rayman et al., 1981) is produced. Rayman et al. (1979) report the presence of *Salmonella* spp. in both egg containing and no-egg pasta in four out of 654 samples. Furthermore, the presence of *Escherichia coli* is reported (Rayman et al., 1981), however, in the calculations, this microorganism is eliminated in the extrusion process. Obviously, there are *E. coli* strains that are more heat resistant than the ones included in the databases. In storage tests, *E. coli* is not found to survive in pasta after 10 days. Spicher (1985) reports the presence of spores (1 to $1 \cdot 10^3$ cfu/g), coliforms (absent to 24 cfu/g), fecal streptococci (absent to $1.4 \cdot 10^4$ cfu/g), *Staphylococcus aureus* (absent to 62 cfu/g) and moulds (<10 to $1.1 \cdot 10^4$) in spaghetti. In the calculations both the fecal streptococci and *Staphylococcus aureus* are eliminated during the extrusion process. In practice, the extrusion process seems less able to eliminate reported microorga-

Table 7
Results of the production of dry spaghetti

Processing	Organisms	Log_{10} (Nos.) per gram
Ingredients	>20 species	6
Extrusion	7 species	1.2
Tunnel dryer	*Clostridium* spp.	0.4
	Bacillus spp.	0.3
	Salmonella spp.	−2.7
	Xeromyces spp.	−4.3

nisms, therefore, the process parameters of the extrusion process should therefore be reassessed.

6. Possible extensions of FDSS

The results of the simulation of the production of a food should be interpreted by means of an expert system that assesses the numbers of microorganisms (quality) and possible deviations from safety regulations (safety). Knowledge from food microbiologists can be modelled and incorporated into an expert system shell that performs the checking. Interpretation of the results should take place in two stages. The first stage of the interpretation of the results takes place during the simulation of the production of a food. The second part assesses the shelf life of the developed product and the safety of the final product including the distribution chain phase. Each step in the entire production chain of the food should be assessed.

In each step the number of spoilage microorganisms should be lower than a general cut off value (10^7 microorganisms/g) to provide for good quality intermediate products. The number of pathogenic microorganisms should be below the specific cut off value of each organism, which can be very low, for food safety reasons. If these values are exceeded, the program should warn the user and explain how modifications should be made to the simulated food.

Because of rapid developments in several fields of food technology, the information in the databases should be maintained and regularly updated, which is one of the ways FDSS can be updated and improved. At the moment part of the data and models in the databases, is validated, part still needs validation. However, the need for good models and data is evident. In predictive microbiology, more data sets are measured and more accurate models become available. FDSS uses the developed models and combines these with expert knowledge and engineering heuristics. The predictions of the microbial growth models are influenced by the inaccuracies of the assumptions in the decision support system. Generalising models for microbial growth, that is, using a model for one microorganism which was developed for another, also decreases the accuracy of the predictions slightly. Attention should be given to developing rules for more general application of models for groups of microorganisms. The accuracy of the assumptions in the decision support system also has to be assessed. If improved data and models become available, they can be incorporated into the databases of FDSS, although, at the moment, the system already performs well.

If modes of action should change because of new insights, FDSS is set up in such a way that parts can be taken out, reprogrammed and put back into the system. The system is programmed in different libraries. Each of these libraries performs its own task regardless of the rest of the system. Because FDSS is set up this way, it is relatively easy to take one library out, alter it, and put it back into the system. The library that needs to be altered should be looked up and the conventions for that library should be followed, but calculations, inferences, and data handling can be altered at will.

The last way in which FDSS can be improved is by the addition of new libraries. Then the system could, for instance, be used for the prediction of chemical and physical spoilage of foods. Other types of models have to be developed, but the method of combination and prediction is largely equal to the those of the developed system. Chemical and physical spoilage play important roles in foods and food products in which no microorganisms can grow (e.g., dry foods), microorganisms grow slowly (e.g., dried meat), when microorganisms are not present (e.g., sterilised foods), or when large numbers of microorganisms or certain chemical compounds keep other microorganisms from growing (e.g., fermented foods). The characteristic times for each of these spoilage reactions should be calculated so that the most important decay reactions can be assessed. Models for prediction of chemical and physical spoilage can easily be added to the databases and libraries of FDSS, creating an even more versatile system for the assessment of quality of foods.

7. Conclusions

A computerised decision support system is set up that can be a helpful tool in developing and optimising food products. Several product formulations can be tested with respect to changes in formulation and during storage. Microbial consequences of trial product formulations can be determined, so that on the

spot decisions can be supported objectively. Consequences of different temperatures in the distribution chain can be calculated. This may allow the determination of optimal distribution chain conditions with respect to the microbial load and minimisation of costs associated with cooling and storage.

Several types of models are used ranging from qualitative (e.g., tree structure) to quantitative (e.g., microbial growth models). Resulting predictions will always be affected by inaccuracies resulting from the combination of these models and the inaccuracies of the models. However, the transparent way in which the calculations and predictions take place, and the possibility to alter information and models, result in a flexible system in which improved models or improved data can easily be implemented.

The predictions should be seen as an indication of possible occurrence and growth of microorganisms, rather than absolute numbers or predictions. The results of the prediction, can be used as an indication, and also as reminder. Predictions of the computer system should be interpreted by food manufacturing experts to assess the relevancy to the food product. Furthermore, the developed system can be used for training production staff and quality engineers.

The HACCP concept requires insight in the relevant processes for decreasing and controlling certain risks in production and consumption of foods. The developed system can help quantifying effects of control measures on the microbial load of foods. Therefore this system can be a discussion tool for the team that implements the HACCP methodology into food production and distribution chains.

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