Proteinous cellular network model

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THE DREAM Project Book of Results

Design and development of
REAlistic food
Models with well-characterised micro- and macro-structure and composition

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Chapters

Foreword

DREAM, standing for "Design and development of REAlistic food Models with well-characterised micro- and macro-structure and composition", was an EC-funded FP7 large-scale integrating collaborative project which started in 2009, lasting almost five years. DREAM embarked 18 partners from nine countries on a very stimulating scientific and technological adventure focusing on the question: how could the consumer demand for safe, high-quality food be supported by developing modelling approaches?

The DREAM ambition was to develop food models realistic enough to be used by the industry and sufficiently versatile to be used as predictive tools to understand the impact of changing composition and/or processing conditions on food quality. The ultimate goal is to save time in the development of an innovation and to provide decision-making support for food professionals.

In this book we present the results obtained by the different teams on the four generic food categories. These categories were chosen according to their generic structures: filled cellular solid (fruit and vegetables), proteinous cellular network (meat), combined gelled/dispersed systems (dairy products and cheeses) and open solid foam (cereal products such as bread and biscuits). In practice, on each product, the DREAM project has developed three types of models. First, generic model foods for which the relationships between the structure, chemical composition and functional properties are known. For these realistic physical models, several parameters can be varied (fibre content in cereal products, type of fat in dairy matrices, etc.), leading to a series of samples representative of each type of food studied. Second, in-silico food models which allow simulation, for example of the role played by the temperature, pressure, chemical composition, etc. on the food structure and resulting material properties. Third, integrated knowledge models to bring together the technical expertise gained by professionals and the data obtained from research. This modelling uses the most advanced recent cognitive science and complex systems science to extend the methods developed in other food products. Such models also allow assessment of the impact of processing conditions on the nutritional food properties and safety issues.

The applicability of the model foods and food models was assessed before transferring the protocols and disseminating the knowledge gained to industry and other stakeholders through demonstration training. To support the practical application of realistic food models, a Practical Guideline on the use of models was developed. The main objective of the guideline was to provide an overview of different food models and of modelling tools/software for industrial users in order that they may benefit from models to optimise their existing processes or to come up with new ones to develop innovative products.

Dissemination to the general public, students, scientists, industry and, food authorities was made via the DREAM website, E-news releases, peer reviewed publications, workshops, training and congresses and at the DREAM international conference. All results are available on the DREAM web site: http://dream.aaeuropae.org/.

Finally, I would like to thank all colleagues and teams who have contributed to the DREAM project and congratulate them for their achievements. It was also a stimulating collaborative public-private research challenge and an incredible human adventure.

Monique Axelos

INRA - Head of the division for science and process engineering of agricultural products

DREAM Project Coordinator

Mathematical knowledge integration for food-model numeric simulation

Is this information important for me?

Consumers	●	○	○	○	○
Food Industry	●	●	●	●	○
Regulatory Authorities	●	●	●	●	○
Scientific Community	●	●	●	●	●

WP-1

Workpackage

numeric simulation
mathematical knowledge

Introduction to WP1

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Aims and background

The challenge of the WP1 was to develop or adapt new applied mathematical tools able to predict the emerging organisation of a food model at different scales and the functions associated with it, so called IKMs (Integrated Knowledge Models). To do so, several authors had demonstrated the need to resolve the enormous challenge of unifying complex and dissimilar data, knowledge and models, specifically to understand the dynamics of such a complex food system (Perrot *et al.*, 2011). This is particularly true when applied to real systems. Food structure prediction and structure-function relationships are only well- established for simple – or "simplistic" food models (gels, emulsions, dry foams, etc.), which are far from the foods they are intended to represent, at least for their composition and function, and thus useless with respect to industry needs. Nevertheless the improvements to food processes by optimisation methods are restricted to the few applications where the mathematical modelling is complete (Banga *et al.*, 2003). In this context the development of mathematical approaches having the ability to take into account heterogeneous knowledge and simultaneously uncertainty on the system were promising and has been investigated in DREAM.

Prospects

Promising results were achieved to facilitate the task of numerical modelling in food science. Such models can be of precious help in a context of sustainability, either through helping towards a better understanding of the emerging organisation of the food model during its elaboration or by optimising of the process based on numerical simulators.

Task 1.1

Generic structure for the modelling approach: The objective of the task was to propose a structure of the way in which to integrate knowledge that could be available for all cases studied in WP2 to 5.

Task 1.2

Construction of the numeric food model and uncertainty management: In-depth interaction with the researchers of WP3 to 6, mathematical concepts and methods were established and applied to DREAM food models. The main objective in this task was to integrate the knowledge generated by the experimental trials in WP3 to 6, the technical expert knowledge extracted from WP1T1.1 and uncertainty on the knowledge as to reconstructing the dynamic network, at each time linking the scales of the system under process conditions.

Task 1.3

Reverse engineering using the numeric food models: In this task, the challenge was to develop methods able to help determine the sequences of actions directing the food process along admissible evolutions and requirements. The problem was turned into a theoretical adaptation of a viability approach initially developed by Saint-Pierre (1994) for dimensions lower than 6.

Main outcomes

Numeric IKMs able to respond to the issue fixed within the WPs have been developed. Managing the uncertainty and lack of knowledge on certain phenomena was a prerequisite. Approaches for modelling, coupling stochastic and mechanistic approaches in the form of equations or graphical models were thus developed and applied to food models. For example, an IKM has been developed and validated to contribute to understanding of the structure and texture dynamics of a dairy oil-in-water emulsion. It has been applied to a dairy dessert (Foucquier *et al.*, Descamps *et al.*) and generalised to a cream-cheese model (Jelinko, D.) in collaboration with INRA Nantes and IFR Norwich. An IKM mimicking the thermal treatment of broccoli including quality degradation and microbial inactivation has also been developed to be used for decision support purposes in collaboration with the WUR Wageningen (Gaucel, *et al*) and the ADRIA Quimper. A graphical model of biscuit baking was also tested at INRA, GMPA in collaboration with UB. Theoretical developments at the interface of applied mathematics and computing were proposed in parallel (1) to help and simplify the modelling task (Tonda, Lutton *et al.*, 2013). (2) to help the reverse engineering task by coupling viability theory and methods of clustering (Alvarez *et al.*, 2013) and optimisation.

In-silico comprehension and prediction of the structure and texture of a dairy dessert

Dairy products have been experimentally shown to behave like complex systems: their resulting textures depend on various factors, including their composition and their processing conditions. Out of these processing conditions, the most influential are the nature of heat treatment, and processing parameters applied during acidification and during the homogenisation process. Nevertheless, being able to predict the texture based on process conditions is an interesting challenge for the industry. The work developed under the WP1 was to answer to this challenge by developing an in-silico model able to integrate the available knowledge and the uncertainty on the domain. The originality of the approach is in the integration of recent theoretical developments crossing over applied mathematics and computing science. The predictions of the model were validated on experimental data achieved under the WP4, applied to different neutral dairy emulsions and generalised to a cream-cheese model.

Research aims and background

Dairy products have been experimentally shown to behave like complex systems: their resulting textures depend on various factors, including their composition and their processing conditions. Out of these processing conditions, the most influential are the nature of heat treatment, and processing parameters applied during acidification and during the homogenisation process (Foucquier, 2011). From an industrial point of view the texture of dairy products is of crucial importance.

Consumer appreciation of dairy desserts such as gels, yoghurts or cream-cheese variants is influenced by the texture of the product. Due to difficulties in thorough experimental product characterisation along the production chain, mathematical simulation and modelling approaches are well-suited tools to gain deeper understanding of how the composition and some of the processing parameters can be related to the final structure of the product. Nevertheless the task is not easy because of the complex interactions that can occur between key variables at different scales (Perrot, 2011) if we want to mimic a real system. The model proposed is based on knowledge originating from different domains (physical chemistry, microbiology, computer science, applied mathematics, etc.). For dairy dessert, the story starts at a lower scale: the nanoscale level (Descamps, 2013) (Figure 1).

A dairy dessert is an oil-in-water emulsion stabilised by milk proteins. The organisation of the macrostructure of the gel depends on the behaviour of each of the types of particles, denaturated whey proteins or native whey proteins, aggregates of proteins and casein micels, with particles in competition to colonise the interface of a fat globule. From this dynamic system a more or less regular and stabilised fat-globule interface is reached. From this individual interface and the connexion between all of them, a connected organisation will emerge at a higher level. We propose an integrated model that mimics this competition in-silico.

Knowledge of the laboratories working in the WP4 was integrated into the structure and certain parameters of the model. Latest developments crossing over applied mathematics and computing science were included in the mathematical functions, allowing the coupling of deterministic and stochastic algorithms.

Significance and benefits

The model is a coupling between a first-order differential kinetic model of protein denaturation (M1) and a stochastic model simulating of the fat-droplet interface colonisation (M2a) and bridge creation between fat droplets (M2b) (Figure 2). Coupling M1 and M2 makes it possible to simulate the emergence of a network at a mesoscale level from local droplet considerations. The inputs needed are the initial relative concentration of each particle in the solution, the droplet size and volume distribution and the thermal denaturation rate. The fat-droplet local interface organisation is predicted through two dimensions: the interface composition: percentage of the different particles fixed at the interface and interfacial concentration. A good prediction is observed for data achieved during experiments led by the WP4 partners (Descamps, DREAM congress). The macroscopic structure is explored based on the number and organisation of the links between the particles in the space. For example, for the three experiments represented in Figure 3, the percentage of caseins has been evaluated by the experts to have a strong influence on the perception of the texture of the product, which has been shown in the literature to be linked to the number of fat-droplet connections. The prediction is in satisfactory accordance with this knowledge. Thus, for an 80/20 ratio of casein/whey proteins, a weak viscosity is measured (40Pa.s at 0.001s-1) and few local interfaces are predicted to be connected. On the contrary, for a 5/95 ratio, the gel is structured with a viscosity of 2,600Pa.s at 0.001s-1) with the prediction of a highly connected structure.

This approach has been generalised and applied in collaboration with data from the industry to a cream-cheese model (Jelinko, 2013). The experimental data and model simulations show similar tendencies, also demonstrated in previous studies, where increasing homogenisation pressure in cream-cheese production resulted in increased storage modulus (‘G) in the interval of (0 – 50 Mpa) and an increased texture and number of links.

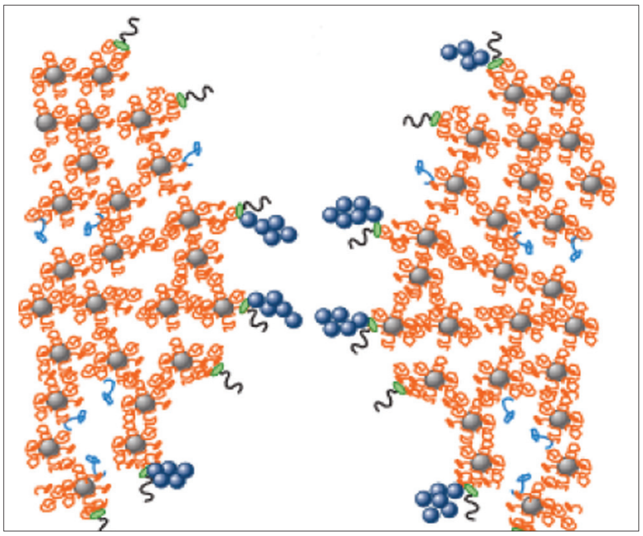

Figure 1. Interaction of casein micelles (only interacting parts are shown), casein from heated milk with attached whey protein/κ-casein complexes. These complexes prevent coagulation even if the κ-casein is removed and provide points of attachment between micelles during acid gelation (Dalgleish & Corredig, 2012).

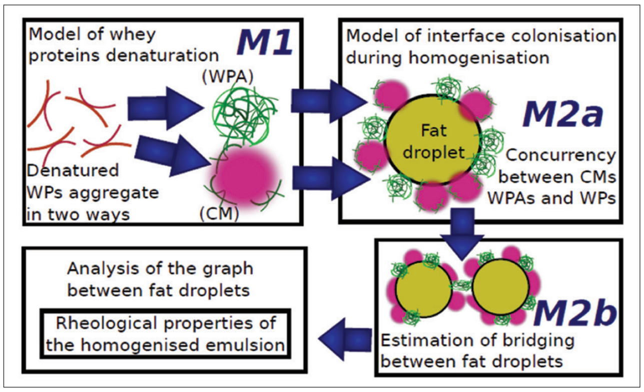

Figure 2. An IKM in-silico model of a dairy dessert including heat treatment and homogenisation.

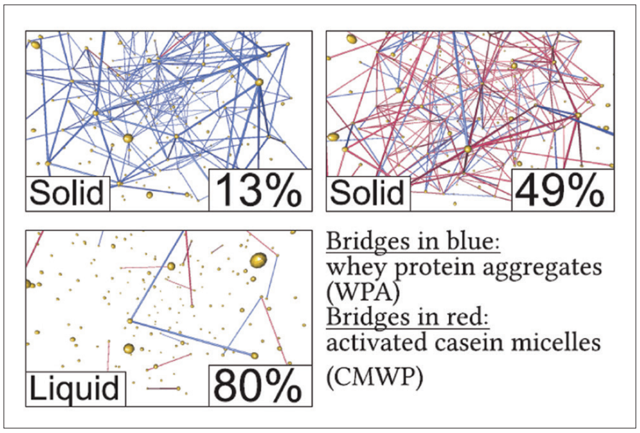

Figure 3. Example of the in-silico IKM prediction at the macroscopic level.

Prospects and challenges

This work is a first contribution able to predict real dairy dessert structures crossing over the scales. The fertilisation of the different disciplines: food, computing and applied mathematics has led to a model of understanding and comprehension that can be used by the industry for optimisation or sustainability purposes.

Results and applications

A generalisation of this approach is needed to be sufficiently generic in order to cover the wide range of dairy desserts produced in the industry. For this a deeper understanding of what takes place at the interface is necessary, coupled with complex system tools developed specifically to handle this understanding and to propose a means of process optimisation.

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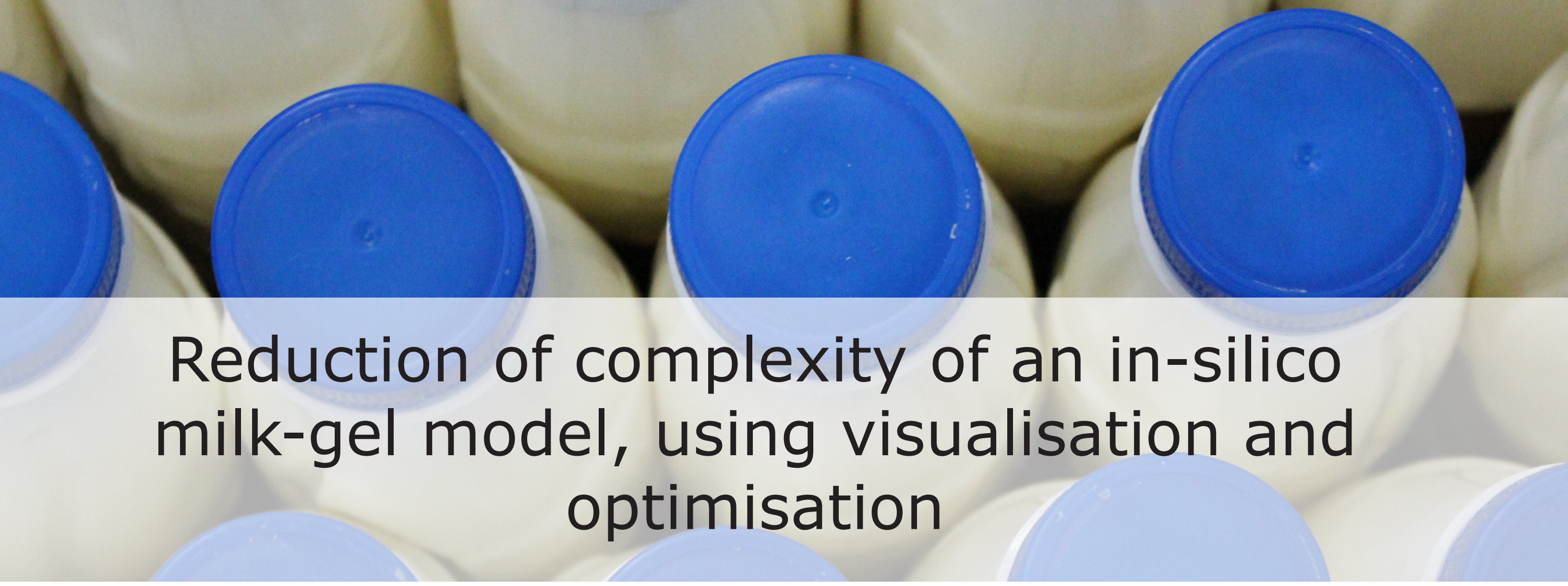

Reduction of complexity of an in-silico milk-gel model, using visualisation and optimisation

Dairy products, complex system, in-silico model, reduction of complexity and visualisation

Replicating the structuring dynamics of food models in-silico is a relevant challenge for a better understanding of these systems. It is thus important to simplify as much as possible the structure and the number of parameters of in-silico food models. Given their intricate structure, however, it becomes hard for experts to thoroughly explore the behaviour of the system and search for meaningful correlations between parameters. In this work, developed under the WP1, we combine visualisation with model exploration to search for correlations in an established computer model of a milk gel, following the subsequent steps: (a) data are collected during the computations of a learning algorithm, (b) data are made available via a multidimensional visualisation tool, (c) subset selection tools and navigation in the multidimensional parameter space help the expert to evaluate the behaviour of the model. Through this approach, we found a correlation between two parameters of the model, which we were able to support with a formal analysis.

Research aims and background

While the structural characteristics of pure protein aggregates submitted to heat treatment are widely studied (Rabe, 2011), research on aggregates of casein coupled to whey proteins (denatured or not) is still in the initial stages (Morand, 2012). The models built are becoming increasingly complex, and necessitate the use of robust and efficient algorithmic techniques. This work is a contribution to the design of such complex models: it addresses the question of parameter learning using robust optimisation techniques and visualisation. The issue here is to show that the observation of the behaviour of an optimisation algorithm yields important information as to the optimisation problem itself, and, as a consequence, on the model studied. The experiments conducted for this work were based on an evolutionary algorithm (EA), a stochastic optimisation technique that relies on the computer simulation of natural evolution mechanisms. EAs are specially well-suited to the resolution of difficult optimisation problems, and particularly for learning the optimal parameters of complex models (Baeck, 1993). Conventional uses of EAs only consider the best individual of the last population as an estimation of the optimum, but recent work points out the potential benefit of visualising data collected during the execution of an EA (Lutton, 2011), and shows how a multi-dimensional visualisation tool, GraphDice (Bezerianos, 2010), can help to efficiently navigate inside the data set collected during the execution of an EA.

Significance and benefits

Even for skilled scientists, it is often extremely hard to validate the behaviour of an in-silico model: due to the complexity an extensive exploration of the search space is often impossible. The proposed methodology generates a limited amount of data that is likely to be of interest for the user.

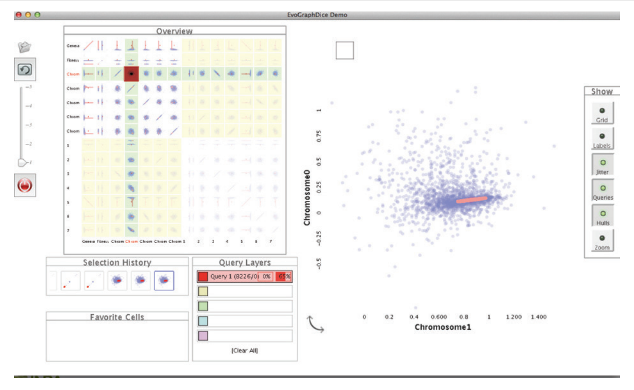

Figure 1: In-silico model

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Results and applications

Data was collected during two emulsification experiments (used as training and validation sets, respectively), where the continuous phase of the emulsion is formed by dissolving milk proteins in permeate. The analysis is based on a model developed previously (Foucquier, 2011) that predicts the structure characterised by the percentages of adsorbed caseins and native whey proteins, and the interfacial concentration. This model depends on five unknown parameters that can be learned from experimental points (learning set), using an EA that searches a five-dimensional space. A visual exploration (using GraphDice, see figure) of the set of points visited during the optimisation process shows a convergence towards a rather large area of values for a couple of parameters (see red points in figure below), highlighting evidence of a possible dependence between these parameters. This evidence was then confirmed by a mathematical rewriting of the differential equations of the model, allowing four unknown parameters to be considered instead of five. An optimisation run within this reduced search space yielded a good matching of the four-parameter model. These results were confirmed on the validation set.

Prospects and challenges

This work can be extended to a general methodology for model exploration. Such a technique could be invaluable to assist experts in assessing the validity and the weak points of their in-silico models, both in agri-food and other domains.

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Coupling viability theory and active learning with kd-trees

Viability theory, kd-trees, controlled dynamical system

The mathematical viability theory is very useful when trying to confine controlled dynamical systems into a set of desirable states. It defines the state area (the viability kernel) where the system can evolve safely. Unfortunately the computation of the exact kernel is a complex and computationally intensive task.

We propose a method coupling viability algorithm and active learning with kd-tree in order to provide a compact representation of the viability kernel and to limit the call to the model, which, in case of food models, is generally time consuming. Viability theory is a set of mathematical and algorithmic methods proposed for maintaining the evolutions of controlled dynamical systems inside a set of admissible states, called the viability constraint set. This framework has proved, in the recent past, to be useful for food control in a domain where knowledge of what exactly is a good candidate objective function for optimisation is not so clear (Sicard *et al.*, 2012). Unfortunately the algorithms that are available presently have a complexity which is exponential with the dimension of the state space. This presents a severe limitation to the use of the method in real applications. The work we present aims at providing compact storage of the set being computed, in order to limit the number of calls to the dynamical model. It also aims at being reusable.

Results and applications

An algorithm based on kd-tree was developed in order to learn the boundary of a hyper-volume (Rouquier et al., submitted), considering the viability kernel as a classification function (Alvarez *et al.*, 2010). The objective was to limit the number of calls to the underlying model. A second algorithm was developed in order to compute the viability kernel of a viability problem (a dynamical system defined as a black box and a set of desirable states), using the previous kd-tree storage algorithm. This new algorithm has been proved to converge to the true viability kernel (Alvarez *et al.*, 2013).

Research aims and background

This work is a crucial step in order to provide a complete set of tools to compute the viability kernel and capture basin of viability problems. The algorithm code is open-source and will be freely available at the ISC-PIF forge. Sustainability problems (such as resilience study) and control problems, which can be defined as viability problems, could then be studied with the algorithm we provide.

Prospects and challenges

This method focuses on the boundary of the viability sets rather than on the sets themselves, so allowing state space to be considered with one additional dimension; but it still suffers the curse of dimensionality. Further work is in progress in order to parallelise the refining part of the algorithm.

Real application of the algorithm will also be implemented in order to validate the platform.

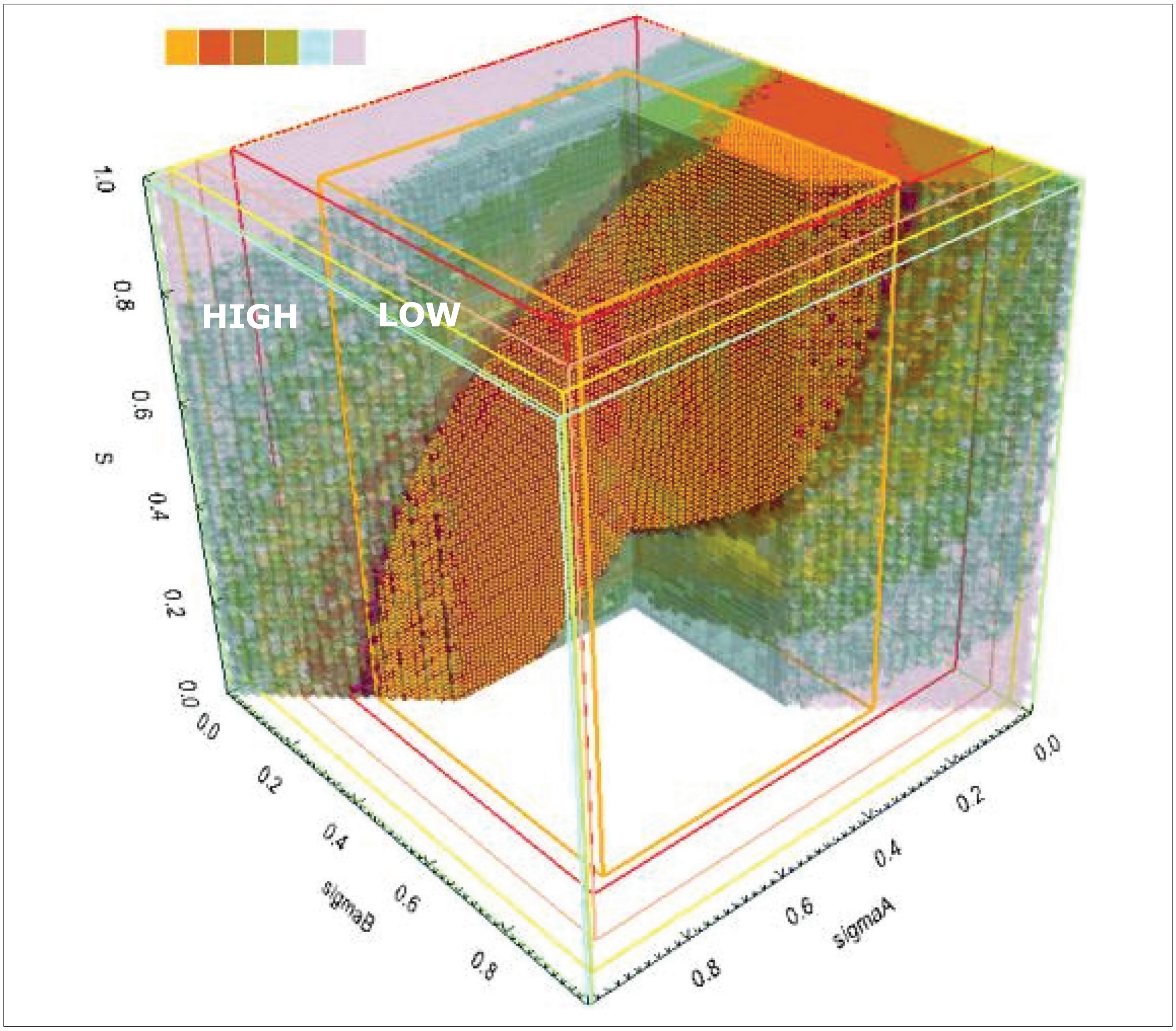

Figure 1. Level sets of the capture basin of a viability kernel (bilingualism), to define the resilience of the system.

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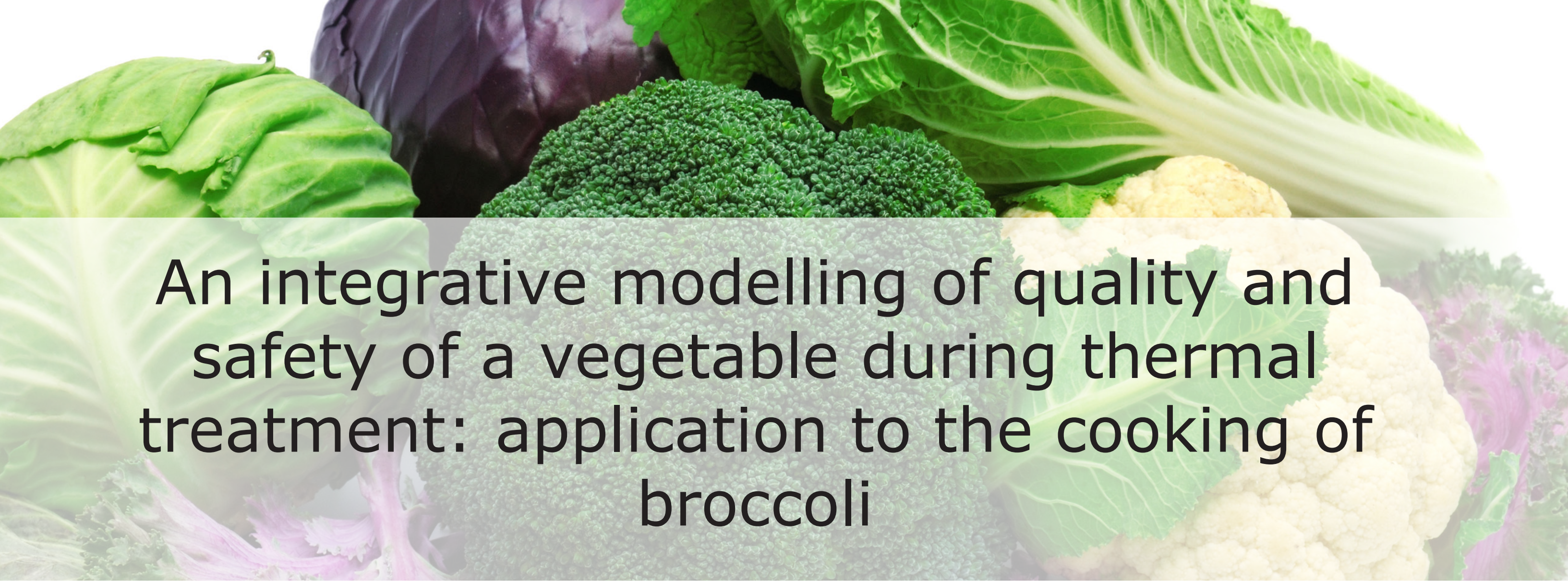

An integrative modelling of quality and safety of a vegetable during thermal treatment: application to the cooking of broccoli

Mathematical modelling can be very useful in the food industry for the control and design of processes. Thermal treatment is a widespread process and literature provides several models, from mechanistic to purely data-based. Unfortunately, these often focus on the process itself or on a single macroscopic indicator of the food product. As a consequence, model coupling is a required step in order to provide an overview of the food macroscopic characteristics. Process control thus involves finding a tradeoff between the complexity of the model and accuracy of the prediction, allowing the use of control-theory tools. In this work, we propose a model taking into account food quality, including consumer acceptability, and food safety, applied to the cooking of broccoli. The results show a satisfactory prediction, albeit improvable, of the experimental data. Furthermore, the low complexity of the model makes it a good candidate for control application.

Research aims and background

Glucosinolates (GSs) are beneficial components present in Brassica vegetables, which have demonstrated an ability to reduce the risk of several cancers. The concentrations of these compounds are strongly affected by the processing of vegetables, especially heat treatment. A model has been developed to describe the fate of GSs during thermal processing (Sarvan *et al.*, 2012). However, this model alone is not suitable for process control as maximisation of GS concentration corresponds to raw cabbage. Indeed, optimisation of the control temperature only makes sense for models requiring antagonistic constraints on temperature , e.g. low temperature to preserve the GS content and high temperature to ensure food safety. Our aim is to extend the previous model to other macroscopic features of a vegetable during heat processes, related to consumer acceptability (colour, texture) and food safety. Literature provides simple models for this purpose, dealing with texture (Rizvi and Tong, 1997) and colour (Tijskens *et al.*, 2001). Inactivation of foodborne pathogens is extensively studied but recent works mainly focus on the Weibull frequency distribution model (Mafart *et al.*, 2002).

In addition, the efficiency of the tools from control theory is directly related to the dimension of the model. The issue of this work is to show the feasibility of accurately predicting the dynamical behaviour of several macroscopic characteristics in a low complexity model.

Results and successful application

A model has been developed in order to reproduce the dynamics of the concentration of a single (or mean) GS in vegetable and cooking water, colour and texture of the vegetable and concentration of the biological pathogen. The single control variable is the temperature, which is assumed to be homogeneous in both vegetable and cooking water and equal to the temperature of the heating device. As there is no data available on thermal inactivation of a specific biological pathogen for this study, a "virtual" biological pathogen is considered, allowing to test different thermal resistances to be tested. Finally, the enzymatic degradation of GSs was neglected so that all sub-models (GSs, texture, colour and biological pathogen) are independent, the only temperature dependency. The corresponding mathematical system (not shown) is a set of seven ordinary differential equations with 16 parameters. Parameter estimation has been performed on data from the cooking of broccoli. The matching between experimental and simulated results, for certain state variables, is shown in Figure 1. Due to the low complexity of the mathematical system, analytical solving was performed, leading to the expression of direct function of time for all the state variables (result not shown).

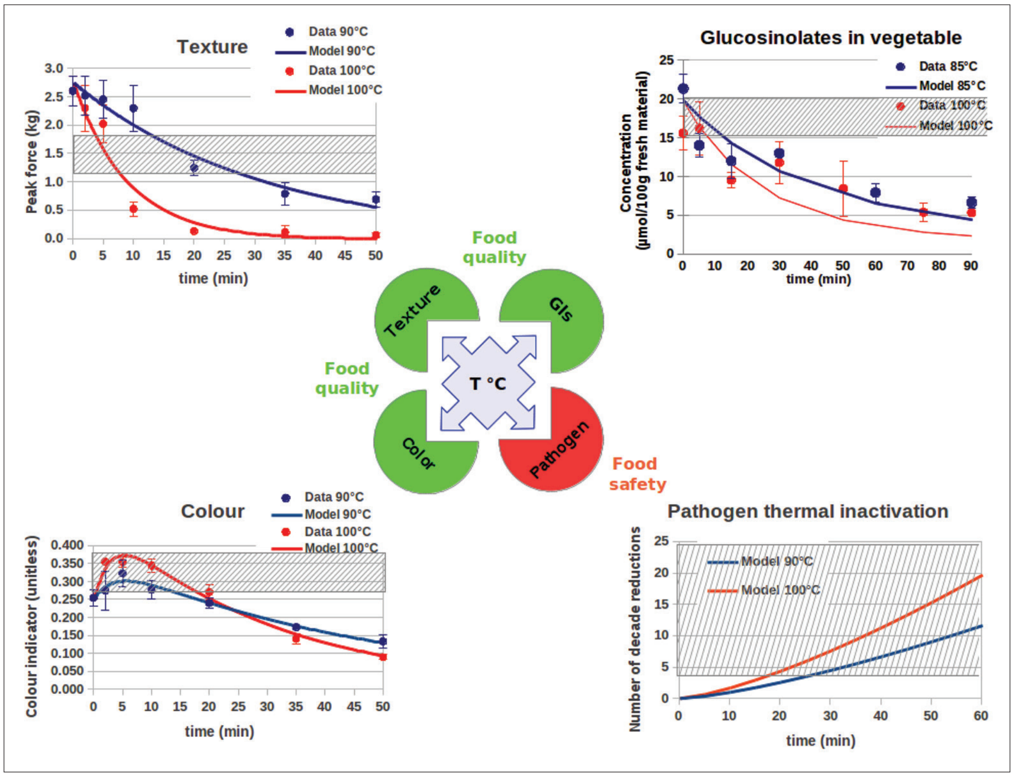

Figure 1. Matching between experimental and simulated results for certain state variables for istothermal heat treatments. The hatched areas correspond to targets at the end of the process.

Prospects and challenges

While the model presented shows an acceptable matching of the experimental data, it must be extended to a larger range of control temperatures, including kinetics. Further work is in progress to apply viability analysis tools in order to find control temperature kinetics leading to the identified targets.

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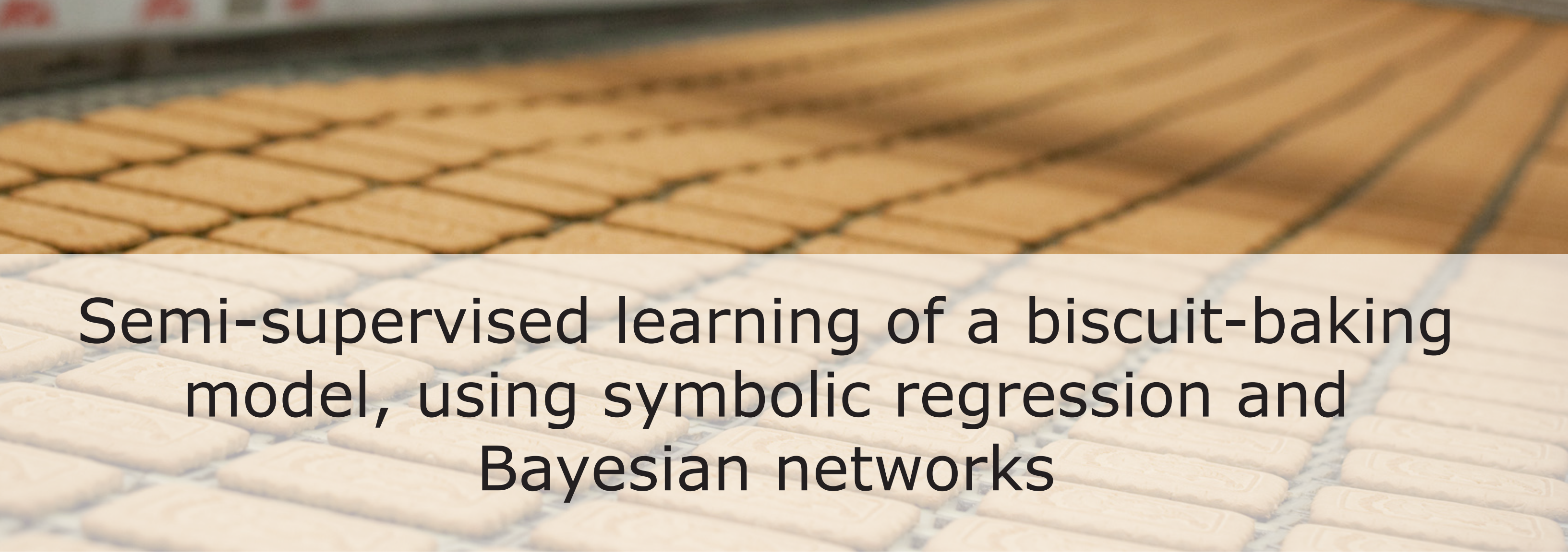


Semi-supervised learning of a biscuit-baking model, using symbolic regression and Bayesian networks

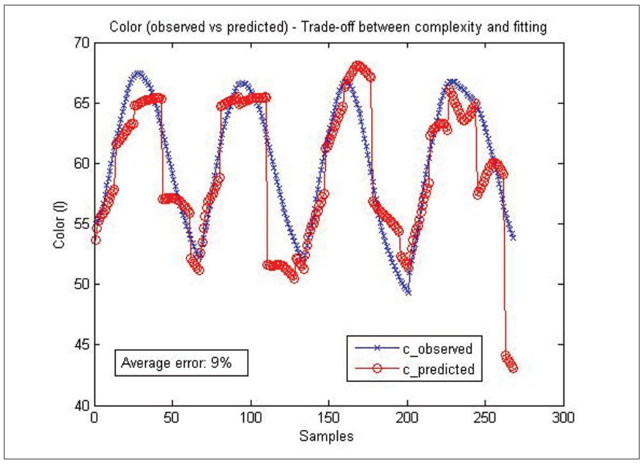
Machine learning methodologies can be an important aid to modelling experts in the food industry, allowing them to obtain reliable models with more efficiency. While human expertise cannot be replaced, it is possible to exploit automated techniques to obtain several candidate models from which an expert could later choose the best, or draw general conclusions on recurring patterns. In this work, developed under the WP1, we perform a feasibility study to learn the model of an industrial biscuit-baking process, using two different machine-learning paradigms. Symbolic regression is employed to obtain a set of equations, starting from raw data; and an interactive approach is used to learn a Bayesian network model, after discretising the original dataset. The results show a good prediction capability, albeit that further improvements must be studied in order to produce physically meaningful models.

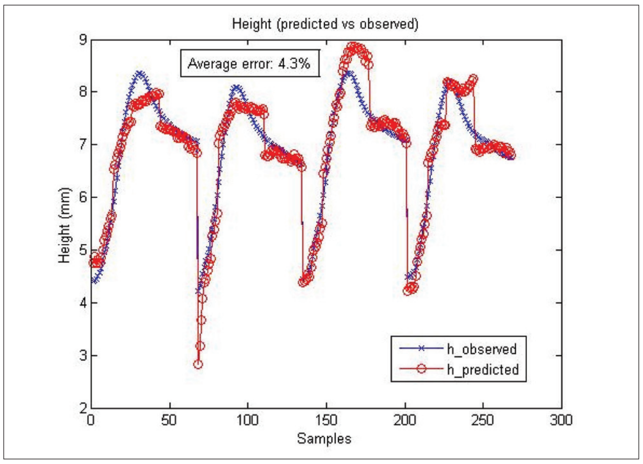
Research aims and background

Machine learning techniques have gained increased popularity in recent years, mainly due to the increasing complexity of problems faced in industry. Symbolic regression, an evolutionary technique based on Genetic Programming (Koza, 1992), is able to automatically reconstruct free-form equations from data, uncovering hidden relationships between variables in a dataset. Commercial software using symbolic regression is already available in the public domain (Schmidt, 2009). While symbolic regression can work on the original data with no modification, models produced can be very complex and not adherent to the physical reality of a process, thus being hard to understand for a human expert. Bayesian networks are graphical probabilistic models that work with discretised variables. They represent a set of variables and their conditional dependencies via a directed acyclic graph, and are widely used to represent knowledge in many different domains, ranging from computational biology to decision support systems. While the discretisation of variables might introduce further sources of error, Bayesian network representations are intuitive for the end user; they can be validated by experts of a specific process with little to no knowledge of their inner working; and they can even be manually modified. Several research lines work on the automatic and interactive reconstruction of a Batesian network starting from data (Tonda, 2012), and several libraries have been developed for the purpose (Druzdzel, 1999). Our aim is to perform a feasibility study on the application of these techniques to the food domain, verifying whether it is possible to produce reliable models for a specific industrial process.

Results and successful application

Data was collected during 16 runs of an industrial baking process by United Biscuits: 12 runs were used for training and four for validation. The variables measured are top and bottom flux of heat in the oven, colour, height, and weight loss of the biscuits. Additional features include the temperature in each zone of the oven, which might vary between different experiments. Both machine learning techniques are attempting to find models that predict the variable considered, at instant t+1, with access to observable values only (such as top flux, bottom flux, heat in the different zones of the oven at time ‘t’, and initial value of the variable considered, at time t=0). Symbolic regression is able to find several good equations to predict colour, height and weight loss, also performing well on the validation set.





The Bayesian network obtained through an interactive learning approach shows several relationships between variables that also appear among the best models produced by symbolic regression, thus supporting the findings of the previous step.

Significance and benefits

Modelling experts usually require a long phase of trial and error before finding a satisfying model of a complex process, as is often the case in the food industry. Semi-supervised learning techniques can generate several candidate solutions with good matching in a small amount of time, from which the expert can then choose the most promising or physically sound. An added benefit is the possibility of examining the candidate models for recurring patterns, which might unveil certain unknown relationships between variables of the process.

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Prospects and challenges

While the models obtained demonstrate satisfactory performance even on unseen data, the machine learning algorithms completely ignore the physical meaning of the models themselves. Further studies on semi-supervised approaches are needed, in order to obtain high-quality results coherent with the physical phenomena underlying the processes.

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Filled cellular solid model

Is this information important for me?

Consumers	● ● ● ○ ○
Food Industry	● ● ● ● ●
Regulatory Authorities	● ● ● ● ●
Scientific Community	● ● ● ● ●

WP-2
Workpackage

thermal impact on fruits & vegetables
mechanical impact on fruits & vegetables
mathematical model describing observed changes

Introduction to WP2

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Aims and background

To develop well-characterised, realistic, food models for plant foods able to serve as tools for integrating and harmonising food and nutrition research on plant food products. Fruit and vegetables are physiological active products that, even for within same variety, show variation in many characteristics depending on the cultivation conditions (location, soil, weather, light, etc.) and post-harvest conditions. Thus, even with standardised protocols variation will remain. Therefore, there is a need to link processing behaviour with measurable characteristics that are determining kinetics of nutritional changes. Mechanistic mathematical models are needed that are robust in dealing with natural variation and still give meaningful results to be used for product and process optimisation with respect to nutritional, sensory and safety quality attributes.

Main outcomes

Selected varieties of brassica vegetables, tomatoes and apples have been studied for their chemical, physical and nutritional properties. For brassica vegetables the main focus has been on developing a mathematical model for thermal processes that can describe the content of phytochemicals (glucosinolates) in the products as a function of processing conditions. In addition, kinetic models have been developed for the texture and colour of the products. For the tomato the focus has been on relating the processing conditions with the content and accessibility of lycopene. For apples the focus was on the distribution and absorption of polyphenols in the cell walls and on texture development.

Task 2.1

Selection of three plant food models taking into account works undertaken in FP6 projects, especially EU-SOL, ISAFRUIT, FLORA and FLAVO: (INRA, WUR) In this task the specific varieties and cultivation conditions obtaining the biological material on brassica vegetables, apples and tomatoes for the further studies where have been defined.

Task 2.2

Processing of the three plant food models to represent mechanical and thermal treatments of fruits and vegetables by industry: (INRA, WUR) For brassica vegetables the effects of thermal processing on the content of glucosinolates, texture and colour have been investigated. For the tomato the effect of hot/cold break on the content and accessibility of lycopene was investigated. For apples the texture and the characteristics of polyphenols in cell wall polysaccharides were studied.

Task 2.3

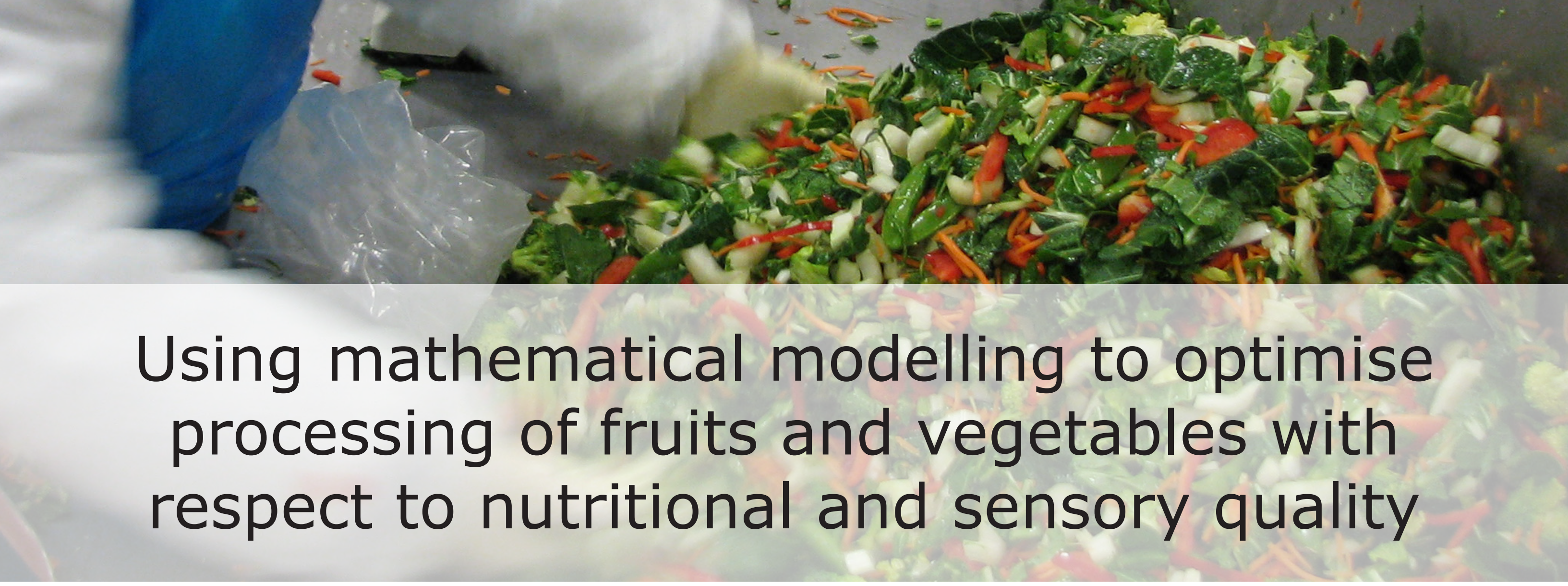
Characterisation of the macro- and microstructure in the fruit and vegetable GMFs before and after processing in terms of different kinetic, mechanical, chemical and enzyme events leading to changes in the bioavailability of selected phytonutrients: (IFR) The changes in cell wall structures and composition during processing were investigated by imaging techniques.

Task 2.4

Mathematical modelling (in connection with WP1) to describe the main mechanisms of changes in product structure, phytonutrient (content and availability) and sensory properties during processing: (WUR) A mathematical model was developed that describes the content of glucosinolates in brassica vegetables, based on the various mechanism that occur during thermal processing: cell lysis, leaching, enzymatic degradation, enzyme inactivation and thermal degradation in different compartments. Kinetic texture and colour models were developed.

Prospects

The developed approaches to studying fruit and vegetables, as illustrated on the selected varieties and quality attributes in this workpackage, can serve as guidelines to studying nutritional and sensory related product properties in fruits and vegetables with a much broader perspective. With limited additional experimental efforts, the parameters of the thermal process model developed can be estimated. With these specific parameters the model can be applied to simulate and optimise the content of many phytochemicals within fruit and vegetable varieties.



Using mathematical modelling to optimise processing of fruits and vegetables with respect to nutritional and sensory quality

Mathematical modelling for improved food quality

The phytochemical content of processed fruit and vegetable products is highly variable and unpredictable. By studying the underlying mechanisms of changes in the contents during processing, mathematical models were developed to simulate and optimise the thermal processing conditions with respect to the phytochemical content in the final product. Combining these models with models describing texture and colour changes depending on the conditions allows multi-criteria optimisation of overall fruit and vegetable quality.

The modelling approach was illustrated with brassica vegetables and the phytochemicals from glucosinolates. This case study can serve as a blueprint for the application of mathematical modelling to enhance the nutritional properties of plant foods, while respecting the sensory quality, in a much broader sense.

Research aims and background

Fruit and vegetables are an important part of our diets. The intake of fruit and vegetables is associated with reduced risk for many diseases such as cancers, cardiovascular diseases and type-2 diabetes, etc. Phytochemicals in fruit and vegetables show important biological activities related to their health promoting effects. The content of these phytochemicals in current fruit and vegetable products is highly variable. Next to breeding and cultivation, processing and preparation have been shown as main sources of this observed variation.

Understanding the changes in the phytochemical content during processing and preparation allows the development of mathematical models to describe the effects of processing conditions on the final level.

With these models, product and process optimisation can be conducted in order to enhance the phytochemical composition of the final product, while in the meantime the sensory quality attributes of the products are respected.

The results of this research in terms of developed models and the approach to extend the applicability to a wide range of phytochemicals in fruits and vegetables can be used by the food industry to efficiently improve the quality of plant foods with respect to their health-promoting and sensory qualities.

Results and applications

As a case study the thermal processing of brassica vegetables (broccoli, cabbages and Brussels sprouts) was studied in detail. By investigating the mechanisms that are responsible for changes in the phytochemical (glucosinolates in the case of brassica vegetables) composition during thermal processing, models were developed to describe:

- Cell lysis kinetics
- Glucosinolate and enzyme leaching kinetics
- Enzymatic conversion kinetics
- Enzyme inactivation kinetics
- Thermal degradation kinetics of glucosinolates in vegetable tissue
- Thermal degradation kinetics of glucosinolates in

processing water.

By means of specific experimental set-ups the parameters in these models can be efficiently estimated. In addition to the phytochemical model, semi-mechanistic models to describe the kinetics of texture and colour changes during processing have also been developed and their parameters have been estimated. With the developed set of models, process conditions can be optimised with respect to product quality (health-promoting effects as well as sensory quality). The developed approach was illustrated on a specific group of phytochemicals in specific vegetables. However, the same approach and often even the same models can be used on a much broader range of plant foods and their specific phytochemicals. What is needed in order to apply this is to estimate the specific parameters in the models for each case. The experimental procedures developed in this project can serve as a guideline for this.

Significance and benefits

With the developed models and experimental approaches for estimating model parameters it is now possible to efficiently describe and optimise the phytochemical content of plant food products, while respecting their sensory quality. The results can be used by the food industry to efficiently improve products, but also by nutritionists wishing to have an overview of the phytochemical contents of plant foods after processing and/or preparation. Most nutritional databases only mention the contents in raw materials and perhaps one standard processed or prepared product. With the developed model the effects of many process and preparation conditions can be estimated and used to improve the quality of intake data in e.g. epidemiological studies.

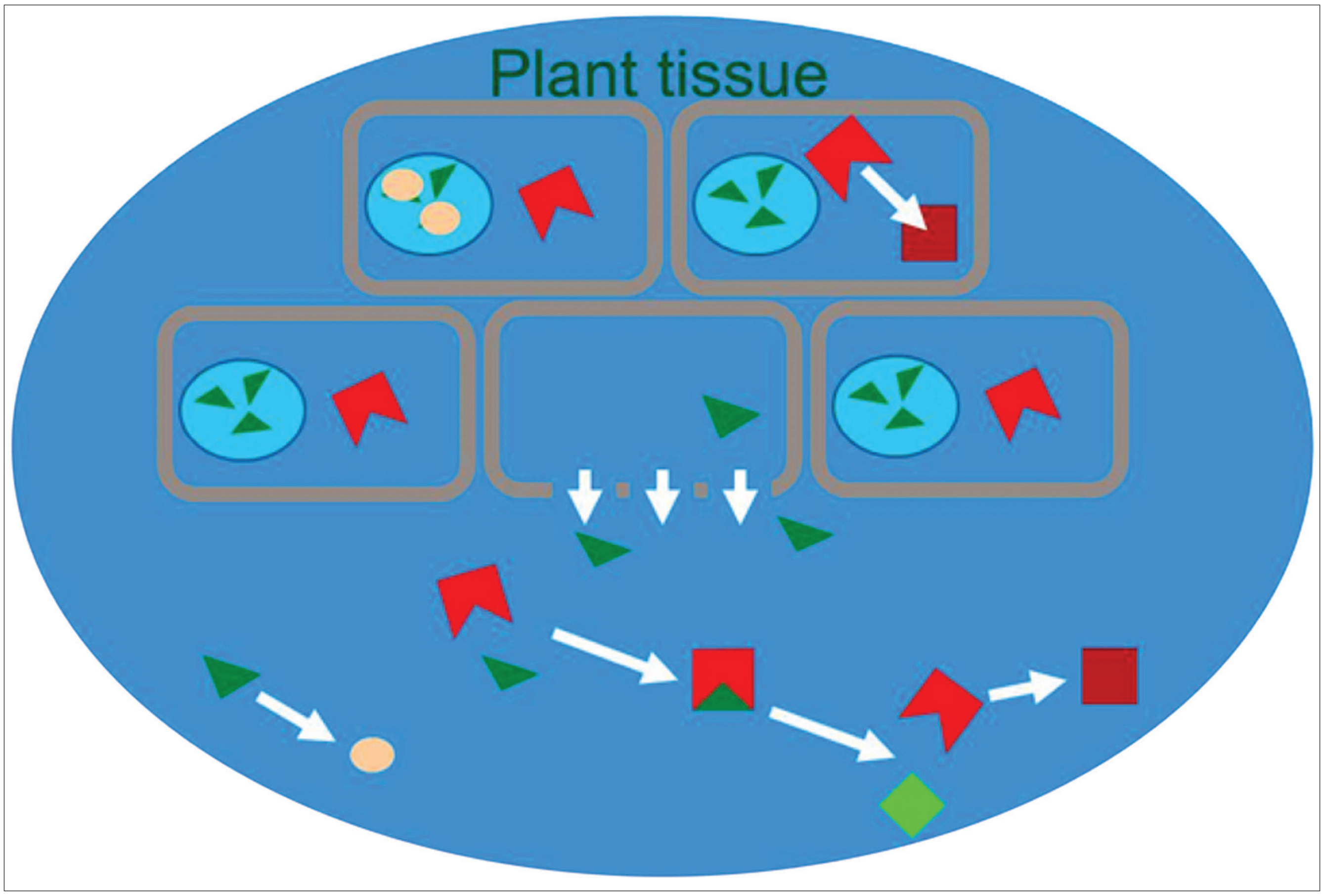


Figure 1. Schematic representation of mechanisms that effect the content of phytochemicals during thermal processing of vegetable tissue (green triangles: phytochemicals, red squares: active/inactive enzymes, beige circles: thermal breakdown products, green squares: enzymatic breakdown products).

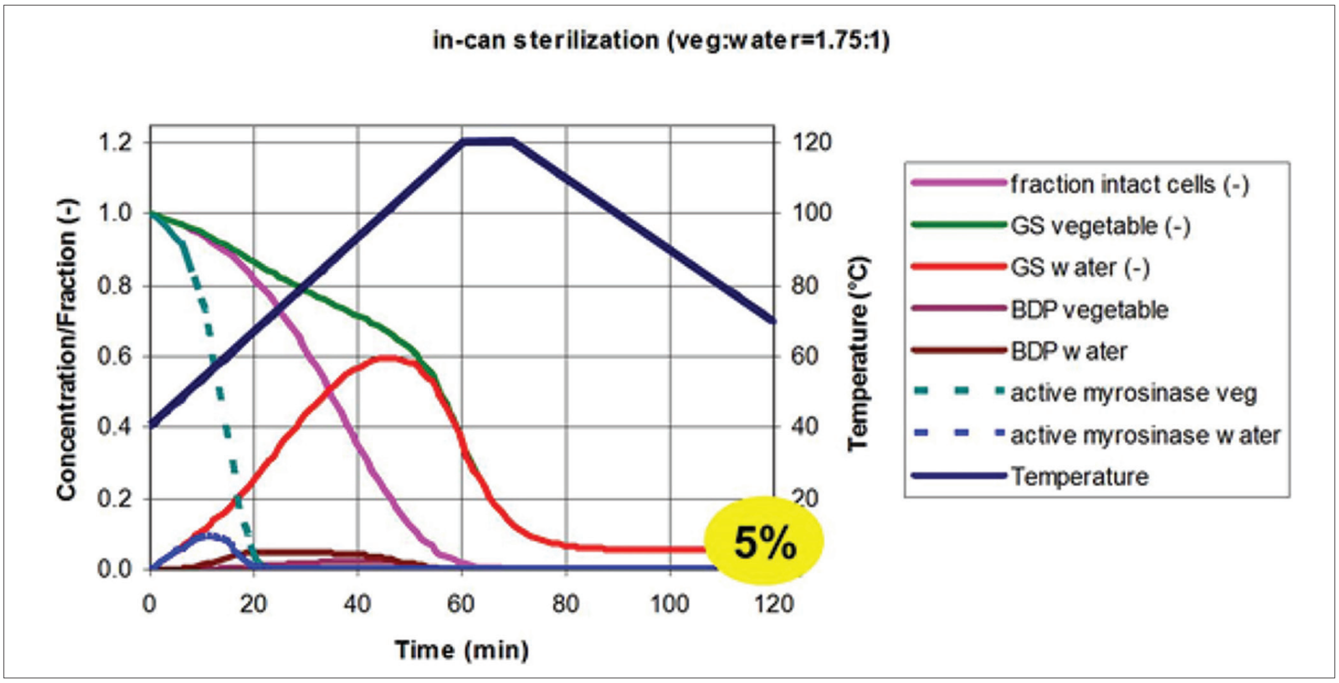
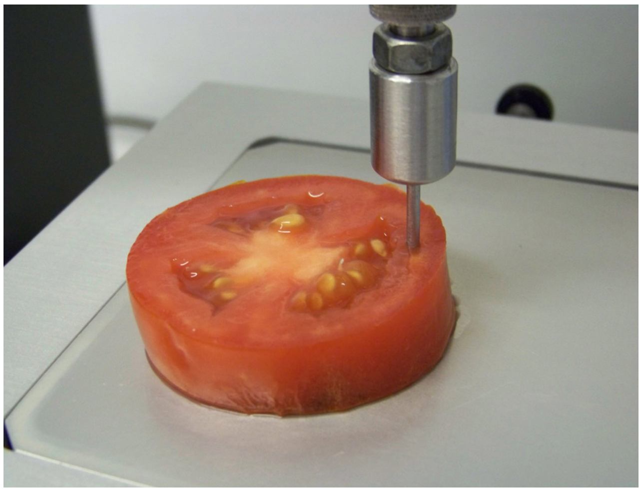


Figure 2. simulation results of the effect of a sterilisation process on the content of phytochemicals (GS) and breakdown products (BDP).

Prospects and challenges

The developed approaches for studying fruit and vegetables, as illustrated on the selected varieties and quality attributes in this workpackage, can serve as guidelines for studying nutritional and sensory-related product properties in fruits and vegetables from a much broader perspective.

With limited additional experimental efforts, the parameters of the developed thermal process model can be estimated. With these specific parameters the model can be applied to simulate and optimise the content of many phytochemicals within fruit and vegetable varieties.



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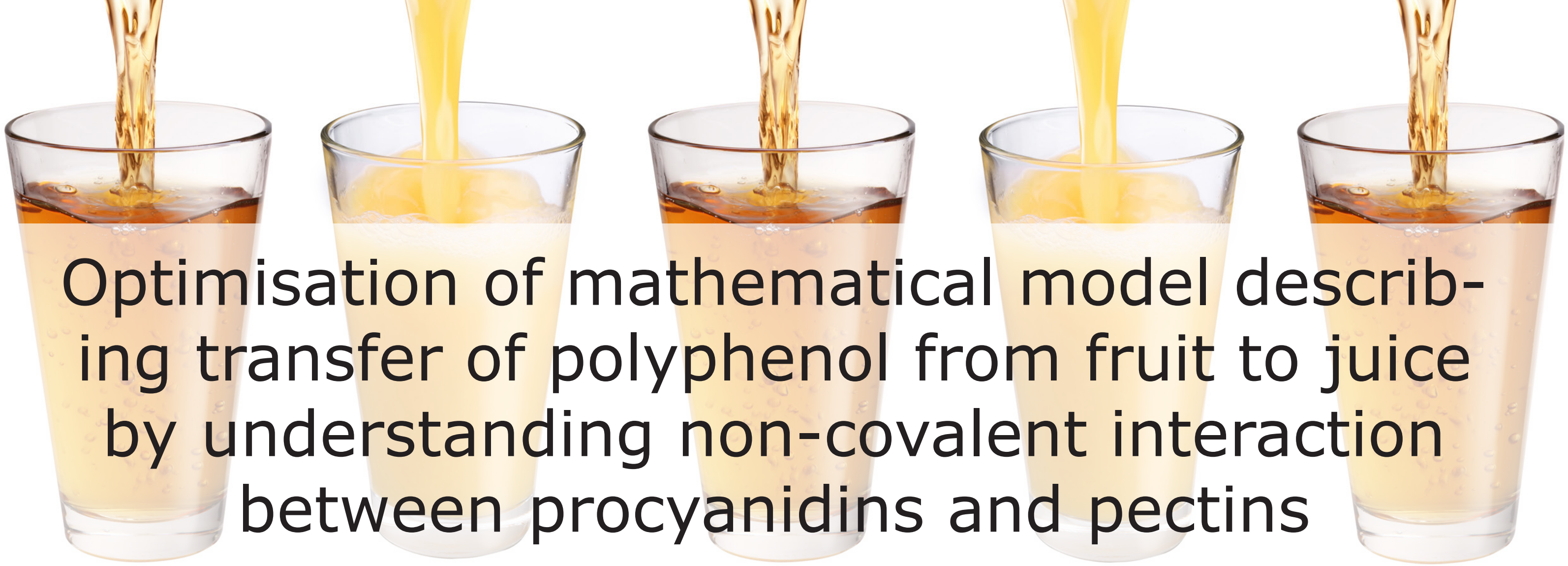

Optimisation of mathematical model describing transfer of polyphenol from fruit to juice by understanding non-covalent interaction between procyanidins and pectins

Non-covalent interaction between procyanidins and pectins

Procyanidins are the main phenolics in cocoa and many Rosaceae fruit, and play a major role in their bitterness and astringency, as well as their potential health benefits. Disruption of the natural matrix during processing and interaction between procyanidins and cell walls may have a strong influence on the release, bioavailability and biological activity of procyanidins. A mathematical model has been developed, which is already applicable to predict retention of procyanidins by cell walls, e.g. in juice extraction processes. However, it needs to be improved by adding the influence of pectin characteristics that are a degree of methylation and neutral side-chain composition, in order to be used by the food industry to enhance food quality.

Research aims and background

Polyphenolic compounds, including procyanidins, are commonly perceived to be found mainly in the vacuoles of plants, where they are separated from other cellular components. However, many may also be associated with cellular components, such as the cell wall, especially after cell injury when vacuoles rupture during processing. This results in the release of phenolic compounds which may then associate with cell-wall polysaccharides through hydrogen bonding and hydrophobic interactions. These interactions have a strong influence on the release but also on the bioavailability and biological activity of procyanidins.

The cell-wall capacity to bind procyanidins depends upon compositional and structural parameters, such as the contents and structure of the various cell-wall polymers, stereochemistry, conformational flexibility and molecular weight of procyanidins, and cell-wall and procyanidin concentrations. It also depends on the surrounding conditions, such as temperature, ionic strength or ethanol content. A mathematical model has been developed to describe the transfer of procyanidin from fruit to juice. Among the different polysaccharides classes (cellulose, hemicelluloses and pectins), pectins are those that have the greatest affinity for procyanidins. However, the mechanism by which procyanidins and pectins interact and the structural and compositional parameters that influence their association are not known.

Understanding the influence of structural and compositional parameters during procyanidin-pectin interactions may allow the initial model to be optimised in order to better describe the effect of mechanical processing on juice procyanidin concentration.

The model developed may be used by the food industry to identify the parameters influenced and to simulate them in order to optimise their process and enhance food quality.

Results and applications

The interactions between procyanidins and pectins were studied in detail by varying the composition of both procyanidins and pectins. Experiments compared B-type procyanidin from apples, with various degrees of polymerisation, to the different pectin substructures, such as homogalacturonan presenting various degrees of methylation, rhamnogalacturonan I with various neutral-sugar side-chains and rhamnogalacturonan II as monomer or dimer.

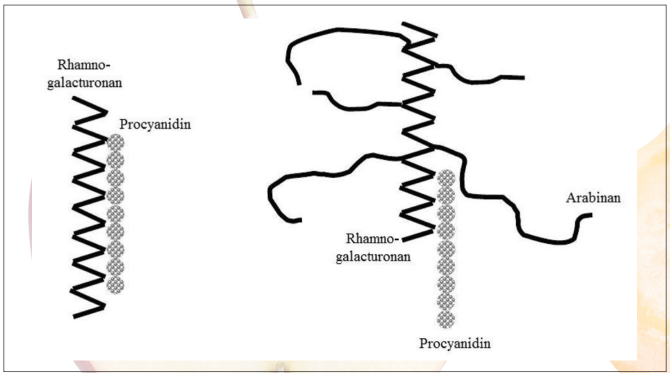

Figure 1: Neutral sugar side chains of pectins limit interactions with procyanidins

The affinity constants of procyanidin-homogalacturonan interactions in solution are highest when both the procyanidin degree of polymerisation and the homogalacturonan degree of polymerisation are highest. Procyanidins interacted with high-methylated homogalacturonan mainly through hydrophobic interactions.

Associations between rhamnogalacturonan-I fractions and procyanidins involved hydrophobic interactions and hydrogen bonds. No difference was found in association constants between rhamnogalacturonan I with different neutral sugar side chains and procyanidins with a degree of polymerisation of 9 was found. Nevertheless, rhamnogalacturonan I rich in long arabinan chains showed lower association constants, and rhamnogalacturonan without neutral sugar chains showed higher association with procyanidin with a degree of polymerisation of 30. Only very low affinities were obtained with rhamnogalacturonan II. It seems that the ramification state of rhamnogalacturonan I limits their association with procyanidins. This might explain some of the variation in the transfer of procyanidins from fruit to juice with maturation, as one of the maturation features is loss in galactose and/or arabinose from the cell walls. The influence of degree of methylation of pectins could now be integrated into the mathematical model in order to optimise it and could be used by the food industry to optimise the process to enhance food quality.

Significance and benefits

Interactions between procyanidins and pectins have been studied in detail and could now be integrated into the mathematical model describing the transfer of procyandins from fruit to juice after mechanical treatment. The result obtained could be used in the food industry to improve food quality.

Moreover, the process of fining for the removal of procyanidins for clarification and astringency reduction in wines traditionally uses protein extracts in its application. The wine manufacturer could use the result obtained here to optimise their fining treatment by using fibres as an alternative to fining with proteins in winemaking.

Successful applications

The impact of temperature and duration of pressing that were identified in the initial model have been validated by the *Institut Français des Productions Cidricoles* for use in cider apple pressing.

Prospects and challenges

The two main research prospects at this point are:

- Application to understanding the impact of maturation on procyanidin extraction, with a thesis starting on that topic (applied to pears due to their simple phenolic composition and existence of a large range of degrees of polymerisation);
- Validation of the impact of the interactions on the colonic fermentation patterns for cell-wall – procyanidin complexes.

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Tomato-processing method modifying the bioaccessibility of its lycopene

Modulation of tomato carotenoid accessibility through appropriate processing

The tomato product is the main source of lycopene in our diet. Its accessibility, i.e. its liberation from the food matrix, and its bioavailability, i.e. the subsequent transfer to its cellular targets at the end of the digestive process, determine its true health benefits against several cancers and degenerative diseases. The accessibility is greatly influenced by the physical properties of the food matrix and especially, it is enhanced in cooked products. Hot-break (HB) and Cold-Break (CB) treatments used by industries to control the viscosity of tomato purees was shown to partially control the ability of the tomato lycopene to diffuse from puree to an oil phase. Food particle size and lycopene/matrix interactions were identified as the main factors affecting the diffusivity.

Research aims and background

Modelling the lycopene availability in response to processing was the objective for the tomato model within the DREAM project. Lycopene has already been identified as a health-benefit product. The initial step of the digestive process for such lipophilic micronutrients consists of diffusing from the plant matrix to reach the lipid phase of the emulsion of the bolus. For lycopene, the major tomato carotenoid, bioavailability is known to be enhanced in cooked products. Indeed, while most industrial tomato processes do not much modify the overall lycopene content, its bioaccessibility can be greatly affected. The aims of the research were therefore to identify the factors limiting lycopene diffusion and how these factors are modified by the processes applied to fruits. Controlling the carotenoid bioaccessibility by the process is a challenge for the fruit and vegetable industries in order to boost the nutritional value of their product.

Results and applications

The starting hypothesis to set up the model linked particle sizes to the ability of lycopene to diffuse to an oil phase. Tomato is a filled-cellular model, and then: 1- The smaller the particles generated by the process (grinding and cooking temperature), the quicker the diffusion of one nutrient, according to Fick's second law and 2- Depending on the numbers of intact barriers (i.e. intact cell-walls or membranes) that may remain in the matrix between the lycopene and the intestinal membranes. The case study chosen for the project was that of two tomato purees obtained either using cold-break (CB) or hot-break (HB) processing, which exhibited a contrasting lycopene diffusion rate when they were mixed with oil in a standardised protocol. Our first results indicated that no clear difference in particle sizes could explain the contrast that we observed (Page et al., 2012). Wet-sieving experiments indicated that most of the HB/CB difference was explained by the behaviour of the smallest particles (Figure 1). Using one standard commercial tomato juice we also studied in more detail , the other physicochemical parameters affecting the lycopene diffusion, including pH effect, temperature and how much the diffusionis including pH effect, temperature and how much the diffusion was modified when tomato purees were mixed with an emulsion instead of pure oil. For the latter, the rate of the diffusion rose, but the partition factor of the lycopene between puree and oil was not greatly affected. Furthermore, it was reduced by certain interactions with the emulsifier (Degrou *et al.*, 2013). These last results indicated that molecular interactions between lycopene and other components of the matrix may affect the availability of the lycopene, making the model more complex than expected, and making a set of new experiments necessary in order to recover variables that should be implemented in the tomato model.

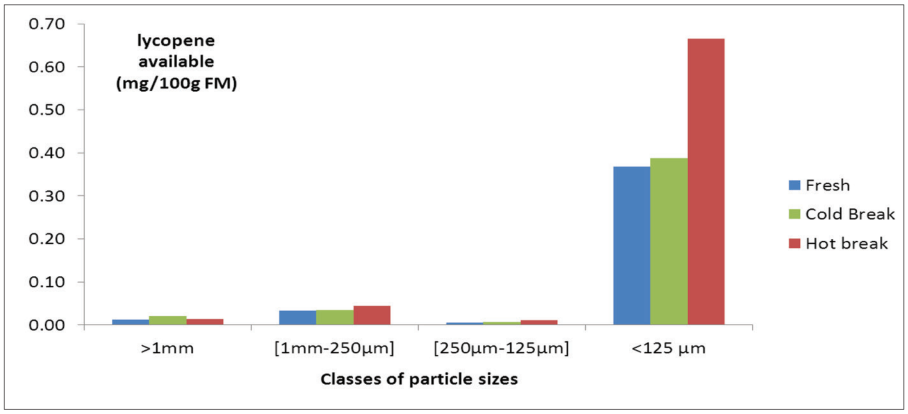

Figure 1. Threshold effect on particle size. Most of the available lycopene is included in the smallest class of particle sizes (limit at 125µm, i.e. roughly the average fruit cell size).

Prospects and challenges

At the end of the DREAM project, the main factors affecting the diffusion of lycopene from the matrix have been identified. Modelling now needs to be performed in order to set up a mathematical model that could predict the availability of the carotenoid from the processing parameters. Moreover, the identification of the smallest particles as the main factor of the contrast between HB and CB puree make it a further research challenge to understand the biochemical change in fruit tissues that leads to lycopene release. The structural description of these small particles is a challenge.

Significance and benefits

From the DREAM results, it is now clear that carotenoid bioaccessibility can be deeply modified by the processing methods, particularly if the very first temperature ramping (i.e. during the first minutes of heating, which correspond to the main difference between HB and CB purees) is efficiently applied, leading to a quick rise in the initial temperature. In this case a significant quantity of carotenoid is made bioaccessible.

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Proteinous cellular network model

Is this information important for me?

Consumers	●	●	●	○	○
Food Industry	●	●	●	●	●
Regulatory Authorities	●	●	●	●	●
Scientific Community	●	●	●	●	●

artificial mimetic gel model
heath impact on mimetic gel
microscopic image analyses of meat tissues

WP-3
Workpackage

Introduction to WP3

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Aims and background

Heating is one of the most important processes applied to animal tissues, since meat is usually consumed after cooking at industrial or domestic scale. This physical process induces structural and chemical changes that can affect the nutritional value of meat. The work developed in WP3 focused on meat and the impact of heating on its protein physicochemical changes and digestibility. Homogeneous muscle models are needed to evaluate the effect of different processing parameters on the nutritional quality of meat. One objective was to define the best experimental models representative of meat products by selecting and assessing meat tissues or by creating artificial mimetic samples. Another objective was to evaluate the effect of compositional and structural properties of proteinous foods on the reactions promoted by heating.

Prospects

Two models were developed: three meat categories (pork muscles) differing in their structure and composition, and a mimetic model (suspension of myofibrillar proteins). The pork muscles allowed their structural variability to be characterised by means of imaging and histology, a non-invasive noble method (MRI) to be set up, and heat-induced protein changes linked with *in-vitro* digestion to be identified. The mimetic model allowed the evaluation of the effect of iron content and temperature on the kinetics of myofibrillar protein oxidation and denaturation. A mathematical 'stoichio-kinetic' model was developed to investigate, based on calculations, the main chemical reaction routes involved in protein changes.

Task 3.1

Rationalisation of meat tissue selection. Three meat categories were characterised in composition and structure and two distinct muscles were selected (Longissimus thoracis and Masseter). Main raw meat parameters associated with the nutritional target property (*in vitro* protein digestibility) were identified. Guidelines to select categories of raw meats based on *in vitro* digestion were developed.

Task 3.2

Prospective investigation to build artificial mimetic gel models representative of animal tissues. Meat tissue structure could not be represented using gel models. Thus, kinetic laws which govern changes in proteins' physicochemical state induced by heating were measured using an *in vitro* model: myofibrillar proteins in a buffer with the various compounds that can be found in different types of meat: Fe, ascorbate, oxidants and anti-oxidants. Heat treatments were applied at 45°C, 60°C, 75°C and 90°C for up to 120 min.

Task 3.3

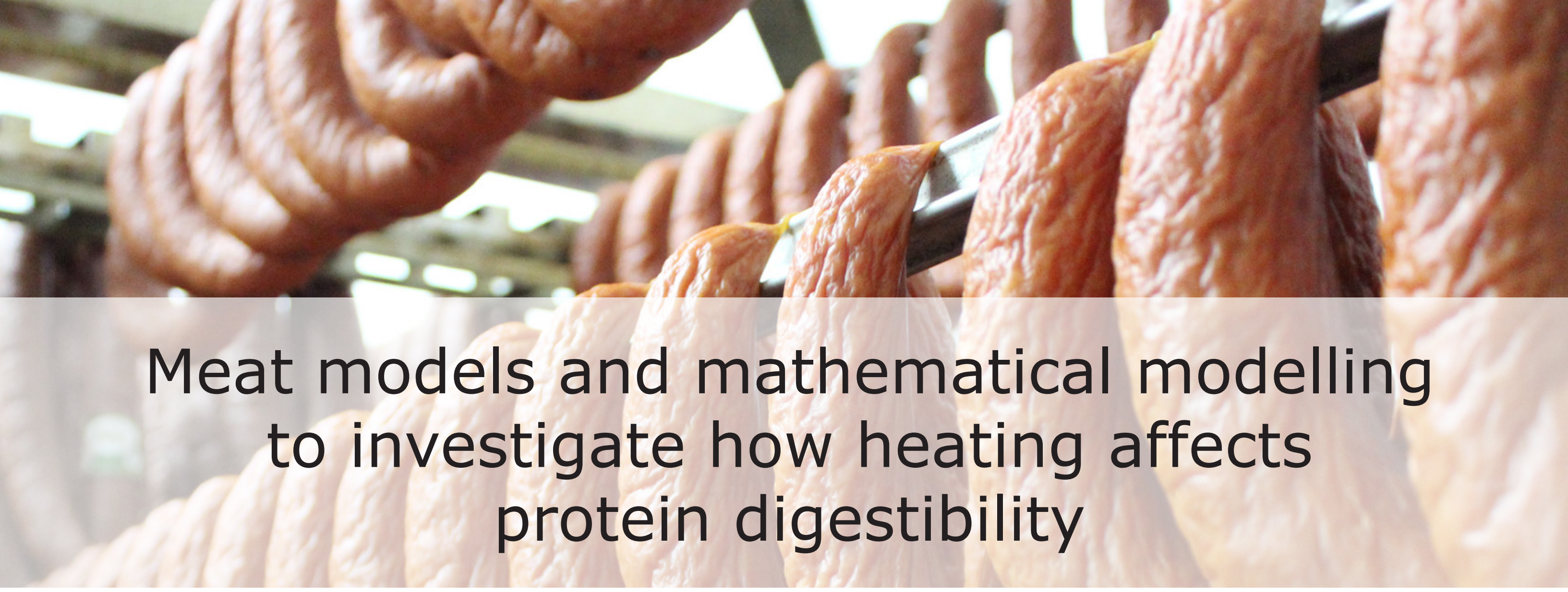
Microscopic image analyses of different typical meat tissues to assess their structural characteristics. Methods and algorithms to semi-quantify in situ the morphology and distribution of cell types in muscle tissue from histological images were developed and applied to the meat categories. It was shown from statistical analysis that connective tissue and fibre type distributions vary considerably with muscles and / or collection areas. The overall structure was also assessed from MRI images using a Diffusion Tensor Imaging technique.

Task 3.4

Use of artificial gel models to understand reaction routes promoted by heating of animal tissues. While thermal denaturation can be considered as a unique first order reaction, oxidation is more complex since many interactive chemical reactions are involved. A mathematical model that accounts for this complexity was successfully developed to analyse and predict the effect of (i) iron content which differs depending on the meat type, and of (ii) the heating conditions through the time-temperature couples.

Main outcomes

The physical and mathematical models developed in WP3 proved to be useful tools in order to evaluate the impact of heating on *in-vitro* protein digestion. These models could be used to evaluate the impact of other conditions or processes applied to proteinous foods on nutritional, sensorial or technological target properties of scientific or industrial relevance. Further research should focus on sensory properties using the defined meat categories, and the mimetic and mathematical models will be progressively completed to include all the possible compounds in meat.



Meat models and mathematical modelling to investigate how heating affects protein digestibility

Models to better analyse and control meat cooking

Meat cooking is an important process applied at industrial or domestic scale that has a nutritional impact. Two experimental models were developed to investigate how meat characteristics and heating conditions, respectively, affect the nutritional quality of meat: (1) meat categories that differ in their structure, composition and metabolic type, and (2) a mimetic model composed of a suspension of myofibrillar proteins, a composition which can be modified by adjusting the concentrations of major meat compounds: iron, oxidant and antioxidant enzymes. In parallel, a mathematical model called 'stoichio-kinetic' was developed to integrate knowledge. The model is composed of differential equations that represent all elementary reactions. Model predictions agree with the experimental measurements. This approach can be applied to other meat processes and sensorial properties.

Research aims and background

Apart from a few exceptions, animal tissues (meat and fish) are eaten after being cooked. Heating is therefore the most important process applied to this type of food either at industrial or domestic scale. This physical process induces structural changes, at microscopic and macroscopic levels, and promotes protein changes that can have nutritional impacts.

A great number of works have been carried out on meat and fish products to assess the impact of production parameters (genetic, breeding, feeding, slaughter conditions, processing conditions, etc.) on meat product quality. This is usually done by comparing samples that undergo a treatment specific to a reference sample. However, in technological or laboratory tests it is rather difficult to satisfactorily control and measure all parameters that can have an impact on a specific output. This often prevents the generalisation of conclusions of a particular study and leads to contradictions between studies because of the interactions between sample properties and phenomena involved.

With the aim of improving the generalisation of laboratory results, our work focused on the of experimental and mathematical models. We worked in two main directions:

- To define the best way to prepare samples representative of meat products either by selecting and assessing meat tissues or by creating artificial mimetic samples;
- To evaluate, using the above meat models and mathematical modelling, the effect of meat tissue characteristics and cooking conditions on the reactions which are promoted by heating and can have nutritional consequences.

The tools that were set up during the DREAM project can help engineers to develop precooked or cooked industrial products with better nutritional properties. They can also be used by scientists to investigate a larger range of processing conditions: other meat tissue characteristics and other processes.

Results and applications

Parallel works were carried out to develop two complementary experimental models: (1) extreme examples of meat tissues representing three "meat categories" that differ in their structure, composition and metabolic type (Realini *et al.*, 2013 a & b), and (2) a mimetic model composed of a suspension of myofibrillar proteins (Promeyrat *et al.*, 2013 a &b).

Changes in protein state and nutritional value were related by applying two extreme time-temperature heating couples (10 min, 75°C or 45 min, 90°C) to the two extreme meat categories. The nutritional value was evaluated from in-vitro digestion tests using either gastric pepsin or trypsin and α-chymotrypsin. It is clear from Figure 1 that the variables associated with protein changes in conformation and those linked with oxidation are positively and negatively correlated, respectively, with rates of *in-vitro* protein digestion. The mimetic model was developed to avoid the confusing effect of uncontrolled biological variability generally observed in animal tissue. Its composition can be modified by independently adjusting the concentrations of the major chemical compounds in meat (Figure 2): iron, oxidant and antioxidant enzymes. This experimental model makes it possible to easily determine kinetic laws governing changes in protein state and to assess to what extent the kinetic parameters are affected by initial product characteristics and cooking conditions. Thermal denaturation can be modelled by a unique first-order reaction. Oxidation is more complex (many interactive chemical reactions that are differently affected by pH and temperature). Thus, a mathematical stoichio-kinetic model that accounts for this complexity was successfully developed (Promeyrat *et al.*, 2012). Simulation calculations make it possible to analyse and predict the effect of (i) iron content, which differs from one meat to another and of (ii) the heating conditions through the time-temperature couples (Figure 3). The predictions are accurate enough to be used for practical purposes.

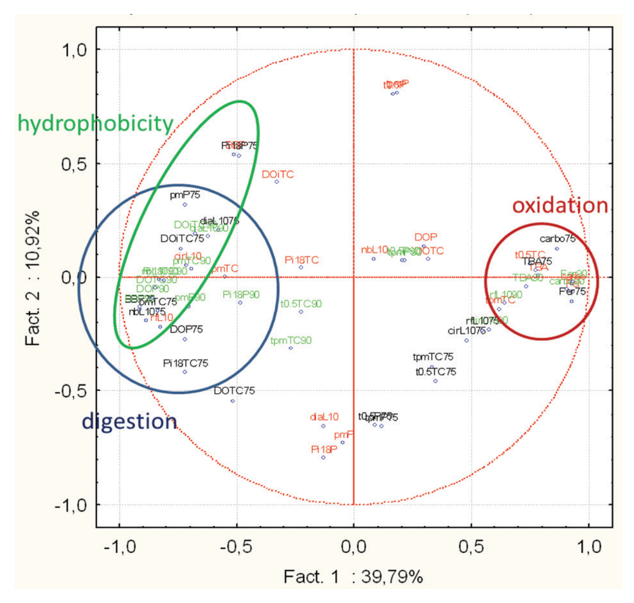


Figure 1. Two meat categories were cooked for either "10 min, 75°C" or "45 min, 90°C". A Principal Component Analysis showed that protein denaturation (hydrophobicity) and oxidation were correlated to digestion rates measured *in-vitro*.

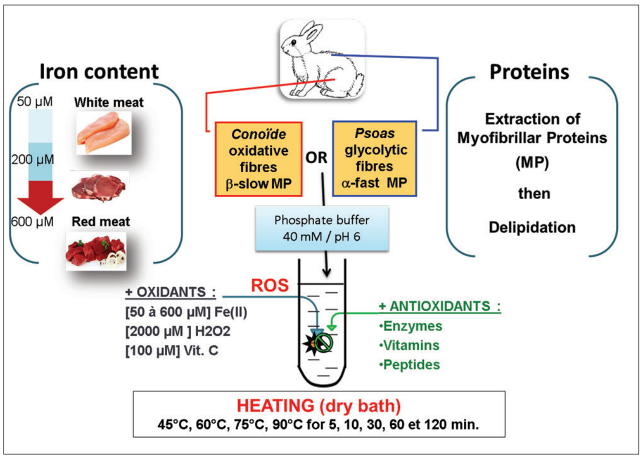


Figure 2. Kinetic laws of protein denaturation and oxidation were determined using a mimetic model: aqueous suspension of pure myofibrillar proteins, control of both physico-chemical environment (pH, ionic strength) and compound contents to mimic many kinds of meat.

Significance and benefits

Our collaborative work provides a sound basis to build a mathematical tool, or simulator, that can predict the effects of various processes such as chilled storage, modified atmosphere conditioning, curing, heat treatments, etc. on the sensorial and nutritional qualities of processed meat products.

This approach requires new scientific knowledge to be progressively added to improve our simulator by assessing parameters associated with each individual phenomenon or chemical reaction. The strategy based on experiments with both realistic and mimetic models is certainly the best way to achieve this goal.

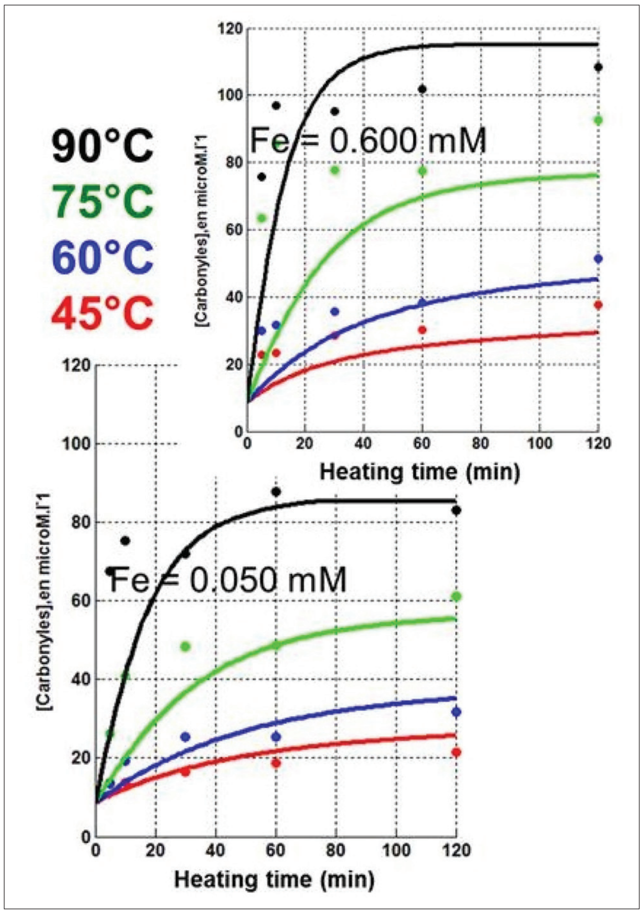


Figure 3. A mathematical model based on differential equations representing numbers of interactive chemical reactions can predict kinetics of protein changes; for example, carbonyl production according to Fe content and heating conditions.

Prospects and challenges

We took a major step forward in predicting the impact of practical cooking conditions on protein denaturation and oxidation through the use of both experimental and mathematical meat models. These phenomena affect protein digestibility but also various other technical and sensorial qualities. For example, the kinetics of protein denaturation is certainly linked to cooking losses and oxidation of myoglobin is known to determine colour. Thus, our strategy could be applied to many other targets. Using a mathematical model is essential to extrapolate laboratory results to industrial process conditions. For example, protein denaturation and oxidation can now be predicted for time-variable cooking conditions, since all the reactions are represented by differential equations. Moreover, these calculations can be easily inserted into other mathematical models that predict the time evolution of the temperature distribution within meat pieces during cooking (Heat-transfer mathematical model based on Finite Element technique).

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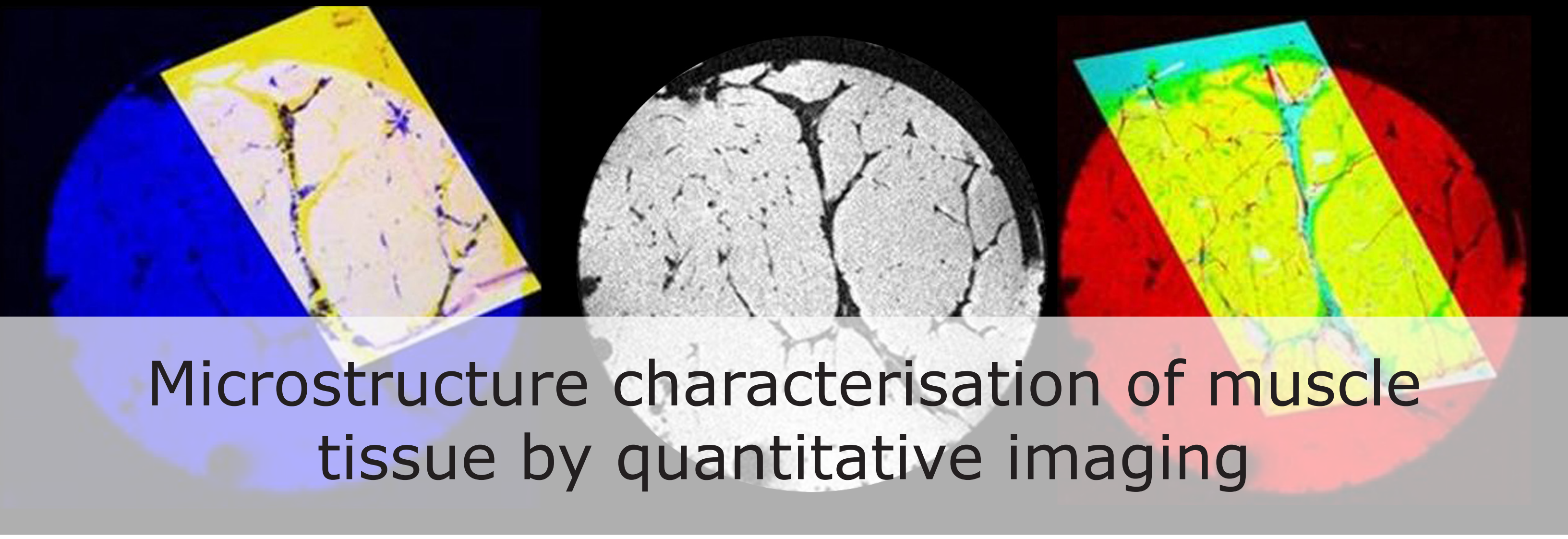

Microstructure characterisation of muscle tissue by quantitative imaging

In situ high resolution imaging of meat tissue microstructure by MRI using Diffusion Tensor Imaging (DTI)

Meat results from the post-mortem transformation of animals' skeletal muscles. These muscles are mainly composed of water (75%), muscle cells of three different types (I, IIA and IIB), connective tissue and fat (3 to 5%). The muscle is strongly organised in fibre bundles more or less aligned depending on its type and functionality. The muscle's structural architecture can be roughly modelled as a square lattice array of fluid-filled cylinders surrounded by fluids. With the MRI technique used here, we look at diffusion: the physical parameter related to the local water motion. Diffusion in tissues differs from diffusion in free solutions because compartments made by fibres hinder and restrict water motion. The structural meat architecture is hereby assessed, not directly and destructively as done by tomography microimaging (microscopy) but indirectly and non-destructively.

Research aims and background

While diffusion quantitative magnetic resonance imaging is a generic method for assessing Brownian random motion of molecules, it has been mostly applied to water, which is abundant in tissues and visible by MRI. Both muscular-cell size and muscular-cell shape as well as interactions within the different compartments of muscular cell can influence the diffusion properties. If the structure is anisotropic, as in muscle, water diffusivity also displays anisotropic behaviour. As muscle, and then meat, is highly organised, the diffusion of water is facilitated in the fibre direction, meaning that, in a group of fibres having the same direction, the apparent diffusion coefficient is: maximum in the fibre direction and minimum orthogonally to the fibre direction. We decided to make use of this anisotropy to indirectly and non-destructively characterise meat microstructure. The anisotropic water diffusion can be modelled voxelwise using ellipsoid by means of a first-order tensor, according to Diffusion Tensor Imaging (DTI). Moreover, by varying the intensity of the magnetic gradient field, one can obtain the diffusion decay. This decay is then fitted by a bi-exponential curve, at each voxel, in order to obtain quantitative mapping at low- and high-gradient field values, exhibiting hindered and restricted diffusion, respectively. One initial objective was to obtain high-resolution imaging of meat tissue microstructure *in-situ* by MRI using diffusion tensor imaging (DTI) at different b-values in order to assess by quantitative imaging the fibre structure of muscle tissue at the mesoscopic scale. Moreover, knowing that the muscle structure can be roughly modelled as a square lattice arrangement of fluid-filled cylinders surrounded by fluid, we can plot the theoretical diffusion decay. This plot exhibits deep gaps in attenuation curves that were directly correlated to the geometry of the cylinder lattice.

We thus attempted, in a second objective, to determine whether such attenuation behaviour can be found in the real meat structure made of aligned fibres. The tools that were set up in this part of the DREAM project can be used as input for creating artificial mimetic meat samples and to feed mathematical models.

Results and applications

Regardless of the sample orientation relative to the magnet, diffusion-weighted signals were obtained with gradient fields applied in six directions and then a calculation (tensor diagonalisation) was performed in order to consider diffusion in the meat fibre-oriented frame. The huge advantage of this approach is that the diffusion (closely linked to the spatial fibre organisation) is then assessed free of the effects of local fibre orientations. After diagonalisation, the first eigenvector corresponds to the main fibre-axis direction. The second and third eigenvectors correspond to the two orthogonal directions of the fibre axis. The same process was applied to each six-direction dataset at increasing b-values (in the range 100-20,000 s/mm²).

Quantitative mapping

Parallel and perpendicular decays both deviate from the Gaussian diffusion, expressed by a mono-exponential decay since they follow a bi-exponential shape (Figure 1). This highlights the hindered and/or restricted diffusion of water, out of and into muscle fibres, or exchanging between the two compartments. Diffusion maps reveal details due to spatial variations of structure at a resolution much below the acquisition resolution.

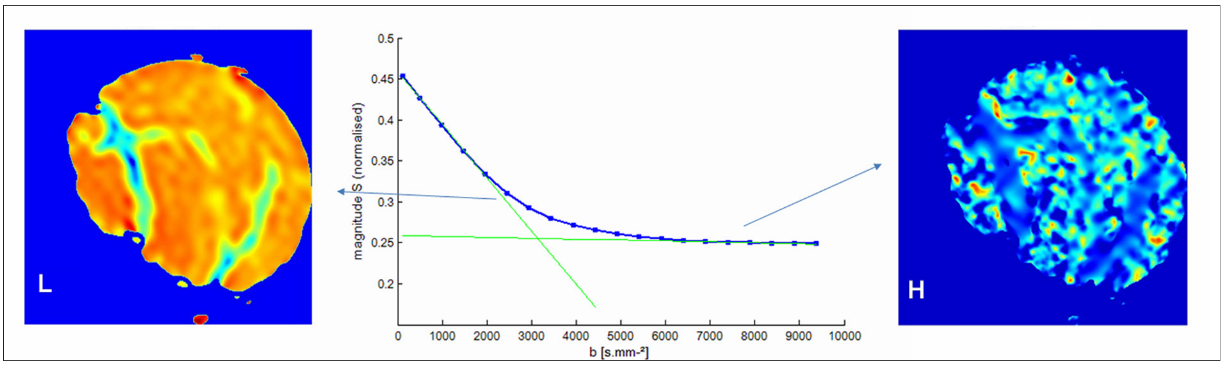

Figure 1. Diffusion-weighted intensity attenuation images from the trace of the diffusion tensor matrix. Image L (left) is at low b-value, image H (right) is at high b-value, inhibiting high diffusion corresponding to hindered diffusion and low diffusion corresponding to restricted diffusion, respectively.

Identification of structural and morphologic components

After MRI experimentation, samples were frozen at -180°C to avoid muscular cell degradation and microscopic histological observations were performed. After spatial registration, histological images were first superimposed onto high-resolution images (susceptibility-weighted gradient-echo images, with 300×300 voxels) to identify morphologic components (fat/collagen network), and subsequently superimposed onto quantitative diffusion maps (Figure 2).

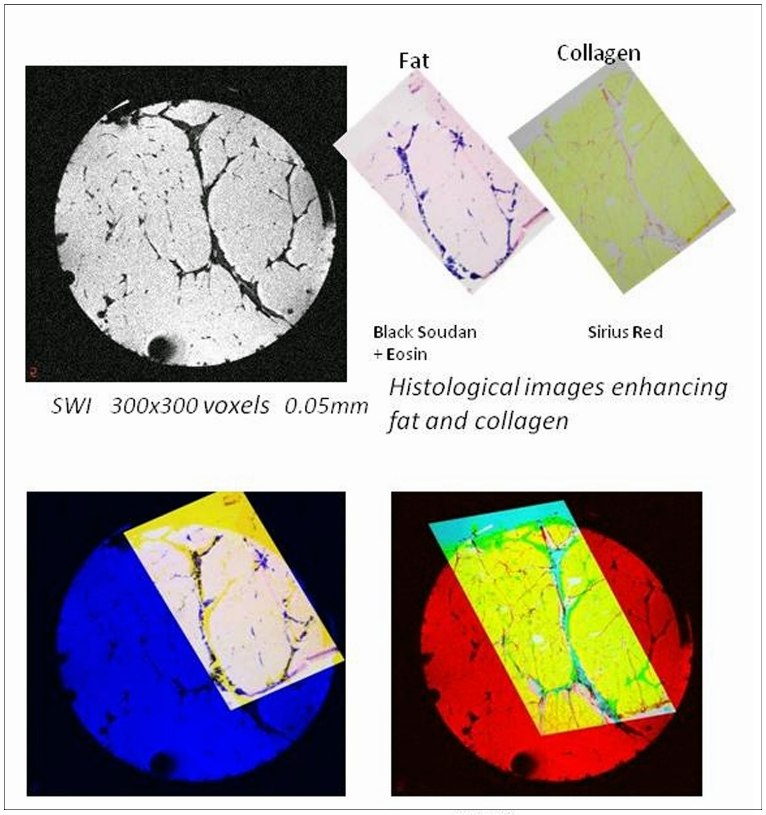

Figure 2. Superimposition of histological and diffusion image.

Relationship between diffusion and muscle fiber types

To assess the architecture of the muscle, we investigated the relationship between diffusion and muscle fibre types. Histological cuts (approximately 1mm x1mm) were observed after histoenzymological ATPase staining with pH 4.35 preincubation. At low b-values, diffusion parameters seem to correlate with the metabolic characteristics of meat fibres, as highlighted by photomicrography of areas characterised by histoenzymological ATPase staining (Figure 3).

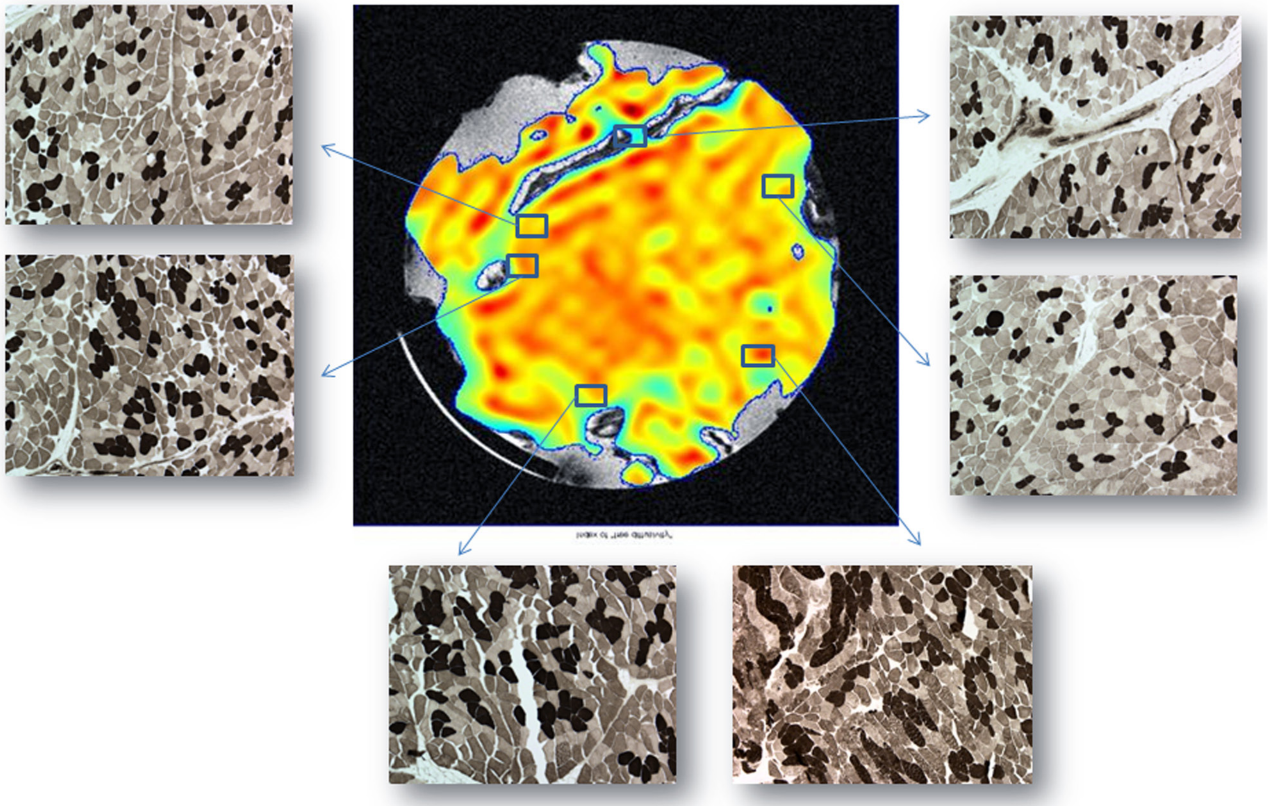

Figure 3. Superimposition of histoenzymological ATPase stained and diffusion images. On the histoenzymological images the three intensities are black (type I), white (IIA) and grey (IIX plus IIB). Diffusion is mapped with a blue/green to orange/red scale.

Variability of the dimensions of structural components

Less deep minima amplitudes on acquired data in the homogeneous region are observed compared to the prediction of the mathematical models. The experimental data plot deviates from the theoretical plot mainly due to the heterogeneity in the fibre diameter, the lack of strict parallelism of the fibres and also perhaps the lack of strict impermeability of the fibre membranes.

Significance and benefits

It is essential in the building of a mimetic model where structural components are involved to precisely access these components *in-situ* on real material. The tools that were set up in this part of the DREAM project and results describing structural meat components can be used as input for creating artificial mimetic meat samples and could be applied to many other targets. We have showed that characterising the behaviour of water diffusion within a voxel provides a means for describing the inner microstructure at a cellular scale, taking into account apparent diffusion coefficients measured in muscle. Using the anisotropy of water diffusion due to the highly fibrillar structure of meat, we modelled this diffusion in three dimensions using tensors. We used Diffusion Tensor Imaging (DTI) with different b-values to obtain high-resolution diffusion parameter mapping of tissue, which were registered to high-resolution susceptibility-weighted gradient-echo images and histological images to determine whether relationships existed between meat microstucture and diffusion observed at a meso-scale.

Prospects and challenges

The results of this research are a step towards the construction of realistic food models such as meat and will make it possible to feed the models built in the other workpackages. Promising results were obtained showing structural details correlated with metabolic characteristics. To the best of our knowledge, it is the first time that a scatter-like behaviour has been observed in a biological matrix, which seems very promising for quantifying structural information from the resulting diffusion attenuation plots. Future efforts will be focused on the differentiation within type of meat muscle and meat fibre types and on the variability of the structural components. Furthermore, developed methods could be applied on other food products.

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Combined gelled/dispersed/aerated systems model

Is this information important for me?

Consumers	●	●	●	○	○
Food Industry	●	●	●	●	●
Regulatory Authorities	●	●	●	●	●
Scientific Community	●	●	●	●	●

WP-4
Workpackage

chesse model development
additional research on existing dessert model

Introduction to WP4

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Task 4.1

The objective was to produce and characterise a range of gelled/dispersed aerated generic model foods. The primary model was a dairy dessert that could be used for risk assessment and was tested for use in following lipid oxidation. The changes in properties of the dessert were described as a function of the ratio of caseins to whey proteins.

Task 4.2

This task focused on producing a range of model cheese systems that could be used for assessing the effect of changes in formulation or processing on industrially-relevant parameters. In particular, the effect of salt reduction was assessed in the micro-cheese, the generic cheese and the standardised pilot-scale cheese-milk models.

Prospects

At the start of the project there were no gelled or dispersed model systems that could be consistently reproduced and that could be made widely available for testing nutrient, allergen or toxicant release, microbiological safety, etc.

Therefore, we aimed to produce well-characterised, realistic, food models for these types of food systems, including cheeses and desserts, that could serve as tools for harmonising food quality, safety and nutrition research on these types of food products.

We also aimed to produce mathematical models that could relate model composition such as fat content, protein ratio and processing to model functionality such as nutrient release and texture.

Aims and background

The two main models produced from this WP both have great potential for the future but the development of the models also leaves a number of questions unanswered.

The standardised cheese-milk model is already used by Actalia in the TeRiFiQ project and a simplified version was developed by Soredab for use with SMEs who do not have the expertise or equipment to use the complex model. Additionally, results from the dairy dessert model are being combined with other data from the literature to build an integrated knowledge model of protein-based emulsion systems that will be much more predictive in nature.

Main outcomes

This workpackage was split into two tasks, each looking at a different food group, namely dairy dessert and cheese. For the main dairy dessert model, three kinds of rheological behaviour and four different interfacial structures were characterised. In the first group, the emulsions were liquid, showing no connections between droplets.

In the second group the emulsions were structured, the droplets being weakly connected by aggregated WP .

In the third group the emulsions gelled, the droplets being connected by CM/WP complex or in other cases by aggregated WP. In the same task the impact of enzymatic cross-linking of the protein was demonstrated and in a slight variation on the basic model the impact of homogenisation pressure on the textural properties of cream cheese was also demonstrated.

The studies on cheese models yielded a generic cheese model for studying the effect of the composition of texture and bacterial growth. The use of a micro-cheese model for high-throughput screening of bacterial growth was also demonstrated.

Finally, the primary cheese model yielded a robust protocol for the standardisation of the milk used for pilot-scale production of experimental cheeses with very low variability. The usefulness of the approach was demonstrated for a wide range of cheese types including Camembert, Brie and Swiss cheese.

The Dairy dessert: a model for designing tailored interfaces in food systems

Composition and structure of interface impacts texture of emulsions

The main objective of this work was to understand the impact of interfacial composition and organisation on the connectivity between fat droplets and the microstructure of oil-in-water emulsions.

Four kinds of object were obtained by different processes applied to protein solutions containing various protein ratios. Their different properties led to competition between these objects at the interface, generating four types of structure with different connectivity, leading to various rheological properties: liquid, structured or gel. In complex dairy desserts, only the presence of aggregated whey at the interface increased the firmness of these desserts. When emulsions and dairy desserts were enriched in PUFAs, the oxidation of lipids remained low after two months' storage at 4°C.

Research aims and background

Most processed foods contain gels and dispersions of some sort that consist of small particles such as fat or protein dispersed in another medium. There are currently no gelled/dispersed model systems that can be consistently reproduced and that can be made widely available for testing nutrient, allergen, toxicant release, microbiological safety, etc. The work described here addresses this issue with a standardised dairy dessert model. The production of the dairy dessert is built on experience at IFR (UK), INRA and Soredab (France) in studying and understanding proteins/surfactant interactions in emulsions and foams, and fat composition, and on the use of biopolymers such as starch or pectin as thickening/gelling agents. We hypothesised that changes in protein structure caused by heat treatment could induce different structures of the interfacial layer (difference in thickness and in homogeneity) with or without disulfide bridges.

These different morphologies would then have an impact on the emulsion structure and texture, which could moreover affect the release and bioaccessibility of nutrients contained in fat (Poly-Unsaturated Fatty Acid ω-3, for example) or the digestibility of proteins. Consequently, the aim of this study was to evaluate the combined effect of heat treatment and CM/WP ratio change on the structure of nterfaces, in relation to the impact on the texture of O/W emulsions.

To that end, our strategy was to generate emulsions with a range of different, well-defined interfaces and combining different compositions (CM-to-WP weight ratio: 80:20 to 12:88) and heat treatment of milk proteins (60°C or 80°C).

Results and applications

The results of the work on the dairy dessert have been published in a series of papers from INRA Nantes and INRA Grignon (Foucquier *et al.*, 2011; Surel *et al.*, 2013). The way the dessert model is made is shown in Figure 1. Initial measurements determined the mean size of the casein micelles (CM) to be 140-160nm regardless of processing temperature (60°C or 80°C), whereas the whey protein (WP) increased in size from 6 to 100nm as the processing temperature increased.

The emulsion droplet size was remarkably insensitive to either CM/WP ratio or temperature.

The primary controlling factor of the model was the interfacial composition as a function of CM/WP ratio and processing temperature. When the ratio was below 0.2, the interface was dominated by WP and at 0.2-0.3 there was a minimum in the amount of protein adsorbed to the interface. At CM/WP ratios above 0.3 the interface was dominated by the CM and the effect was more marked at higher temperature. These differences in interfacial composition also had a marked effect on the interactions between the droplets and thus the rheological behaviour of the emulsions.

The overall effect is shown in Figure 2, in which the first group with a liquid texture consists of emulsions whose proteins were treated at 60°C regardless of the CM/WP ratio, and those with a ratio of 0.8 or more treated at 80°C. The second group producing a structured liquid with higher viscosity includes emulsions with CM/WP ratios from 0.19-0.26 treated at. The final group of gelled systems were all treated at 80°C and have CM/WP ratios of below 0.15 or from 0.3 to 0.5. In these last systems the emulsion droplets are all interconnected by aggregated protein causing the system to gel. In parallel with the experimental work undertaken to develop the physical model, a mathematical model was developed that aimed at predicting the texture of the final model based on a number of inputs, including the amount of casein and whey, the size of the whey aggregates, the processing temperature and the homogenisation pressure. From this information a number of internal variables are generated that provide information on the amount of adsorbed CM and WP, the amount of aggregated WP adsorbed and the emulsion-droplet connectivity. From these variables the structure of the resulting emulsion system can be predicted.

Equipment required in order to produce the model is relatively basic, comprising stirrers, heaters and an Ultra Turrax to make the pre-emulsion that is then passed through a high-pressure homogeniser capable of delivering 50 bar.

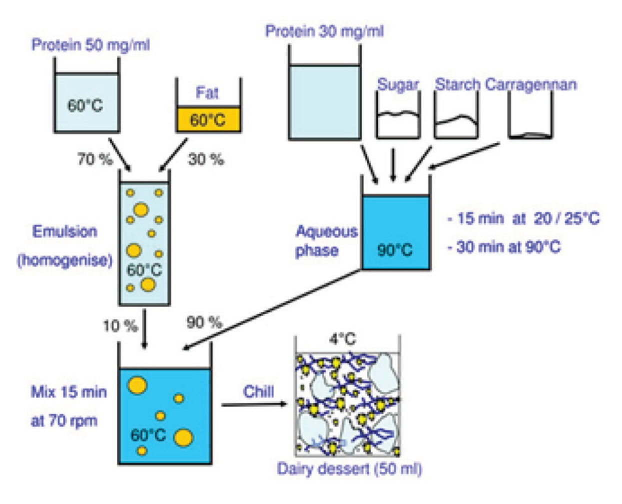

Figure 1. Flow diagram for the production of the Dairy Dessert.

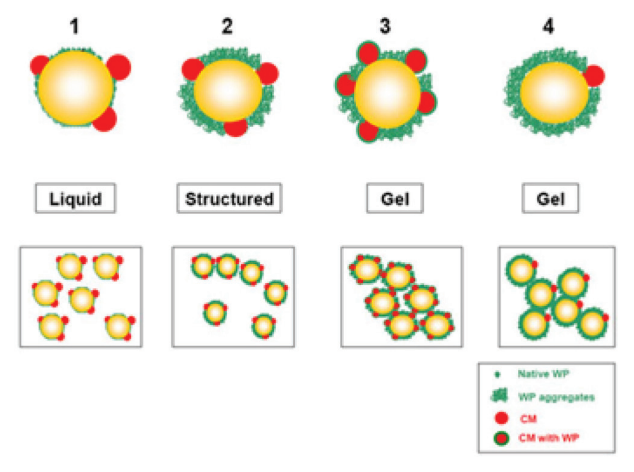

Figure 2. Schematic of the different structures induced by composition and processing.

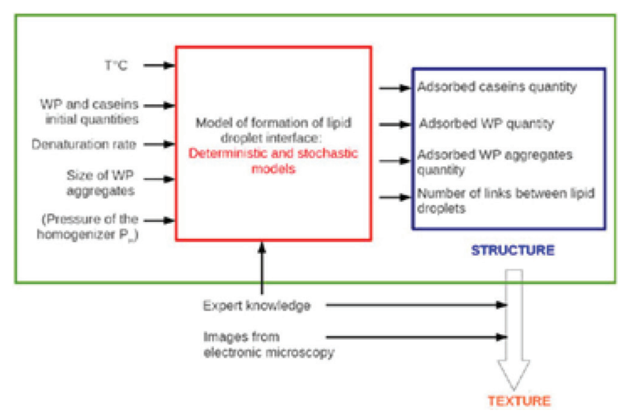

Figure 3. Schematic of the mathematical modelling approach used to link formulation and processing to texture.

Significance and benefits

This model offers the possibility of using a standardised dessert model with a range of textural properties. The texture of the dessert can be predicted from the amount of micellar casein and whey protein added and from the thermal treatment and the homogenisation pressure used to make the emulsion. The standardised and predictable nature of the model makes it ideal for use in risk assessment involving the growth of pathogenic or spoilage organisms or involving toxin contamination. In addition it is also suitable for use in studies on bioaccessibility or bioavailability using *in-vitro* or *in-vivo* methods, respectively.

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Prospects and challenges

This model has successfully been used to determine lipid oxidation rates after the incorporation of kiwiseed oil containing high levels of ω-3 polyunsaturated fatty acids into the formulation. No statistically significant differences were seen in the levels of oxidation after two months of storage at 4 °C, regardless of formulation or processing temperature.

Successful applications

The development of mathematical models able to predict the formation of structure and thus the texture of dispersed systems represents an interesting prospect for the future. It also offers the possibility of broadening the range of dispersed food systems that can be included in the modelling.

In particular, coordinated approaches to producing healthier food systems with lower salt and/or fat and/or sugar are becoming increasingly important. The development of standardised models of significant food types offers the possibility of designing healthier foods with the desired textural properties and shelf-life.

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A pilot-scale model for the reproducible production of soft cheese

A pilot-scale model for the reproducible production of soft cheese

A realistic cheese model (Brie-cheese manufactured with industrial technologies, Figure 1) was built as a tool for experimental studies on cheese. Great attention has been paid to the authenticity and repeatability of these small-scale models (around 1kg). Twenty replicates per cheese model were made to determine the repeatability of around a hundred state-variables and control-variables: from the milk composition to the cheese qualities. Their coefficient of variation was around 1%-1.5%. For each of these variables, statistical analyses were performed to characterise the dispersion of the data and the origin of the variability, in order to improve the models. Reliability of the models was confirmed in experiments dealing with the influence of salt content in cheese on Bifidobacteria in Brie-cheese.

Research aims and background

Many problems in the field of dairy research and development require the implementation of cheesemaking trials. These trials include technological topics such as process modifications, yield, raw material, spoilage microorganisms, sensory studies (effect of starter or adjunct cultures), nutritional questions (reduction of salt or fat content, decrease of the proportion of saturated fatty acids in fat and the use of probiotics and/or prebiotics) and food safety issues (survival of pathogens and presence of harmful chemicals).

However, cheesemaking experiments are expensive and time-consuming, even on a pilot scale. They require specific equipment and the required environmental conditions are difficult to control. Therefore, several alternatives have been suggested for experimental studies on cheese. The improvement of cheese models and the proposition of a strategy for the development of cheese models, as proposed in our study, are useful for the cheese industry and its suppliers (e. g. enzymes, lactic and ripening cultures, proteins, etc.). Indeed, cheese models are too often considered as black boxes in certain laboratories and as such their improvement of knowledge regarding dairy science. More particularly, experimental results on food safety (e.g. growth and survival of pathogenic bacteria in cheese) or on the cheese-milk quality are very important for cheesemakers and require suitable cheese models. The screening of ingredients for cheesemaking must also be performed using viable models.

Finally, the strategy of characterisation of the representativeness and repeatability can be applied to the pilot plant in the cheese factories.

Results and applications

Preparation of the cheese milk as outlined in the schematic diagram in Figure 2, starts with the heat treatment of raw milk (88°C/1 min). This is to denature the whey proteins and to inactivate vegetative cells of bacteria present in the milk. This is followed by the preparation and addition of protein concentrate to increase the casein content of the cheese milk. The next stage is to adjust the fat and recoverable protein content, which in turn controls the fat-in-dry-matter of the final cheese.

The last step in the process is the microfiltration of the skim milk (1.4µm) and heat treatment of the cream (120°C for 1 minute) in order to remove spores and thermo-resistant bacteria.

The cheese itself is prepared as follows: the milk is prepared with starters and acidifiers at 39°C for 30 min in order to standardise the pH at renneting. The milk is then coagulated with recombinant chymosin to gel the milk, which is then cut into 1.7x1.5x1.5cm pieces to promote syneresis. The vat containing the milk gel is then drained and the cheese placed in moulds, which are in turn drained at 32°C for 3 hrs then 18°C. After 1 day the cheese is placed in saturated brine at 12°C for 55 min and then ripened for 12 days (12°C, 96% RH) on grids before wrapping and storing. Mean value and standard deviation were measured for the composition of the cheese milk, day-1 cheeses and the ripened cheeses, respectively. A good reproducibility was obtained for all state variables with the coefficient of variation around 1-1.5%.

The equipment needed for milk standardisation is: pilot-scale microfiltration with 1.4µm ceramic membranes, Pasteuriser, Tri-blender (or mixer) and a skimming centrifuge. Cheese manufacture requires a cheese vat, cutting blades or wires, cheese moulds and a thermostated cheesemaking room. Finally, cheese ripening requires wire grids and a ripening room (RH and temperature controlled).

Figure 1. Brie-style soft cheese produced using the cheese-milk model.

Significance and benefits

A detailed, realistic and reproducible cheese model has been built and characterised. The model is currently used in our laboratory and could be used as a basis for model development in research institutions or industrial laboratories. A simplified version of the model has been developed in collaboration with Soredab

Successful applications

This model has been successfully applied to study the influence of salt in moisture on the growth and survival of Bifidobacterium lactis BB12. The experimental data obtained from the model was in agreement with previous studies, showing an inhibitory effect of the increase of the salt in-moisture on butyric acid fermentation. Our results obtained in Brie cheese also confirm previous findings which showed little influence of salt content on the survival of B. lactis BB12 in cheese.

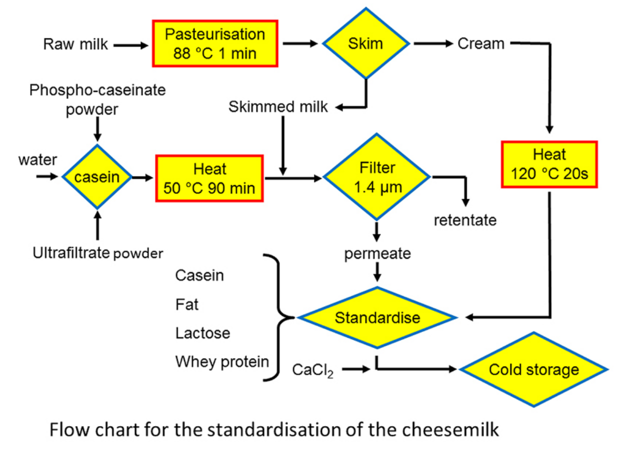

Figure 2. A flow chart for the standardisation of cheese-milk in the soft-cheese model.

Prospects and challenges

This model offers a way of producing pilot-scale cheese with low variability. One of the main limitations of the model is its complexity. Therefore, one task for further development is the simplification of the model so that it may be used more widely in the cheesemaking industry.

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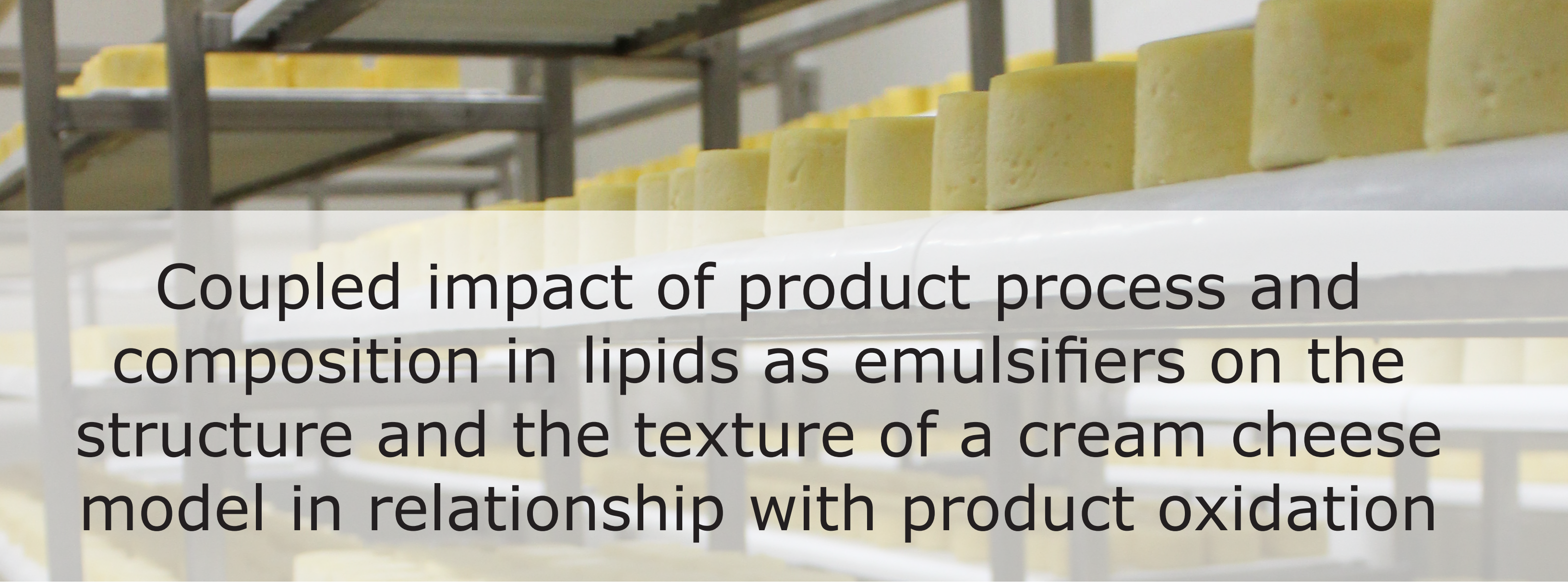

Coupled impact of product process and composition in lipids as emulsifiers on the structure and the texture of a cream cheese model in relationship with product oxidation

Impact of product process and composition on cream-cheese texture and oxidation

A cream cheese is a dairy emulsion where proteins act both as emulsifiers at the fat-globule interface and as protein network components. The objective of this work is to understand the impact of the process and the addition of lipid emulsifiers on the interface composition then on the model texture. The most discriminating step of the process on the product's rheological properties is homogenisation. Nevertheless, its influence is modulated by heat treatment. The addition of lipid emulsifiers decreases the connectivity and hence decreases the product's firmness. These molecules compete with proteins and replace them at the interface. The cream-cheese model is not sensitive to oxidation either after intense thermo-mechanical treatment, storage or enrichment in polyunsaturated fatty acids.

Research aims and background

The issue was to have an easy-to-produce cream-cheese model (Figure 1), with a well-characterised composition in order to understand the impact of the process and its composition in lipid and protein emulsifying agents on its structure, texture and oxidation stability.Previous works on the impact of product process on product texture exist (Sanchez *et al.*, 1996).

However, there is a lack of information regarding the influence of each process step on the final product. Moreover, the emulsifying capacity of phospholipids is well-known but the influence of its addition on fat-globule interface, product structure and texture remains little-known.

Results and applications

Regarding the impact of the process (described in Figure 2) on the structure and texture of the cream cheese, the project showed that the final homogenisation pressure has a large impact on the cream-cheese model texture. When the pressure increases, the fat-globule size decreases. This leads to an increase in the specific surface of fat, the number of interactions between particles and consequently the cream-cheese model firmness.

The pH at the end of acidification has a very limited impact on the rheological characteristics of the model, but it has a significant impact on its sensory properties: products acidified to pH 5.2 are considered more spreadable and brighter than products acidified to pH 4.9 (Coutouly *et al.*, 2013).

Regarding the impact of enrichment of the cream cheese with lipid emulsifiers, the project showed that phospholipids prove to have a larger affinity for fat-globule interface than proteins. As low molecular weight surfactants (Mackie *et al.*, 1999), they replace proteins at the interface (Figure 3). Consequently, the number of interactions between particles decreases and the cream-cheese model firmness consequently decreases. The presence of phospholipids results in the partial coalescence of fat droplets, which yields softer and smoother final products.

Finally, regarding the stability of the cream-cheese model, enriched or not with polyunsaturated fatty acids, and whatever the process to manufacture it, the cream-cheese model proved to be very stable with regard to lipid oxidation, during three months of storage at 4°C. This project allowed better understanding of how the interactions between particles and microstructure impact the final cream-cheese texture.

Significance and benefits

The project was performed with cream-cheese models analogous to actual products. The cream-cheese model's manufacture integrated a process and certain ingredients commonly used in the dairy industries.

The different parameters studied here (process parameters such as heat-treatment temperature, final acidification pH and homogenisation pressure; or ingredients such as proteins or phospholipids) can be tested in a straightforward manner in the dairy industries.

The project outsides can give direct applications/ solutions for industries. Thorough characterisation of the product was achieved at each stage in the process and at different scales.

The consequence of each variation of the process or of the formula has been characterised from nanoscale through electron microscopy to macroscale through rheology and sensory analysis.

The project made it possible to obtain an overview of the possible parameters that can be used to modulate cream-cheese texture. These parameters include both technological and formulation factors.

Successful applications

The cream-cheese model could be used in other research projects.

The direct results provide information to link process, formula and product structure and texture.

Moreover, this work allowed the production of various data, which are currently used for mathematical modelling. Two studies are in progress: modelling protein aggregate formation in tubular exchanger during heat treatment and the modelling colonisation of the fat-globule interface upon homogenisation and induced connectivity.

Figure 1. Cream-cheese model

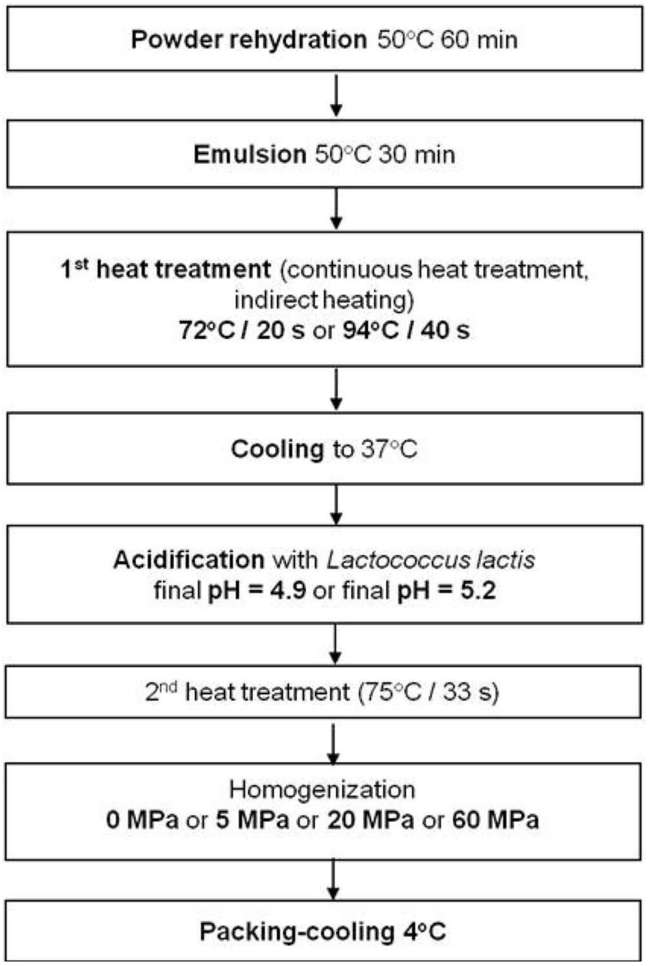

Figure 2. Cream-cheese process

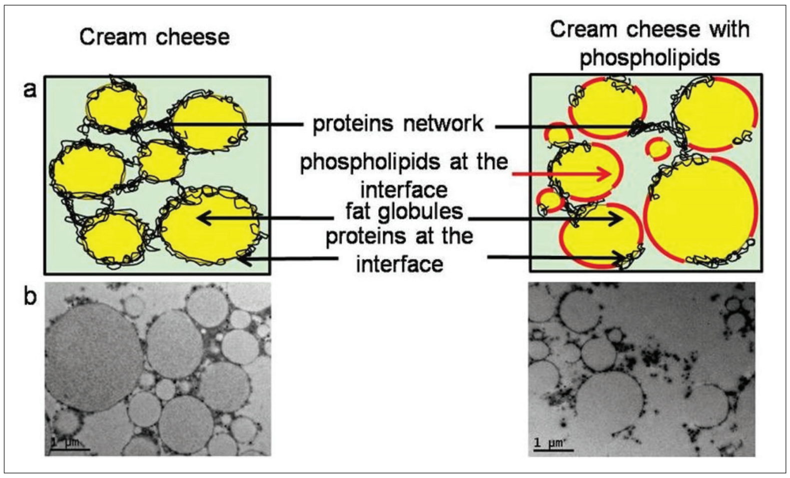

Figure 3. Schemes (a) and transmission electron microscopy images (b) of cream cheese with or without phospholipids

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Prospects and challenges

This work raises various perspectives. Firstly, the analysis of the fat-globule interface has to be more specific. In order to reach this goal, a method for the characterisation of the fat-globule interface in the final product should be developed. Moreover, for further work, a source of purified phospholipids or other emulsifiers should be used. Indeed, in this work we used buttermilk isolates as a source of polar lipids. Finally, it will be necessary to quantify the connectivity and link it practically with rheological properties and the texture of the product.

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Open solid foam model

Is this information important for me?

Consumers	●	●	●	○	○
Food Industry	●	●	●	●	●
Regulatory Authorities	●	●	●	●	●
Scientific Community	●	●	●	●	●

WP-5

Workpackage

input data for numerical R&D
researching cereal structure-function relationships

Introduction to WP5

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Aims and background

Open solid foams represent the structure of baked cereal products, the properties of which are closely related to the intrinsic properties of the solid material, its density and cellular structure. The solid phase is a composite material blend of biopolymers and components of lower molecular weight. The size and distribution of pores is also important in the product behaviour. Fracture properties and dynamics of water in the matrix are important for the sensory quality of products based on solid foam structure. The micro- and macro-level structure is likely to have an important effect on digestibility and delivery of small molecular weight components in the human gastrointestinal tract.

The aim was to develop models for open cereal solid foam foods with special reference to the effects of wholegrain and fibre on structure.

Prospects

The results showed the importance of models in understanding the role of food formulation and process variables at different structural levels of the product and further on nutritional properties, stability and safety. In bread, important nutritional benefits include high fibre content and glycaemic response. In the former, maintenance of good sensory texture is critical, and in the latter, food structure has a decisive role. In biscuits, fat quality and amount of sugar should additionally be considered. Fundamental understanding and modelling of structure formation helps to develop solid foam foods with consumer benefits.

Task 5.1

Definition of the work domain and relationship with WP1 and WP6: Food models and process and recipe variables were selected. Processes required for manufacturing the food models were detailed according to the possibility of control and in-line measurement. They were transferred to WP6 for safety and nutritional tests. The available numerical models and the know-how for structure-property and structure-processing relationships (BKM) were collected.

Task 5.2

Cereal foam structure design and processing: Laboratory scale processes, and in biscuit model also pilot processes, were investigated to elucidate the most essential phenomena for cereal foam design. Samples were taken during and after processing for further analysis, or measured *in-situ* during processing. The phase/state changes were assessed at different structural levels, by determining starch digestibility, rheological properties, porous architecture by X-Ray tomography, electron and light microscopy, as well as water distribution by NIR and calibrated colour imaging.

Task 5.3

Improving (numerical) models and generating pathways for cereal model foams: Partners' know-how and expertise were combined for specific process operations (mixing, bubble formation and baking) and product specifications in order to complete BKMs, where differential equation (PDE) -based models are too complex or not available; the existing models were extended to the computation of other variables (colour during baking, for instance), in WP1. Integrating BKMs will allow complete pathways to be designed for cereal food processing.

Main outcomes

Generic model foods (GMF) were developed for solid cereal foams, bread and biscuits, and accurate methods to characterise these were developed. A preliminary cake model was also developed.

Structural changes during processing were ascertained for bread, with emphasis on the creation of the cellular structure and its heterogeneity. The liquid phase of dough, including sugar and fat, was studied as a stabiliser of the air bubbles in the dough and bread matrix. We used and further specified the model for bread in the ring test, and protocols for the bread model were validated and disseminated for end users. Effects of oven heat flux on biscuit moisture distribution and colour were studied, and a model for bubble growth and biscuit thickness was made. The models were used to study the effects of dietary-fibre/bran addition to bread and biscuits, and to study the effects of fat and sugar in bread.

Structural challenges in nutritionally-improved biscuits

How can one produce wholegrain and high-fibre biscuits with slow starch digestibility and high sensory quality?

Biscuits are an important cereal food category, made most often of white flour, fat and sugar and consequently typically have high calorie but low nutrient density. We wanted to understand the effects of adding dietary fibre (wholegrain flour and wheat bran) on biscuit microstructure, texture and *in-vitro* starch digestibility. Fine and coarse wheat bran were used to make five different biscuits with varying dietary fibre content (5-15%). The biscuits with small bran particle size had the best sensory texture. The generally low biscuit starch digestibility *in-vitro* was increased slightly by adding wheat bran.

Research aims and background

There is a large consumer and public-health demand to increase the nutritional profile and expected health benefit of cereal-based snacks. Biscuits, with white flour, fat and sugar as major ingredients, are popular snacks and also breakfast items. The production steps during biscuit manufacturing do not allow starch to gelatinise completely in spite of the baking process, and the glycaemic response of biscuits is typically lower than that of bread. On the other hand, the nutritional profile of biscuits is not optimal. Making biscuits from wholegrain flour or adding dietary fibre to the recipe would improve their nutritional profile, but poses challenges to the open solid foam structure determining the mechanical properties and sensory quality of biscuits.

We wanted to elucidate the role of dietary fibre in the form of cereal bran, as well as that of wholegrain flour on biscuit structure and starch *in-vitro* digestibility of biscuits. The aim was to be able to change the process conditions so as to maintain good sensory perception of texture and low starch digestibility while increasing the amount of cereal fibre and associated phytochemicals in the biscuit formulation.

The results are important for the baking industry and biscuit manufacture in the development of more nutritious products. Knowledge of the interactions of dough components and bran particles also benefits producers of other baked snacks and dry products.

Figure 1. Biscuit assessment methods: Texture (2mm rod penetrometry).

Results and applications

Five types of biscuit were produced containing 5-15% dietary fibre, including a standard recipe and biscuits made with coarse (260-560μm) and fine (25-160μm) wheat bran. Textural measurements were made with a three-point bending test. Further measurements were made using a penetrometry method for 40 types of biscuit with a wider range of fibre variations including bran and soluble inulin fibre. Starch crystallinity was analysed by differential scanning calorimetry, and *in-vitro* starch digestibility rate was determined as a hydrolysis index using an enzymatic method.

Biscuits became darker with increasing bran content. Bran particle size had little effect on average colour, but the particles were visible as specks. The mechanical properties of the bran-containing biscuit matrix were affected by both bran content and particle size. The addition of wheat bran increased the penetration energy ('firmness'), only slightly increased the elastic modulus, and reduced the number of penetrometry force peaks ('crunch'). Inulin also increased firmness but, unlike bran, resulted in a high initial penetration force. Bran particle size reduction had little effect on firmness, but increased the elastic modulus and hardness measured by three-point bending. The bran supplementation level had a greater effect on penetrometry tests than particle size, but particle size had a greater effect in three-point bending. The failure strain at maximum bran loading level was the lowest among the coarse-bran-supplemented biscuits. These samples had very low strain at failure, which varied between 1.1-1.4%, which is unique to brittle materials.

Structural factors had more impact on the *in-vitro* starch digestibility rate compared to the status of starch, which was measured by degree of gelatinisation. Biscuits with finely-ground bran had a visually more compact structure without any surface or internal defects and were harder than those with a coarse bran particle size. Increasing fibre content from 5 to 15% increased the hydrolysis index by 20%. The effect of bran particle size reduction in biscuit formulations did not influence hydrolysis index.

Figure 2. Biscuit assessment methods: Colour.

Figure 3. Biscuit assessment methods: Mass.

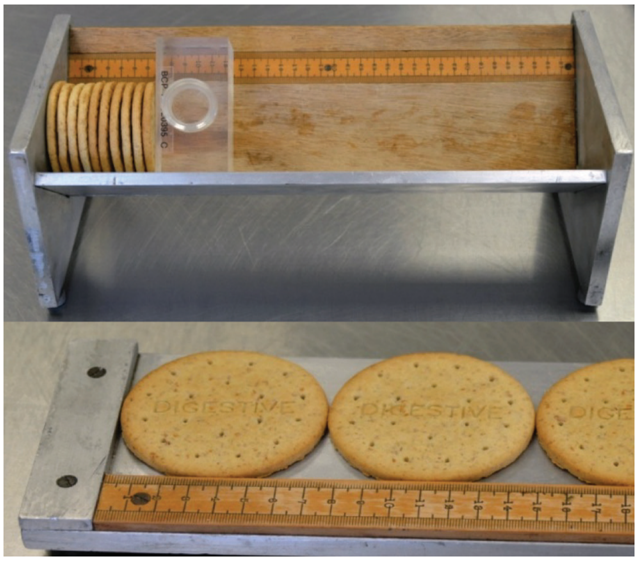

Figure 4. Biscuit assessment methods: Dimensions.

Significance and benefits

It is a food engineering challenge to increase dietary-fibre content in biscuits while retaining structural and sensory characteristics, including texture, colour and taste. There are very few reports available on the addition of dietary fibre to biscuits, and the effects on these characteristics or starch digestibility. The use of wholegrain flour or bran seems a logical way of increasing the fibre content of biscuits, but no reports of their use are available. Fundamental understanding of structure-function relationships in biscuit structure and fracture properties is also limited. Current milling techniques enable efficient bran particle size reduction, delivering new types of ingredients for the baking industry. Their applications have hitherto been reported to a limited extent. The approach of this work thus provided many aspects as a novelty.

The results, when applied, would encourage the use of finely-milled bran and wholegrain flour as biscuit raw materials, to produce biscuits with good sensory texture and colour, and retain the naturally low starch digestibility in biscuits. The benefit for biscuit manufacturers would be the production of new, healthier products, providing consumers with healthier options. The use of bran in food production would also increase sustainability, as a side stream could be utilised in a mainstream food product.

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Prospects and challenges

We hope that the results will encourage biscuit manufacturers in development of high-fibre products, thereby diluting the amount of refined ingredients in the product. The nutritional and health claim regulation by European Food Safety authority would allow a claim for fibre content of products with adequate nutritional profile. The idea of bran pre-treatment prior to incorporation in baking could also be developed further in collaboration with milling and baking industry.

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Creation of bread cellular structure

Designing bread texture thanks to the solid foam model

The growth of gas bubbles in viscous matrices is the main mechanism responsible for the structure of open solid foams, like bread.

The creation of the cellular structure in wheat flour dough and its heterogeneity was ascertained at different structural scales, focusing on proofing. The liquid phase of dough, including sugar and fat, was studied as a stabiliser of the air bubbles in the dough and bread matrix. The contribution of each scale was integrated by adapting a capillary number. We used and further specified the model for bread in a ring test, in order to increase its fibre content, and protocols for the bread model were validated and disseminated for end users.

Research aims and background

The texture of bread is a fundamental element of its acceptability by consumers, and has a strong impact on its nutritional properties. For instance, increasing the fibre content leads to denser, less-acceptable breads. Like solid foam mechanical properties, the texture depends on the bread's density and cellular structure. Therefore, there is a need to better understand the mechanisms of cellular structure creation during dough processing and provide models to better control process and final properties.

Wheat flour dough contains about 45% water (tot. basis) and its cellular structure is created during fermentation, or proofing; during this stage, porosity increases from 0.1 to 0.7 and CO2 bubbles are connected together, although the dough does not collapse. This stability could be due to the formation of a liquid foam, constituted by a liquid phase, co-continuous to the starch/gluten visco-elastic matrix. To determine the role of this phase in the creation of the cellular structure, the aqueous phase, so-called dough liquor (LdP), has been considered as a good model for these interfacial films. In complement, elongational properties of dough can be determined by lubricated squeezing flow test (LSF), which underlines the importance of minor components. Starting from the study of bubble growth and coalescence in model dough systems, the aim of our work was to determine the role of the aqueous phase and the starch/gluten matrix on the mechanisms that govern the creation of cellular structure at microscopic scale, and at macroscopic scale on the loss of stability at the end of fermentation.

The results are important for the baking industry, firstly for manufacturing breads with increased fibre content, without loss of sensory quality. Secondly, it strengthens knowledge on the breadmaking chain by providing engineers with basic knowledge models.

Results and applications

Around twelve dough recipes were processed with varying sugar (0-15%), fat (0-10%) and fibre (0-15%) content, in a range for which a typical bread cellular structure was always obtained. The elongational properties of the starch/gluten matrix, measured by lubricated squeezing flow, largely influenced dough proofing stability, the evolution of which was assessed by 2D-image follow-up and adjusted by an exponential decay; this result could not be singly explained by the bubble growth model. Porosity kinetics determined at macroscopic level were in satisfactory agreement with results determined at microscopic levels by X-ray microtomography (XRT) at ESRF (F38- Grenoble), and both followed a Gompertz model. Analysis of 3D-XRT images showed that most bubbles were connected, for the highest dough porosity (≥0.5). The homogeneity of the cellular structure was defined from the size distributions of gas cells and walls; it was characterised by a critical wall thickness (≈ 1µm), below which the cells were separated by liquid films.

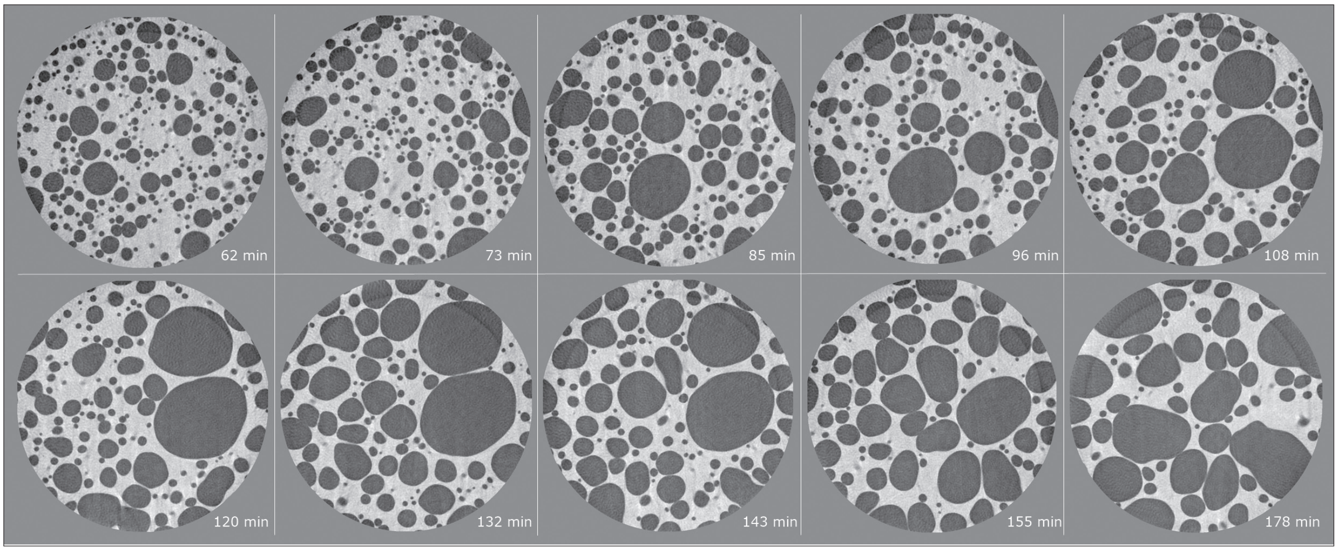

Figure 1. Two-dimensional images of dough from the beginning (66 minutes) to the end (178 minutes) of proofing, diameter 5mm. Images from A. Turbin-Orger, E. Boller, L. Chaunier, H. Chiron, G. Della Valle and A.-L. Reguerre (2012a). Kinetics of bubble growth in wheat flour dough during proofing studied by computed X-ray micro-tomography. J. Cereal Sci., 56, 676-683. Images obtained from the European Synchrotron Radiation Facility at Grenoble, France.

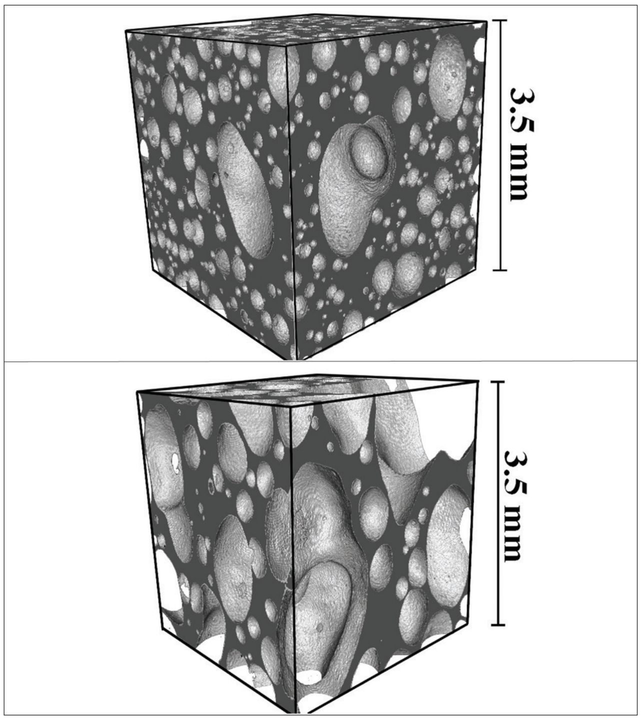

Figure 2. Three-dimensional images of dough at the beginning (66 minutes) and at the end (178 minutes) of proofing. Images from A. Turbin-Orger, E. Boller, L. Chaunier, H. Chiron, G. Della Valle, A.-L. Reguerre (2012a). Kinetics of bubble growth in wheat flour dough during proofing studied by computed X-ray micro-tomography. J. Cereal Sci., 56, 676-683. Images obtained from the European Synchrotron Radiation Facility at Grenoble, France.

The fermented dough could thus be considered as a three-phase medium: visco-elastic matrix/gas cell/liquid phase.

Dough liquor was taken as a model of this liquid phase, and extracted from dough; it behaved like a macromolecular solution, and was characterised by the surface tension (≈ 40mN/m), related to the presence of polysaccharide-protein complexes at the interfaces.

The contributions of the different levels of organisation of the dough were then integrated by defining a (dimensionless) capillary number, which ruled the overall behaviour of the dough. These results, including process specifications, were used in a ring test to study the effect of fibre addition, in different labs; although various texture properties were obtained, they could all be integrated into the same relationship between texture and density, which ultimately validated the open solid foam model.

Significance and benefits

Improving bread nutritional properties without decreasing its sensory properties and, mainly its texture, is a real challenge in the baking industries. A better understanding of various operations is necessary in order to control the density and cellular structure of these products, which can, in turn, be related to texture by available mechanical models. Within this purpose, a common representation of these operations can be obtained by the definition of Basic Knowledge Models (BKMs), which capture the main physics of the phenomena involved. For instance, the relationship between the capillary number and stability can be considered as a BKM; it suggests that the simple measurement of dough elongational viscosity and knowledge of the dough liquor surface tension can lead to the prediction of the cellular structure of the dough.

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Prospects and challenges

The integration of such BKM requires the upgrading of computer tools. Their use for designing cereal food products requires: (a) the integration of the available know-how and expertise for specific process operations where the use of models based on differential equations is still difficult, and (b) the extension of the existing models to a domain of composition, in order to cope for the necessary increase in dietary fibre, which will greatly modify the rheological behaviour of dough. The use of such integrated models may be thought of to design products with target nutritional and sensory properties, provided their porosity and cellular structure are precisely characterised, and define the pathways for reaching them, according to the so-called reverse engineering approach.

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Model food applicability

Is this information important for me?

Consumers	●	●	○	○	○
Food Industry	●	●	●	●	○
Regulatory Authorities	●	●	●	●	○
Scientific Community	●	●	●	●	●

WP-6

Workpackage

validation

R&D result applicability assessment

Introduction to WP6

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Aims and background

Change in composition or process conditions may deeply impact the microbiological quality and safety of foods, as well as the bioaccessibility of toxic or bioactive compounds and therefore their absorption during digestion. To assess their reproducibility and industrial practicability, Generic Model Foods (GMF) were standardised and validated. Their physico-chemical characterisation can provide information on bioaccessibility of nutrients and/or toxicants, fundamental for understanding the effect of different processes on the bioavailability – *in-vitro* and *in-vivo* studies - of selected nutrients and their impact on consumer health. Additionally, GMF can represent a powerful tool for microbiologists. According to microbial behaviour of beneficial, spoilage and pathogenic populations, the use of GMF can help in optimising formulations, processes and storage - ultimately improving risk assessment - via the implementation of available decision-making tools.

Main outcomes

Protocol standardisation, cross-validation and physical-chemical characterisation were achieved for seven generic model foods - WP2-Brassica and Tomato purée; WP3-Mimetic meat model; WP4-Dairy dessert and Soft cheese; WP5-Bread and Biscuits. The *in-vitro* digestion and *in-vivo* studies highlighted the effect of the different processes in changing the physical and molecular structure of food and consequently the bioaccessibility and bioavailability of nutrients or bioactive compounds. The quantification of the impact of process and storage on microbial food safety and quality was obtained after inoculating GMF, monitoring the microbial behaviour and implementing the decision-making tool to simulate their performance in food.

Task 6.1

In WP6, model foods used for nutritional studies as well for microbiological food safety and quality assessment. It is important to ascertain that GMF are reproducible and well characterized. In this task, protocols for the realization of seven model foods have been standardized and cross-validated among the partners and tested for their practicability by industries.

Task 6.2

Models were further characterized by using analytical methods and high level structural studies. Main physico-chemical features, e.g. firmness, color, bioactive molecule content have been assessed in WP2-models. Protein concentration and oxidation surface hydrophobicity were assessed to characterize WP3-mimetic model. Deep investigation characterized WP4-models for viscosity, fat globule size distribution, protein content/oxidation, while hardness, texture profile, and color have been monitored to describe WP5-models.

Task 6.3

Through the development of appropriate methods and using the most recent analytical technologies, the *in vitro* and *in vivo* studies have been focused at determine how different processes, modifying the molecular and physical structure of GMF, can influence the bioavailability of selected nutrients or bioactive compounds and their kinetics of appearance in blood of minipigs during digestion of a complete meal composed by GMF.

Task 6.4

In T6.4, the impact of environmental conditions on microbial behavior or mycotoxin production have been obtained by inoculating GMF with molecularly characterized spoilage, pathogenic or beneficial strains. The use of experimental kinetics performed during the challenge test has allowed the determination of growth/destruction parameters specific for each combination microorganism/GMF. Mathematical models have been then used to simulate growth for other conditions.

Prospects

Administration of different GMF *in vivo* as a complete meal can highlight the effect of processes in changing the food structure and consequently the nutrient/biomolecule bioavailability, giving a realistic evaluation of possible interactions of foods within the digestive tract. A specific task includes the implementation and consolidation of microbiological data deriving from GMF exploitation in the Sym'Previus decision-making tool. The predictive module will help the scientific community and industrialists to i) select food model formulations and optimise processes and storage; ii) determine the appropriate shelf-life according to microbial behaviour; iii) assess quantitative risk.

Acting on the micro- and macro-structure of meat, cooking conditions can modify the nutritional potential of meat proteins

How does one cook meat to obtain the best health effects?

In addition to the amino-acid composition and the digestibility, new criteria are appearing to fully describe the nutritional potential of proteins: the kinetics of amino-acid absorption, and the potential to release bioactive peptides during digestion. For meat, these parameters can be modified by cooking conditions, which act on the micro- and macro-structure of the product. Drastic cooking conditions lead to protein aggregation, which slows enzymatic digestion of proteins. However, this effect, related to the micro-structure, is limited in comparison to the effect of the macro-structure, and the chewing efficiency of the consumer. Furthermore, a simple difference in cooking conditions significantly modifies the postprandial plasma peptide profile of the consumer, and therefore the potential health effect of meat.

Research aims and background

Conventional criteria for evaluating the quality of a protein source are based on amino-acid composition, and protein digestibility in the digestive tract. It is now known that these basic criteria are not sufficient to fully describe the nutritional potential of a protein. For instance, it has been shown that the rate of protein digestion can regulate postprandial protein retention (Dangin *et al.*, 2003). Thus, the ranking of protein sources according to their rate of digestion is necessary. Additionally, total digestibility is not a good predictor of amino-acid bioavailability Indeed, only digestion in the small intestine is thought to supply amino acids to the body. Finally, all dietary proteins are potential sources of peptides with beneficial health effects.

Previous work on meat shows that modifications at the microscopic scale of the protein cellular network, for instance by protein aggregation during heat treatments, can slow down the enzymatic digestion of proteins (Bax *et al.,* 2013). The rate of meat protein digestion can also be modulated by chewing efficiency (Rémond et al., 2007), probably in conjunction with meat macrostructure. However, the hierarchy between the effects on digestion parameters of the meat micro and macrostructure and mastication remain difficult to establish.

Furthermore, it has been shown that meat digestion reproducibly releases peptides containing amino-acid sequences with antihypertensive activity (Bauchart *et al.*, 2007a), and that a significant amount of carnosine is released into the blood after a meat meal (Bauchart *et al.*, 2007b). This dipeptide has numerous health benefits, such as prevention of pathologies related to oxidative damage, or protein glycosylation. Nothing was known on the effect of the meat structure (micro and macro) on the bioavailability of meat-derived peptides.

In this context we used *in-vitro* and *in-vivo* approaches (using minipigs and rats as animal models) to investigate the effect of structural modifications on the bioavailability (kinetics and quantity) of amino acids and peptides by manipulating meat cooking conditions.

Significance and benefits

We showed that cooking pork meat for 45 min at 90°C accelerates protein digestion, compared to cooking for 10 min at 75°C, but has no effect on the total bioavailability of amino acids (Figure 1). Although these results underlined the importance of the structure of the ingested meat in the determination of amino-acid absorption kinetics, they seem to be in disagreement with a previous study of beef, according to which meat protein digestion was slowed down by increasing cooking temperature from 75°C (30 min) to 95°C (30 min) (Bax *et al.*, 2012). Beside a possible meat origin effect, this suggests that, more than the temperature, the time-temperature couple is important in the determination of protein digestion rate. Furthermore, in the beef study, the meat was minced before meal serving, whereas in our study, the meat was only sliced. An interaction between cooking conditions and the efficiency of oral and gastric meat degradation, could therefore also explain the apparent discrepancy between the two studies. Indeed, in the present study, prolonged cooking at 90°C produced a meat, the structure of which was much more sensitive to mechanical degradation in the mouth, leading to an increased digestion rate.

Cooking conditions did not modify meat carnosine content, and in both animal models (rats and minipigs), the carnosine bioavailability was not affected by cooking.

In order to address the question of peptide bioavailability, we developed an analytical approach, using an LTQ-Orbitrap Velos mass spectrometer and data extraction with XCMS, for the characterisation of the plasma peptidome and the identification of selected peptides. The method developed enabled us to discriminate the plasma peptidome of the minipigs fed with the pork meat cooked according to the two conditions (Figure 2). We identified up to 33 peptides discriminating the cooking conditions. The identification of these peptides was validated by analysis of their fragmentation. Furthermore, the kinetics analysis allowed us to show the postprandial trajectory of the plasma peptidome (Figure 3).

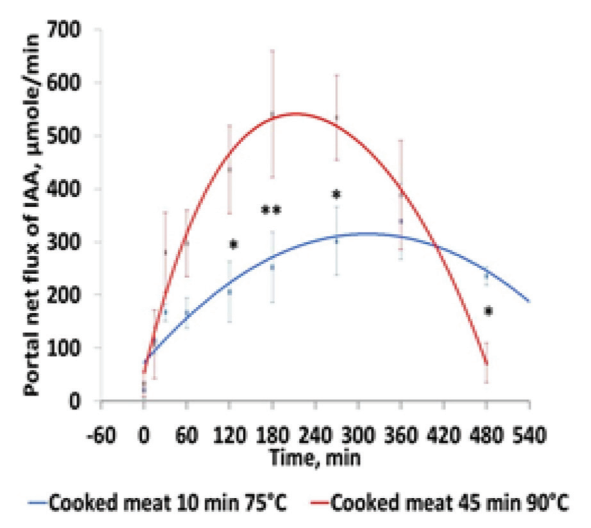

Figure 1. Amino-acid absorption. Portal net flux of the sum of indispensable amino acids (IAA), in minipigs (n = 5) receiving two meals differing by the meat cooking conditions.

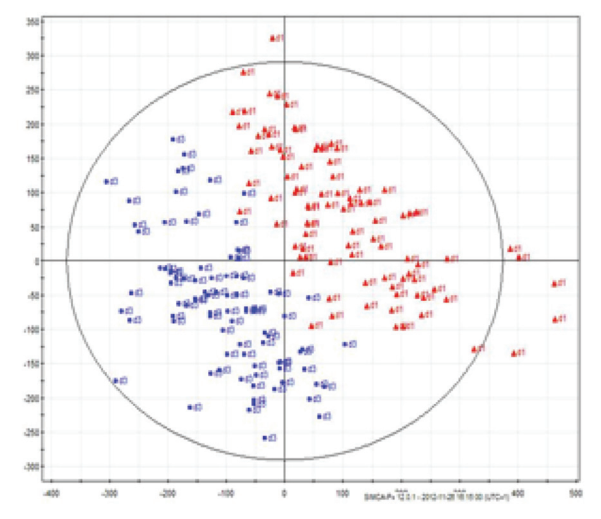

Figure 2: Peptidome. OSC-PLS score plot of plasma peptidome of minipigs fed with pork meat cooked according two different conditions (d1 = 10 min, 75°C, d3 = 45 min, 90°C).

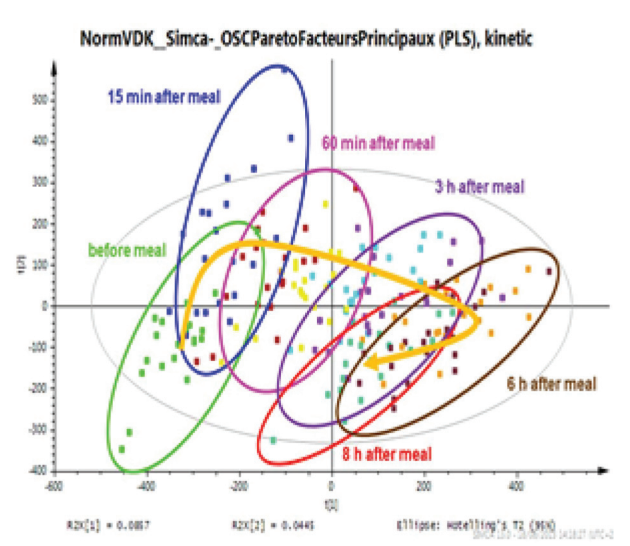

Figure 3: Peptidome. OSC-PLS score showing plasma peptidome trajectory during the postprandial kinetics after ingestion of meat in minipigs.

Results and applications

Our work highlighted the difficulty of predicting protein digestion rate. Although it is clear that protein aggregation slows down the accessibility of digestive enzymes to their cleavage site within the proteins, this parameter appears to have a minor effect when meat is not ground. Indeed, in this case, the resistance of the meat structure to disruption by chewing activity could be the main determinant of the digestion speed. As this is attributable to the chewing efficiency of the consumer, it seems difficult to predict it only from meat-derived measurements (chemical composition, structure characterisation, and *in-vitro* digestion). We have clearly evidenced that for a given meat, a simple difference in cooking conditions significantly modifies the postprandial plasma peptidome of the consumer, and therefore the potential health benefit of meat proteins.

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Prospects and challenges

This work is continued through the study, in humans, of the interaction between meat structure (cohesiveness and tenderness) and chewing activity, in order to assess the final impact on the level of degradation of the swallowed bolus, and the consequences on protein digestion rate and peptide release.

If we identify peptides that are reproducibly released from meat proteins, the next challenge will be to identify their potential biological activity (antihypertensive, immunomodulator, antioxidant, etc.)

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Industrial concerns and needs towards fungal risk assessment

How to assess and take into account the ability of *Alternaria alternata* mould to grow and produce mycotoxin during tomato-purée shelf-life

Alternaria species are reported to be the most common fungi affecting either tomato fruit or plant, causing the so-called black mould of tomatoes. Rapid infection of *Alternaria* in tomatoes may occur on the crop or post–harvest, yielding high financial loss due to spoilage of industrialised products such as tomato purée. Moreover, under specific growth conditions, *Alternaria spp.* may also produce various mycotoxins, which represent a serious risk for human consumption of tomato-based products. Within the framework of this collaboration, the ability to grow and produce mycotoxins was determined as a function of tomato purée pH and storage temperature. These boundaries and growth simulations will help food industrialists to further optimise tomato-based food formulation and shelf-life.

Research aims and background

Predictive modelling and microbial risk assessment have emerged as a comprehensive and systematic approach for addressing the risk of microbial pathogens and spoilers in specific foods and processes. Within WP6.4, food shelf-life or the impact of physico-chemical factors (pH, aw, temperature) on microbial behaviour were determined after (i) artificial inoculation of the microorganism of interest in developed model food, (ii) the matching of experimental kinetics in food and (iii) the prediction of shelf-life for various scenario in static or dynamic storage conditions.

Challenge tests in DREAM model foods were performed according to guidelines and standardised protocols based on the current NF V01-009 on guidelines to conduct microbial challenge tests. Experiment matching and shelf-life determination were performed with recognised mathematical models available in the Sym'Previus decision-making tool (www.symprevius.org). While simulation with a large variety of characterised strains of pathogenic bacteria is possible, few spoilage fungal strains are available in the database. Similarly to the the modelling approach reported by Huchet *et al*. (2013) predicting mould appearance time on pastries, an adaptation of the gamma concept of Zwietering (1992) was used to characterise fungal strain and to model its growth.

In tomato-based products, *Alternaria alternata* represents a relevant microbial hazard since it is responsible for black mould spoilage (Figure 1) yielding high financial losses (Bottalico & Logrieco, 1992). In order to model the effect of environmental factors on the development of mould on a tomato medium, in-depth characterisation of the strain was performed for a wide range of temperature and pH values at a given water activity of 0.99.

Moreover, to further screen the conditions yielding to mycotoxin production, a similar experimental set-up was used and analysed.

Results and applications

A toxigenic strain of *Alternaria alternata* (ITEM8176) isolated from tomato fruit affected by black mould (Somma *et al.*, 2011) and deposited at the ISPA collection, Italy (ITEM accession: http://www.ispa.cnr.it/Collection/) was used for growth and mycotoxin production assessment.

Growth ability and mycotoxin production of this strain were determined on similar samples, after inoculating fungal ascospores (seven-day-old culture) on WP2 cold-break tomato purée supplemented with agar. Adequate controls and a complete factorial design with a total of six pH levels (2, 3, 4, 5, 6 and 7) and ten temperature levels (6.5, 10, 15, 20, 25, 30, 35 and 37°C) were used (60 conditions in total), for three replicates, to define which pH and temperature conditions supported (i) fungal development and (ii) mycotoxin production. Growth ability was determined on a tomato-based medium by regular observations of the fungal development, and additional experimental data in broth were produced to determine the strain cardinal values, i.e. minimum, optimum and maximum pH and temperature values allowing growth. When plates were covered by the fungus, mycotoxin quantification (tenuazonic acid, TeA; alternariol, AOH and alternariol methyl ether, AME) was performed by HPLC coupled with UV/DAD detection, according to an adapted protocol from Solfrizzo *et al.* (2004).

After a maximum incubation time of 1 month, growth was observed in 35 conditions. A pH of 3 was the lowest pH value enabling growth. Lower and higher temperature values allowing growth were further validated with experimental data. Among the mycotoxins investigated, only TeA was produced by *Alternaria alternata* ITEM8176 in the conditions studied.

The impact of pH and temperature on growth and TeA production of the strain on a tomato-based medium are indicated in Figure 2 and Figure 3, respectively. Interestingly, optimum growth (24.5°C, pH5.5) and optimum mycotoxin production (15°C, pH3.5) occurred for opposite conditions, suggesting a strong impact of stress conditions on the strain virulence that may represent a health issue for non-adapted storage conditions.

Figure 1. *Alternaria* species are reported to be the most common fungi affecting either tomato fruit or plants, causing the so-called black mould of tomatoes (Bottalico & Logrieco, 1992).

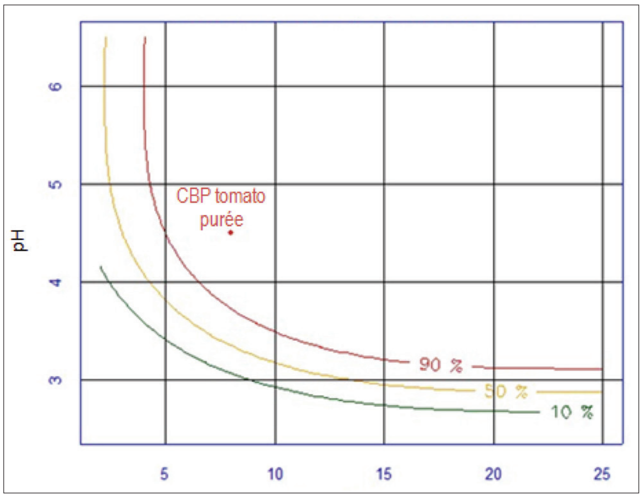

Figure 2. Impact of pH and temperature on growth ability of *Alternaria alternata* ITEM8176 strain on a tomato-based medium. For the conditions tested, physico-chemical conditions supporting growth are indicated in red (>90% growth probability). For conditions close to growth/no-growth boundaries, the impact of annex flora, texture or complex formulation might impact growth ability and experimental testing or challenge testing is needed.

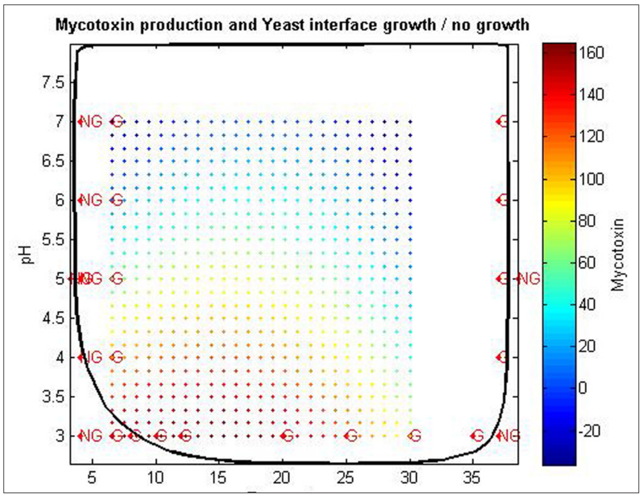

Figure 3. Impact of pH and temperature on TeA mycotoxin production of *Alternaria alternata* ITEM8176 strain on a tomato-based medium. For the conditions tested, dark-red dots refer to environmental temperature and pH conditions yielding higher concentrations of mycotoxin (15°C, pH 3-4).

Prospects and challenges

To our knowledge this is the first time that boundaries representing physico-chemical conditions yielding growth and mycotoxin production of *Alternaria* black-mould spoilage were defined on tomato-based products.

These results were obtained thanks to a productive collaboration with complementary expertise and know-how. These data are brand-new and are currently being disseminated towards public, scientific and food industrial audiences for future successful applications.

Significance and benefits

Alternaria alternata is the major microbial contaminant causing black spoilage in tomatoes, yielding high financial losses. Thanks to these results, the prediction of spoilage development is now possible for static or dynamic pH and temperature conditions on a tomato medium. Future work could address (i) validation for various recipes of tomato-based products, (ii) characterisation of a larger number of strains to take into account biodiversity in growth prediction or (iii) further characterisation of mycotoxin synthesis to predict health issues for various industrial relevant conditions.

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Technology transfer

training
R&D results assessment
researching industry needs

Is this information important for me?

Consumers	●	●	●	○	○
Food Industry	●	●	●	●	●
Regulatory Authorities	●	●	●	●	●
Scientific Community	●	●	●	●	●

WP-7

Workpackage

Introduction to WP7

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Prospects

The use of existing modelling approaches as time-saving and cost-effective tools for assessing and optimising processes and their impact on product quality, and supporting decisions during the process and product development activities is currently relatively limited in the industry, especially at SMEs.

Technology transfer was integrated into the project to promote the model development's conducting in collaboration with food manufacturers through industry needs and feedback approach.

To ensure that the practical needs of the industry, especially those of SMEs, are considered during the development of real model foods; to convert the results of the research into appropriate format that can be used by the industry as simple process and product development tools, and to test their applicability at industry level and provide feedback for further improvement.

Aims and background

According to the industry

- The financial advantages of using models should be emphasised and clearly explained
- Models should be well practically applicable
- Development of models should focus on food safety and the effect of adding or removing components/ingredients to the product or applying new process conditions on shelf life, texture and flavour.

Industry guide for Food Modelling:

The guideline is intended to provide a technical aid to users, but also to create awareness and encourage the use of modelling in the food industry.

Task 7.1

Collecting and mapping the needs of the industry: Identification of the needs of the industry and barriers to using modelling methods in four sectors (vegetable and fruit processing; meat, fish and poultry processing; dairy and bakery industry) and three countries, based on interviews and focus-group discussions (partners involved: ACTALIA / France, CCFRA / United Kingdom and CCHU / Hungary).

Task 7.2

Assessing the practicability of the generic food models and their protocols:
The next step of WP7 was to test the practicability of the models developed by the relevant WPs. Tests was carried out by the WP partners (SOREDAB, ACTALIA, ADRIA, CCFRA and CCHU). After adjustment the improved models and protocols were evaluated for practicality by involving industry partners.

Task 7.3

Development of industry guides:
To support the practical application of the models and to provide an overview of different food models and of modelling tools/software for potential users, a practical guideline was developed by involving industry partners including SMEs from each country. CCHU, SOREDAB and ACTALIA were responsible for consulting national industry partners during the development of the guide.

Main outcomes

As was emphasised for the model developer WPs by WP7, models developed within DREAM should consider the following aspects:

- Models should have practically applicable outputs, clearly described for the user.
- Models should be quick, as product-specific as possible and easy to handle.
- Results should be as reliable and precise as possible.
- The modelling activity shall not require special equipment, but purchasing necessary materials and software is not a barrier. Companies could ensure a food engineer to operate the model.
- Confidentiality should be considered, regarding inputs.
- The main barrier to the use of models by the industry is lack of knowledge, therefore significant effort should be made to remedy those failings.

Industry guide for Food Modelling:

After consultation of the draft version with national industry partners the final version was discussed and adjusted.

Industry guide for Food Modelling

A guideline intended to provide a technical aid to the users but also to create awareness and encourage the use of modelling in the food industry

This guideline can be used as a manual, in which the potential user can find advice on questions related to the use of specific models and also for general considerations on the application and design of food models.

The content of the guideline, including the descriptions of the models, is based mainly on the models that were developed within the DREAM FP7 project and moreover on some models outside the DREAM project that are currently available and frequently used in the food industry.

Brief descriptions of certain general examples of successful practices, and hints for avoiding typical traps and failures are summarised in the guideline.

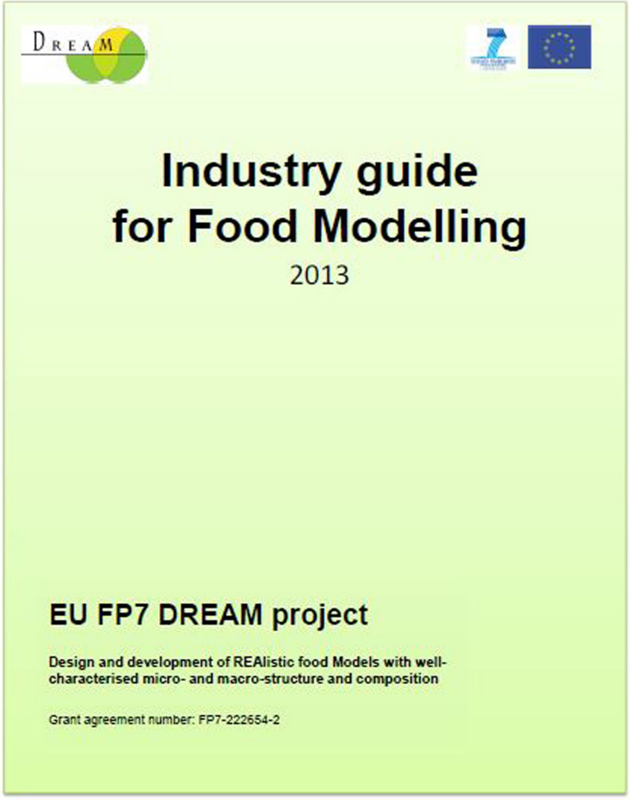
Research aims and background

To support the practical application of realistic food models a Practical Guideline on the use of models was developed. The main objective of the guideline is to provide an overview of different food models and of modelling tools/software for potential users.

Models can be used in many different activities in the food sector, considering the complexity of food and their different applications. As changes in needs and requirements related to food products arise increasingly quickly and frequently, dissemination of available and effective models to the food industry and also to all sectors dealing with food is therefore of high importance.

The target audience of this guideline includes several stakeholders of the food sector, particularly representatives of the food industry (including SMEs) and R&D teams, and decision-makers on food safety, quality and nutritional questions. It is also recommended for food safety and regulatory bodies, nutritionists, food scientists and for marketing specialists who are particularly responsible for the industrial development of food companies.

Food models are useful tools for product and process development, for assessing the safety of product/process design, and can help in understanding the impact of process parameters on the final characteristics of food and yield. However, their use requires an appropriate level of expertise, competence, skills and clear practical guidance.



DREAM

Industry guide
for Food Modelling
2013

EU FP7 DREAM project

Design and development of REAlistic food Models with well-characterised micro- and macro-structure and composition

Grant agreement number: FP7-222654-2

Significance and benefits

One of the main advantages of the realistic food models is to mimic the behaviour of real food products. Furthermore, models can predict the impact of changes to the ingredients, compositions and process parameters. Thus, they can reduce the number of necessary experiments in real conditions, which is particularly important in the case of experiments in factory environments. The use of models can save time and reduce costs. Standardised physical modelling materials and calculations with mathematical models provide a more reproducible benchmark for the impact of different treatments on food properties than experiments with real foods. Because of the rapidly-changing conditions and demands of the market, food producers are required to have a safe but fast process for development. As experiments under real conditions can be expensive and time-consuming, frequently there are significant limitations for under such conditions. In these cases, food models and software models can definitely be good tools to screen options at low cost and to enable experiments with real foods to focus on the most promising test parameters. By using models, waste of the valuable real food product can be significantly reduced during the experiments.

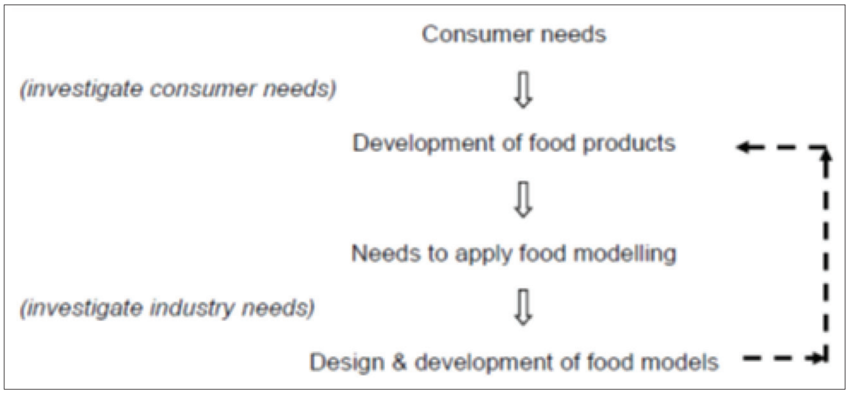


Figure 1. The scheme of the food modelling process driven by consumer/industry needs.

Results and applications

Although a wide range of models exist with different scopes, the model development process is typically divided into five phases:

i) Defining the goal of the model: developing a statement of purpose

ii) Designing and developing the model

iii) Practical testing and verification

iv) Making the model available to the audience

v) Maintenance of the model

This guideline describes these five phases as a systematic procedure and provides a brief description of those steps that it is essential to consider during the model's development. The most important facilities and requirements for application and operation of the models are discussed to help their use and to raise awareness among potential users. The model descriptions are grouped into four major generic structure groups representing vegetable, dairy, meat and cereal products. Furthermore, there is an additional group for models with general applicability, in which these models are discussed according to their function, such as predictive microbial models and heat treatment models.

Prospects and challenges

However, finding satisfactory answers is a time consuming process. Models as time-saving and cost-effective tools provide fairly good support when a company decides to develop a new product: food models can help to reduce the time needed to provide an initial protocol for a production process, and mathematical models can support the simulation of different processes and changes to the parameters (see Figure 1).

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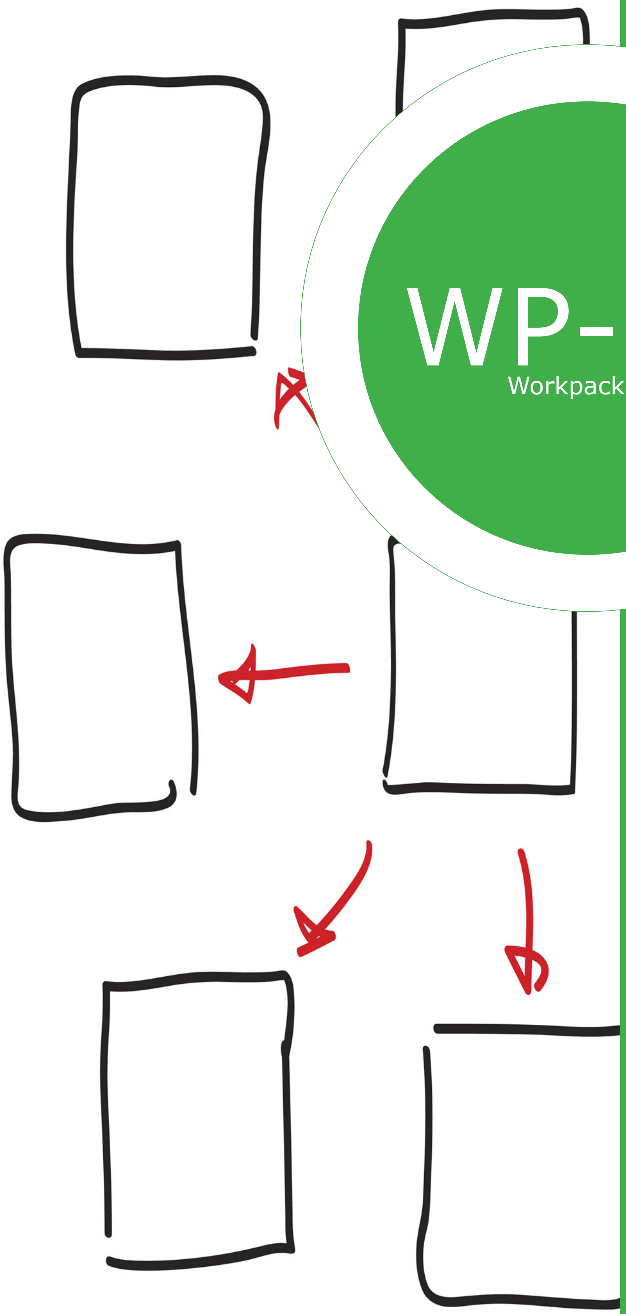
Management & Dissemination

Is this information important for me?

Consumers	●	●	●	●	●
Food Industry	●	●	●	○	○
Regulatory Authorities	●	●	●	●	●
Scientific Community	●	●	●	●	●



WP-0&8

Workpackage

communication
planning and reporting
project graphical identity

Introduction to WP0

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Management tasks

The Management tasks were aimed at strategic steering, project monitoring, and administrative and financial management of the project

Management

The management of DREAM met the – exciting – challenges posed by the project that:

i) Adopts a bold scientific approach consisting of applying state-of-the-art modelling techniques that have so far rarely been used in food sciences

ii) Gathers a truly multi-disciplinary and multi-sectorial consortium made up of physicists, chemists, process engineers, microbiologists, mathematicians, bioinformaticians, etc. in terms of expertise, academia, and technical centres;

iii) Aims to provide concrete answers to an industrial sector facing somewhat contradictory societal demands – taste and tradition, safety and nutrition, product affordability and sustainable production – by searching for solutions in fundamental science. The management needed to be:

i) Sufficiently flexible to enable its work programme to remain relevant throughout external events, whether scientific, technological, or even societal

ii) Transparent and focused enough to make the consortium work together in compliance with the work plan. These main requirements have been achieved by a three-tiered management system integrating strategic

steering (including surveying of the societal background and the scientific state-of-the-art), project monitoring (including the development of a collaborative platform, a management guideline and a risk management plan) and consortium management (including financial and administrative issues).

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Introduction to WP8

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Dissemination

As DREAM encounters important industrial and societal issues while addressing fundamental scientific issues, we paid particular attention to technology transfer since the consortium is convinced that the project results are to improve competitiveness of the European agrifood sector, one of the rationales of the project.

As the project was designed to respond to some of the most important issues listed by the European Technology Platform on Food for Life, which express industrial expectations from scientific research, industrialists will certainly be interested in appropriating the project outcomes.

Another prioritised target of the project is constituted by food authorities. Last but not least, European citizens will certainly be interested by the societal stakes of the project as it responds to some of the "hottest" societal topics that are food safety, nutrition patterns and food supply. For these reasons, it was important to disseminate outcomes as soon as possible to the relevant stakeholders.

Our vision was as follows:

- Make the best possible use of the project results by the food industry and authorities concerned.
- Ensure fruitful exchange with the scientific community, including individual scientists and initiatives.
- Inform European citizens about the societal stakes of the project and the way in which their money is used.

The intention to implement new concepts and techniques not having been widely applied by the industry, such as modelling, was enhanced significantly by practical training sessions and workshops provided to industry and science. However, the special treatment offered to SMEs was conducted in their mother tongue. This was particularly important to achieve a good understanding in the area of comprehensive dissemination activities, which is not as easy as it looks from the beginning since we had to induce awareness for this issue, first with media editors and ultimately with the parties involved.

Task 8.1

Dissemination to the industry and food authorities: Training covered potential applications, the practical benefits, the functions and operation of the models, their limitations, explanation of the practical steps, practices and tips for their use, and warnings about typical traps and malpractices. Training at national level in national languages created awareness and induced a multiplication effect (e.g. spread of use), also through development of the industry culture. A core training package was developed in English, covering each group of models.

Task 8.2

Dissemination to the scientific community: The publication in scientific journals and participation in scientific meetings as well as industrial fairs were found to be a good opportunity to disseminate DREAM developments and results through oral presentation, posters or discussion. We conducted the organisation of scientific workshops and sessions at EEFoST, IUFoST, CEFooD meetings and relevant ETPs aiming at the exchange of best practices.

Task 8.3

Training and career development: For the efficient technology transfer it is important that young researchers understand the needs of the industry, the way in which the industry thinks and operates, and the daily operating requirements in the industry in terms of process, quality and food safety management, as well as the specific priorities, conditions, resources and constraints of SMEs. We provided a practical training session for young participants linked to project events focused on the latest advances in food model development, food process and industrial quality management.

Task 8.4

Communication with the general public: The objective of this task was to inform the general public about the context and achievements of DREAM, in terms of the benefits for society. European citizens were informed about the project values, with special attention paid to communicating to the public through media invitations and via the DREAM website, project popularised publications in brochures, newsletters and lectures.

Figure 1. Active communication among partners. Meeting of the chairs with coordinator Dr. Monique Axelos, fourth from the right, in Nantes where the project started in 2009.

The concept pushed to our research under the terms ‘Generic Model Foods’, ‘Basic Knowledge Models’ and ‘Integrated Knowledge Models’ was very difficult to share with the general public.

It may look very simple and straightforward, however when you ask even professionals about the details you face certain barriers that cannot be applied in a straightforward manner to daily practices and daily life. Let us analyse this particular case in more detail.

The term ‘Generic Model Foods’ (GMFs), defined as realistic physical models in which several parameters can be varied, represents a structured statement but it has to be clearly explained that this type of model has to be established on particular food samples of the kind and is substantially different from the other, which might look to consumer eyes and taste very similar. Additional explanation of the structure and chemical composition makes this issue even more complex and complicated, not just for the general consumer, but sometimes even for practitioners in the food supply chain when they are asked to explain certain details in simple, transparent language. An additional obstacle lies in the research community. All this case development is based on lingua franca English, which is not the mother tongue of the majority of researchers in the project. Consequently, we adopt this thinking for English, and when switching back to our mother tongue we convert this to the mother tongue with the result that it suddenly takes on a different emphasis or even a different meaning. A more scientifically-complex statement has more possibilities of being transposed to another language with deformation, not just linguistically, since researchers in this area do not posses this knowledge, but also professionally.

If we look to more simplistic Basic Knowledge Models or more sophisticated models like Integrated Knowledge Models this problem remains at present and is becoming even stronger. One only needs to take a closer look at the Basic Knowledge Model, which is considered to be simpler since it describes specific aspects of the model, through heuristic or mathematical approaches, which is not clear to average professions in the food supply chain. For example, the description of the role played by temperature, pressure, chemical composition, etc. in the formulation of food structure and (food) material properties is far from simple and has many different implications in different foods.

Lastly, we addressed Integrated Knowledge Models, the dynamic networks based on software systems integrating the operating rules of Basic Knowledge Models, technical expert knowledge, food properties and food processing data from the Generic Model Foods. This complex approach clustered initial experiments and simulations to improve models in order to reveal key parameters and material behaviour and help refine, optimise and establish the food model concept prior to the pilot stage.

All of these issues were elaborated with care and we addressed potential professionals to create awareness of these new concepts and also to convey this message to the general public. This was achieved through scientific meetings that we attended (e.g. IUFoST in Brazil in the session with lectures in global meetings such as: "Food safety consequences arising from the Design and development of REAlistic food Models with well-characterised micro- and macro-structure and composition (DREAM)" or as organisers of certain activities within the programme of regional meetings such as CEFood in Serbia. Beside this we also transferred DREAM experiences and messages to students and teachers in Ljubljana at a joint workshop with the EU USA ToBeSafe project. Moreover, we also approached the general public with a contribution on World Food Day, October 16, 2012 at a national event marking this day with DREAM's contribution to in-depth knowledge of food models and food modelling. This is just to mention the main streams of our activities with dissemination in the project, which will continue via our website and book of results for a further five years, as planned.

Figure 2. DREAM (FW7) & TU_BE_SAFE (ATLANTIS) Joint Workshop, Ljubljana, May 17, 2011, which provided an opportunity to disseminate models to teachers and students in the food domain.

Figure 3. Novi Sad 2012 CEFood congress: DREAM was disseminated to the general public for food in Central Europe at the meeting with 500 participants from academia and industry.

Figure 4. IUFOST (international union of food science and technology) gave DREAM the opportunity to present their achievements in the area of modelling in Brazil, 2012, to several thousand practitioners from all over the world.

Figure 5. Marking the importance of World Food Day on October 16, 2012, Ljubljana (second from left, Prof. Dr. Peter Raspor, Responsible for DREAM project dissemination).

Figure 6. The DREAM Project International Conference: "From Model Foods to Food Models", held on June 24 – 26, 2013 in Nantes. We had a combination of dissemination activities at the event: lectures, poster presentation, round-table discussion and interviews.

Figure 7. The last DREAM project meeting, held on October 15 & 16, 2013 in Bari, Italy. The DREAM project partners (top picture) and DREAM project WP leaders (bottom picture) – from the left: Caroline Sautot *(WP0 management)*, Peter Raspor *(leader of WP8)*, Kaisa Poutanen *(leader of WP5)*, Matthijs Dekker *(leader of WP2)*, Monique Axelos *(coordinator)*, Alan Mackie *(leader of WP4)*, Nathalie Perrot *(leader of WP1)*, Carolina Realini *(leader of WP3)*, Paola Lavermicocca representing Angelo Visconti *(leader of WP6)* and András Sebők *(leader of WP7)*.

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Curious?

Consumer clip for you.

Food Modelling

Model Foods

Food Modelling

Modelling in food science is used to predict/simulate an outcome regarding quality of food, production process or food shelf life. For example, if you are developing a new food product and you are missing certain information on what is going to happen with this food product in certain conditions (heating, etc.) the food models can help you to find the right answer to the question. What makes models answer this question? Food models are records of numerous laboratory experiments conducted by food experts and scientists and collated in a user-friendly form that enables you to reuse them when needed.

Food modelling or food models reduce the number of experiments, time and costs, and provide process optimisation, improve process automation and control, due to results measured in previous experiments or production conditions. What has the DREAM project contributed to food modelling? The DREAM project used real food products for its studies, for example: dairy products, bakery products, meat, fruit and vegetables. The research demonstrated that mathematical models can be successfully adapted to complex food matrices (i.e. food structure, composition, etc.), which are profoundly changed (i.e. visually, nutritionally, etc.) from entering the substrate (i.e. milk, flavour, etc.) to the final product (i.e. Cheese, Bread, etc.).

Model Food

Model food is a material that consists of or contains essential body nutrients, such as carbohydrates, fat, proteins, vitamins and minerals in exactly known amounts. Model food is used for mimicking real food products. For example, the soft-cheese model mimics real soft-cheese characteristics. These kinds of food models are used in research and development circumstances. Why use food models rather than real food? Let us say that you would like to produce soft cheese with a lower salt content. In the early stage of the new product development you can use model food to run the experiments. This means that you may use the soft-cheese model to mimic the real soft-cheese characteristics. By using the model food you may reduce the time taken to obtain comprehensive data in order to design a real new food product. This is achieved by reducing the number of experiments necessary, food material, food waste, packing material and, consequently, cost. Can model food completely replace experiments on real food? No. The model food cannot replace real food, it can simply speed-up the development of new products with designed nutritional and food safety characteristics, e.g. less sugar, salt, fat, etc. What is the DREAM project's contribution to model-food development? One of the main contributions of the DREAM project to model food is its linking of mathematical modelling to physical model foods from different foods (pork meat, soft and hard cheese, bread and biscuits, tomatoes and brassicas). Linking physical model foods with mathematical models provides a good support tool for industry and for research.

by Peter Raspor, UL-BF & Lidija Baša, UL-BF

Food Safety

Food safety aims to assure a high level of food safety, animal health, animal welfare and plant health within the food supply chain through coherent farm-to-table measures and adequate monitoring.

Food Quality

Food quality refers to the minimum technological, nutritional and gastronomic standards for substances to qualify as fit for human consumption

Process Optimisation

From a practical point of view, we define optimisation as an approach which finds the best solution for running a particular process within certain constraints.

by Peter Raspor, UL-BF

Conclusion

by Peter Raspor, UL-BF

Since the DREAM kick-off meeting in May 2009 we have been working in-depth on research but also on innovation aspects with permanent cooperation between different stakeholders (institutions, external industrial partners, etc.). As a trans-disciplinary partnership in nine countries, DREAM focused on the development of realistic, physical and mathematical food models for use as standards to be exploited across all major food categories in order to facilitate the development of common approaches to risk/benefit assessment and nutritional quality in food research and industry.

Since the DREAM kick-off meeting in May 2009 we have been working in-depth on research but also on innovation aspects with permanent cooperation between different stakeholders (institutions, external industrial partners, etc.). As a trans-disciplinary partnership in nine countries, DREAM focused on the development of realistic, physical and mathematical food models for use as standards to be exploited across all major food categories in order to facilitate the development of common approaches to risk/benefit assessment and nutritional quality in food research and industry.

Over a period of four years, we have been constantly improving our capacity and skills in food-model design and application. The multidisciplinary approach adopted by partners in the project integrated the diverse disciplines engaged in food science and engineering, mathematics, physics, chemistry, biochemistry, microbiology, process engineering, nutrition, etc. The knowledge gained on relationships between structure/formulation property functions and structure process functions allowed the tailoring of processes according to the desired end properties such as safety, nutritive value and sensory qualities.

The project delivered several prototypes of food models covering the four major food categories: bread, cheese, meat and vegetables. On brassica vegetables, the effect of thermal processing on colour, texture parameters and the effects of processing on bioconversion and bioaccessibility of glucosinolates were modelled. On apples, a model to predict the transfer of procyanidin from fruit to juice depending on processing conditions was developed. On meat, a mathematical stoichio-kinetic model which assesses how much the kinetic parameters are affected by initial product characteristics and cooking conditions was developed.

On dairy dessert models, the impact of the interfacial composition and organisation on the connectivity between fat droplets and the microstructure of oil-in-water emulsions were characterised depending on the protein type and concentration (casein micelle and whey protein) and heat treatments. The reproducibility of a soft-cheese model and a hard-cheese model developed is three times better than the reproducibility of conventional platforms; it allows the number of trials to be reduced by 3/5 depending on the significant difference to be proved and the alpha and beta risks. The generic bread and biscuit models were developed to study the influence of added dietary fibre on product quality and to develop mathematical models to describe dough formation and product quality. All of these models were standardised and cross-validated and fully characterised in terms of structure and composition. They were also used to assess nutritional properties as well as microbiological food safety. The *in-vitro* digestion and *in-vivo* studies highlighted the effect of the different processes in changing the physical and molecular structure of food and consequently the bioaccessibility and bio-availability of nutrients or bioactive compounds.

The model development was conducted in close collaboration with food manufacturers through a specification-based approach. All of these models were implemented by means of the mathematical approach. This approach realised a complete dynamic description of food processing using an innovative strategy exploiting the very latest advances in cognitive and complex system sciences to allow generalised methodologies to be extended to other food products. Starting from the project outcomes, the industry is able to develop food matrices tailored to requested functions such as controlled nutrient delivery and bioactive compound release, as mentioned above.

During the project, attendance was high at the various DREAM meetings organised in France, Spain, Slovenia, Hungary and Italy and we received very positive feedback from the press and relevant technological and scientific community. Respecting this, we did not focus solely on research but also introduced the dissemination of our findings to relevant environments such as science, industry, consumers and regulators.

Models and protocols developed within DREAM were efficiently disseminated by expert partners via existing scientific and research channels (CEFood, EFFoST and IUFoST congress) R&D channels (ETP and national platforms, CIAA and national federations, EFSA and national regulatory bodies) to be used by scientists, SMEs and multinationals to improve nutritional quality and benefit-risk management of the food supply networks.

Finally, not just research but also industry is now able to develop food matrices tailored to requested functions such as controlled nutrient delivery, bioactive compound release, etc.

In short we can summarise our achievements as follows:

A) Industrial achievements: decision-support systems allowing the realisation of tailored microstructure in the food industry; protocols to produce operating procedures to standardise model foods and practical guidelines on the use of models for industry.

B) Technological achievements: realistic and easily-reproducible in-laboratory food models encompassing large structure variations; optimised methods to characterise relevant structural, chemical and biological characteristics and monitor their changes during processing; critical assessment of the relevance of the developed models to determine relationships between matrix microstructure, biological and chemical composition, and activity, delivery and transfer of bioactive compounds (nutrients, phytochemicals, toxins, etc.) during static (storage) and dynamic conditions (processing, in-vivo degradation, etc.); and critical assessment of the relevance of the developed models to evaluate the impact of environmental changes on the microbial population of real products and, conversely, the effect of microbial populations on food structures.

C) Scientific achievements: mathematical models linking food formulation, processing, resulting matrix structure and material properties; cognitive mapping of technical know-how involved in the construction of food matrices; unified integrated knowledge description of each selected food matrix, and description of the relationships linking molecular and macroscopic structures to functionality.

The DREAM Project International Conference “From Model Foods to Food Models” held from 24th until 26th June 2013 in Nantes.

Perspectives

by Monique Axelos, INRA (DREAM coordinator)

Over the last four years DREAM partners have joined forces to develop models keeping in mind the idea that modelling will allow complexity to be mimicked and make progress in the process-properties relationship in order to be able to design tailor-made food. Even though food processing is a field in which computer modelling is just emerging, the mathematical knowledge integration approach developed in the project appeared to be relevant and useful in giving interesting results as illustrated in this book. Three major issues must be pointed out.

The approach used in DREAM makes it possible to i) integrate multidisciplinary skills, ii) take into account a large number of parameters which could be integrated into decision support tools, and iii) gather heterogeneous and complex data and face the lack of data. While some progress has been made during the project further works must be undertaken. For the future, our findings suggest important avenues for further exploration. There are three that I will mention here.

Addressing issues on the collaboration between science and industry is of major importance in order to be sure that the models developed meet the real needs of the industry. For this purpose, interactions with stakeholders should play a key role and should be held sufficiently upstream of the model development in the laboratory so that opinions from both sides can genuinely be taken into account. Beside direct relationships among project partners, our work showed that the main barrier to the use of models by the industry is a lack of knowledge of what a model can do. Significant effort should be placed in creating awareness and encouraging the use of modelling in the food industry, especially for SMEs, proving that models, as time-saving and cost-effective tools, provide good support for innovation or for improving existing processes in order to reach new objectives. Work should continue on improving the industry guide and training tools that have so far been developed.

The second major avenue of interest is the use of this approach to answer complex, multi-objective new societal challenges like food sustainability. We know that the food system makes a significant contribution to greenhouse gas emissions and gives rise to major environmental impacts like loss of biodiversity, water extraction and pollution, energy and material waste. In order to cope with this challenge, technologies are required to enable the management of elements (such as energy, conservation, waste reduction and efficient use of capacity) but other non-technical data such as consumer acceptance, economic impact, regulation modification, etc. must be taken into account. Knowledge integration as developed in DREAM appears a very adequate and realistic approach in order to take into account a large number of criteria in a dynamic way and to provide a new way of conceptualising this challenge.

The third avenue deals with the increase of knowledge acquisition and integration in-laboratory at the interface between mathematics, cognitive and bio-technical sciences. Even within the academic world this approach is still poorly developed and implemented in daily work practices. It is a real challenge for public institutions to create awareness and encourage scientists to exchange with mathematicians at an early stage in order to determine the lack of knowledge and to work together to build a new modelling approach. Food science has very much to gain by going along this route. Respecting new knowledge and skills in this area will contribute greatly to better quality, greater food safety and more economical food production, preservation and distribution.

The DREAM Project Consortium

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Project Facts

Acronym	DREAM
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Funding Scheme	Large Collaborative Project
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EC Contribution	€5,995,786
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SEVENTH FRAMEWORK
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