QUA-SI-PORK: MODELLING OF MEAT QUALITY IN PIGS

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SUMMARY

Meat science combines several disciplines. Modelling can help in integrating these disciplines, which may improve our understanding of the development of meat quality. Parts of the processes involved have been described in a conceptual way, or even modelled. Present approach (Qua-Si-Pork: Quality simulation of pork) aims to integrate such studies into a more general model. The foreseen model consists of 5 modules: Animal, Temp, Biochem, Denaturation and Meatq. The central philosophy is that knowledge of animal characteristics, pH and temperature provide the opportunity to predict meat quality. This was recently shown in literature. The modules Temp and Denaturation have been developed elsewhere and especially Temp has proven its value by very accurately predicting the course of temperature in pig carcasses. The module Biochem calculates pH and temperature from the glycolytic process in a time dependent way, taking into account animal characteristics like genotype, fibre type distribution and glycogen content. Biochem has been designed in its general structure, but still has to be developed further. It is expected that Qua-Si-Pork will provide a framework to integrate the disciplines involved in meat science by presenting an overall framework and by indicating research areas. Benefits are especially expected from the integration of separate mechanistic modelling approaches.

Key words: Meat quality ; Simulation model ; pigs

Introduction

The process of conversion of living muscle to edible meat is highly complex and only partly understood. To understand the underlying mechanisms, one has to comprehend (and have data on) enzymes, protein denaturation, thermodynamics, biological variability (within and between animals) and several other biological factors. In the last decades, the amount of published information in this area has multiplied significantly. The increased specialism between the research fields involved make it increasingly difficult to keep view on the present state of knowledge. On the other hand, the increased understanding of the underlying mechanisms may facilitate prediction of meat quality. Both for combining different disciplines and for predicting effects, modelling has proven a useful tool in many research areas (Dransfield and Scheffer, 1991).

In the present contribution, the general outline of an integrated system (model) will be described. The major aim of the model is to predict ultimate meat quality as a product of animal and environmental factors. The approach will not be fully original. Several studies in literature have provided essential components for the present approach (among others: Offer, 1991; Dransfield, 1993). These will be referenced when appropriate. Present modelling exercise aims to provide a framework to integrate knowledge. The model is designed as a modular system. In this way, existing models or concepts can easily be incorporated, and verified/validated independently. The main aim of present paper is to present the general structure of the model. Its main parts will be presented concisely. Key concepts in the approach are glycogenolysis, pH, temperature and protein denaturation. This is reflected in the modules.

The proposed model is called Qua-Si-Pork: Quality Simulation of Pork. For the time being, the Qua-Si-studies will focus on pork. Offer (1991) has proposed a model to simulate the process of protein denaturation. This model will be incorporated in the present approach. General features of the model may apply to other species.

General outline

Post mortem, pH decreases while temperature can increase in the muscles due to the *post mortem* anaerobic breakdown of energy sources. The increase in temperature is counteracted by heat loss to the environment, especially after scalding and evisceration. The combination of high temperature and low pH causes protein denaturation, which is a major influence on meat quality. This simplified (and incomplete) view on meat science forms the basic structure of the model, which is presented in Figure 1. The model is designed in modules, which represent discernable concepts in the above described view. In the following paragraphs, each module will be described and discussed shortly.

Starting up: the basal module Animal.

Several animal factors influence the processes in the muscle during and after slaughter. In the basal module Animal, these animal factors are combined. The basal module Animal calculates the physiological status of the animal and its muscles at the onset of the *post mortem* processes.

The basal module Animal is a small model in itself. It calculates glycogen levels in the muscle as a result of animal and environmental factors. The major concept is 'glycogen content', which is a physiological feature. Therefore, the calculations can be validated experimentally. Figure 2 presents the general principle on which pre-slaughter muscle processes are based. The glycogen content, which is an essential feature in the *post mortem* process, is assumed to be dependent on the genotype (breed, presence of Hal^+-gene or rn^+-gene etc.) of the animal and its nutritional history. The glycogen store level can be affected before slaughter through short term (minutes: stress) and longer term effects (hours: increased activity or fasting). Before slaughter, lipid can be involved in replenishing energy stores.

Glycolysis: the bio-chemical module Biochem

The bio-chemical module is a central module in the model. In this module, the *post mortem* conversion of energy substrates into metabolites is calculated. Glycogen (including glucose), ATP and Creatine-Phosphate are regarded as the major energy substrates. During life, each substrate is re-synthesised. *Post mortem*, resynthesis ceases to a large degree. It is explicitly assumed that there is a priority in the exhaustion of energy substrates. This does not imply that there is a similar priority in use of the substrates, but it implies that the metabolites with a higher priority are resynthesized at the expense of those with the lower priority. The assumed priority is: 1. ATP, 2. CP, 3. Glucose, 4. Glycogen (a.o. Bendall, 1973; Fernandez and Tornberg, 1991). These assumptions are based on the experimental observations that the substrates with the higher priority have a later definite decline compared to substrates with the lower priority. A part of the energy substrates can be metabolized before slaughter due to physical exercise or stress. This has been dealt with in the basal module Animal (see above). It is assumed that these *ante mortem* processes are only reflected in glycogen and lactic acid contents, and that the other substrates (ATP, CP) are virtually replenished. This is in line with the assumed priorities. Onset of rigor is assumed to be caused by absence of ATP (Bendall, 1973).

The separate fibre types differ distinctly in compositional and biochemical properties. Therefore, model calculations will be performed at fibre level. Effects on the muscle as a whole will be calculated by combining the effects on separate fibres, taking fibre type distribution (dependent on breed and muscle) into account.

Description of the enzymatic regulation

The mentioned processes are catalyzed by enzymes. The breakdown of glycogen into lactate involves more than 10 different enzymes (Stryer, 1981). Enzyme activity can be described using the Michaelis-Menten approach. The use of Michaelis-Menten parameters has proven to be very useful in modelling, and is described comprehensively by France (1991). In this approach, affinity constants and rate constants of each enzyme involved have to be known. Furthermore, exogenic influences on the process (pH, temperature) have to be described for each enzyme system separately. Experimental data for this are highly lacking. There are indications that there are only a few major 'rate limiting' enzymes involved in the glycogenolysis, at least *in vitro*, mimicking the living muscle (Scopes, 1973). The process can be simplified by describing it as dependent on those few enzymes. However, if there are still drawbacks in parameterizing this approach, an acceptable alternative can be to describe the enzymatic process as a one-enzyme-system. It can then be expressed as with the Micahelis-Menten-method with a hypothetical enzyme. The required parameters then have to be derived empirically on available data. This method is chosen for the present model. A similar approach, describing kinetics for entire transactions in stead of describing the individual reactions within that pathway was used by Pettigrew et al. (1992), dealing with a mechanistic model which could not be parameterized due to lacking physiological data. Using such an approach, the process is described mechanistically, and can easily be adapted when new information comes available.

In its simplest form, the change in pH and temperature as a result of glycogenolysis can be described as in Figure 3. Important in this are the feedback systems, in this example temperature and pH. The mechanism as presented in Figure 3 for the glycogenolysis also holds (in general terms) for the other energy delivering processes. Feedbacks can be more complicated, like ATP breakdown being fed back both by metabolites (AMP) and the environment (pH, again resulting from metabolites).

Figure 3 illustrates that the process can slow down or cease due to different factors: depletion of glycogen or a feedback on the enzymatic process due to the changed pH or temperature. On the other hand, the process can be enhanced by the temperature if heat production permits the temperature to rise to a more optimal temperature. In reality, the process is far more complex, as there are more metabolites involved in the post mortem process. The described interactions between pH, temperature, substrates and metabolites are dealt with by the close connection between the modules Biochem and Temp. The rates of the processes as described in Figure 3 are modelled in the form of Michaelis-Menten method. In this method, effects of pH and temperature can be included.

Calculation of the pH

The Biochem-module calculates concentrations of metabolites. These metabolites (especially lactic acid) affect the pH. However, in converting metabolite concentration into pH, it has to be taken into account that muscle proteins have a buffering capacity, and that the relation between metabolite-concentration and pH is also affected by temperature. In short, the conversion of metabolite concentration into pH is a mechanism which can be modelled separately, but which is still quite complicated and for which a lot of information is incomplete.

Thermo-dynamics: the module Temp

During life, body temperature in homeotherms is maintained within a rather narrow range through a vast array of physiological mechanisms. The actual temperature in the muscle after slaughter is a combination of the physiological temperature (initial temperature), heat production and heat transfer with the environment.

Heat loss as a thermo-dynamic process can be modelled at a mechanistic level using the approach as presented by Veerkamp (1975). Such a model has been developed for pigs and has proven to be able to describe changes in the muscle temperature quite accurately (Van der Wal et al., 1993). This model only describes the physical aspects of temperature. It does not take heat production due to biochemical process into account. For the Qua-Si-Pork-approach, this heat production needs to be included. The produced heat is calculated by the bio-chemical module, and can easily be incorporated in the temperature module.

The module to calculate the thermal behaviour of the carcass (module Temp) requires some compositional carcass characteristics and several thermophysical properties of the tissues (both for the fat layer as for the muscle mass). The program considers the tissue to be in a cylindrical shape, with an insulating fat layer surrounding the muscle. For every time step, the module Temp calculates the (change in) temperature at the muscle location of interest, taking into account the heat loss as determined by the environmental properties and the heat production due to the glycolysis.

Protein denaturation: the module Denaturation

Modelling proteolysis

The process of protein denaturation in the *post mortem* muscle is modelled by Offer (1991). In that approach, myosin denaturation is taken as the major part of protein denaturation and is held responsible for the development of meat quality characteristics like water holding capacity and to a certain extent for colour. Offer modelled the denaturation of myosin as a function of temperature, time and pH. The denaturation process is assumed to cease when the muscle enters the rigor phase. The pH, rate of pH-fall, temperature and onset of rigor are not calculated by Offer's model, but the model presents the effects of these factors on protein denaturation. This approach is very useful for the present Qua-Si-Pork-approach. The modules Temp and

Biochem calculate the pH, temperature and onset of rigor in the muscle. The mechanism as presented by Offer (1991) offers the possibility to convert this into meat quality aspects by means of calculating protein denaturation.

Meat quality characteristics: the module Meat quality

In the module Meat quality, chemical and physical muscle properties will be converted to meat quality characteristics. Major aspects of meat quality are drip loss, colour and tenderness. There is a considerable amount of published information available on each of these characteristics. However, none of them is fully understood. In the present paragraph, the quality parameters water holding capacity/drip loss, colour and tenderness will be dealt with shortly.

Colour

Colour is the result of light scattering of the muscle. Denaturation of both sarcoplasmatic and structural proteins may be involved in the changing colour. The development of colour in pork is still poorly understood, although there is consensus about the fact that protein denaturation is involved (Bendall and Swatland, 1988). Intensity of muscle colour is (among others) affected by pigment level and by surface structure. The first one depends primarily on muscle function, whereas the latter one is influenced to a large extent by pH (Monin and Ouali, 1991). It remains unclear to what extent the associated role of the pH on colour is effected through pH. The definitive concept of describing the development of meat colour still has to be designed for Qua-Si-Pork. Aim is to disentangle confounded factors which are related to colour. Furthermore, possible interactions between influencing factors should not be neglected.

Water holding capacity

In the model of Offer, water holding capacity is regarded to be dependent on the filament lattice spacing, which is a result of the distance between the heads of the myosin molecules. In that approach, water holding capacity can be calculated from the myosin denaturation. Furthermore, water loss from the muscle partly results from glycogen breakdown, as each unit of glycogen holds 2-4 units of water (Fernandez and Tornberg, 1991). This water can be expected to be expelled when the glycogen is metabolized. Finally, a direct effect of pH on water holding capacity can be expected through the pH-dependent charges of the muscle proteins. All these factors have to be combined to calculate the loss of water during *post mortem* changes in the muscle.

Tenderness

Tenderness and texture of meat is a highly complex phenomenon. Protein denaturation may be involved in changes of tenderness *post mortem*. There is experimental evidence that myosin denaturation is involved in changes in extensibility of sarcomeres, and thereby contributes to the subjective impression of softness, at least in PSE muscle (Bendall and Swatland, 1988). Offer (1991) considers the denaturation of myosin to be the decisive event in determining the softness of meat. Modelling denaturation of myosin alone will probably not describe the process of texture changes, due to the fact that several structural proteins are involved (Monin and Ouali, 1991; F.J.G. Schreurs, pers.comm., 1994). In this, enzymatic processes are involved. There is no consensus in literature about the enzymatic regulation of the *post mortem* tenderizing processes. Dransfield (1993) has described the role of the calpain-system in beef tenderization. Tenderness is not a major problem in pork. Still, Dransfield's approach may form a basis for including tenderness in Qua-Si-models. This part requires further attention.

General

Summarizing, it can be stated that the relations between chemical and physical muscle characteristics with meat quality (either objective of subjective) have yet been described only in general terms for the present approach. As there is a vast amount of experimental data, the required predictions seem possible. A foreseen problem is that the influencing factors (temperature, pH, muscle type etc) in the experimental data are often confounded, which may limit parameterisation.

Discussion

Modelling in a modular way

Simulation models have received a lot of research attention in the last two decades. In meat science, the interest is of more recent date. Yet, several useful approaches have been developed and published (see Dransfield and Scheffer, 1991). Present approach is another attempt, but it does not intend to be superior to the others. More generally spoken, present Qua-Si-Pork-approach can be regarded as a modelling approach which models the relation between available models in the field of interest. This approach benefits from the usual advantages in modelling, like being able to draw attention to white spots. At present, it is foreseen that especially description of the bio-chemical process in the muscle requires an integrated quantitative approach. Benefits of present Qua-Si-Pork approach are especially expected from the integration of separate mechanistic modelling approaches.

Central concept of the model

The central concept of the Qua-Si-Pork-model is the combined effect of pH and temperature on the muscle. This is close to the key concept of the model of Offer (1991). The major difference is that temperature and time are explicitly predicted, whereas they are input factors in the Offer-model. The importance of the interaction between pH and temperature on post mortem changes is stressed by results like those reported by Fernandez and Tornberg (1994) on basis of a well conditioned experiment. More generally, interactions between factors make understanding and having grip on data difficult. Models offer the opportunity to study such interactions. In this respect, it is interesting to note that more recent reviews draw more attention to interactions (e.g. Fernandez and Tornberg, 1991), instead of trying to describe a general view together with exceptions or irregularities.

Use of the model

A conceptual view on *post mortem* muscle biochemistry may help in understanding and explaining the variability in meat quality. Both between-batch-variation, between animal variation and within animal variation contribute to the diversity. A model can provide a framework to segregate the underlying factors. An important feature of models like the one presented here is their capacity to calculate '*the effect of*'-relations in a protocollar way. In this way changes in meat quality resulting from changing animal or environmental circumstances can be assessed. An important element in this is the prediction of serious deviations in meat quality. There are several quality deviations in pork, among which PSE, DFD and ACID MEAT are major ones. An important checkpoint for the validity and usefulness of the model is its capacity to predict such deviations in meat quality. Offer (1991) partly judged his model on its capability of predicting PSE-characteristics.

Final remarks

A model is (by definition) a simplified view on the system. This especially holds for the present domain. Much of the mechanisms between muscle and meat are barely understood. The lack of scientific consensus about the enzymological regulation is a good example of this. However, the modelling approach of Offer (1991) has shown that this does not need to be an obstruction for a conceptual view on the process. A general, but essential point is that a model never represents 'the truth' and should be judged in view of the aim of the model. The present approach attempts to be a starting point, aiming research groups to focus on major inadequacies.

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