Development of a multi-physical finite element-based model that predicts water and salt transfers, proteolysis and water activity during the salting and post-salting stages of the dry-cured ham process

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ABSTRACT

With the objective of developing a valuable tool to help professionals find new technological approaches to reducing salt content in dry-cured hams, the aim of this study was to build a 3D multi-physical finite element-based model that would estimate proteolysis, water activity and salt and water content distributions during the low-temperature salting and post-salting stages of the dry-cured ham process. For this purpose, an accurate 3D ham geometry was first constructed from a series of 2D slices of a green ham. The 3D "numerical ham" model built using Comsol® Multiphysics software demonstrated very good prediction of in-ham salt and water content distributions, water activity distribution, proteolysis index, and ham weight loss. The accuracy of the model was evaluated by comparing all the predicted values at the end of the salting and post-salting stages with experimental values measured over the same period of time in samples extracted from 10 Bayonne hams.

1. Introduction

During the dry-cured ham production process, which generally comprises salting (about 10–15 days), post-salting (about 7 or 8 weeks), pre-drying (1 week) and dry-ageing (5 to more than 18 months), salt is a multifunctional element that strongly influences final product quality and food safety. Salt plays a role in developing water holding capacity, texture and flavour, and in combination with temperature, pH and water content, it shapes the time course of proteolysis, i.e. meat protein degradation mediated by endogenous proteolytic enzymes. Salt also inhibits the growth of pathogens and spoilage microorganisms (Arnau et al., 1997; Serra et al., 2005; Taormina, 2010; Toldrá and Flores, 2000). However, although salt is essential to human health, controlling blood pressure and helping the transmission of nerve cell impulses, most surveys in industrialized countries report an average daily salt consumption of 8–10 g per person, whereas 2 g per day is physiologically sufficient for a person weighing 60 kg. This excessive sodium intake has been clearly linked to hypertension, increased

risk of stroke and cardiovascular disease, and even to some cancers (Nazario et al., 1993), together with higher calcium excretion, which can lead to osteoporosis (Karppanen and Mervaalaa, 2006; Lawes et al., 2006). These factors have prompted many studies designed to find technological solutions for reducing salt content in manufactured food products and so obtain healthier foods. In the specific case of dry-cured ham manufacturing, there have been decades of efforts to reduce final salt content without impairing final product quality. However, reducing salt content in dry-cured hams can increase the water activity and also, can alter the texture of the product, which can become too soft, in turn adversely affecting sliceability. NaCl reduction in dry-cured hams is mainly achieved through one of two approaches: (a) direct reduction of NaCl content, or (b) partial substitution of NaCl by other salts. Results of the first approach show that a longer post-salting time is needed for lower-sodium hams to reach the same a_w values as hams normally salted with 100% NaCl, a prerequisite for microbial stability. No more than a 25% salt reduction can be achieved by this first approach. Grau et al. (2008) reported that freezing then thawing hams before the salting process reduced salting time and yielded hams with a lower final salt content, but this approach required special caution to avoid microbiological stability issues and defective final texture due to abnormal proteolysis (Desmond, 2006;

Ruiz-Ramirez et al., 2006). Given these concerns, NaCl substitution by potassium chloride, calcium chloride, magnesium chloride or K-lactate has been explored as a second approach. However, manufacturing hams with low-sodium-content salt mixtures requires lengthening the low-temperature post-salting stage, because of the lower a_w-depressor effect exerted by the salts used to partially replace NaCl (Aliño et al., 2010). Accurately modelling what happens during the low-temperature stages of the dry-cured ham process is thus of great interest for professionals looking to find salt reduction options.

In the food industry, salting and drying are mass transfer processes leading to time-variable water and salt content profiles. It is important to quantify and assess the time course of these two variables, to gain a fuller understanding of their effects on the biochemical evolution and textural properties that develop during dry-cured ham manufacture. Non-destructive methods such as nuclear magnetic resonance (NMR) spectroscopy or computed tomography (CT) imaging are well-suited to estimating local salt and water values in dry-cured hams (Fantazzini et al., 2009; Vestergaard et al., 2005). More recently, Santos-Garcés et al. (2012) and Haseth et al. (2012) used CT imaging to build salt and water content models for different stages in the dry-curing ham process, and concluded that CT was well-suited to characterizing and optimizing dry-cured ham salting processes. However, these analytical tools have to be used repeatedly during the several-month production process in order to track in-ham water migration and salt diffusion patterns. Numerical modelling and simulation could be good alternative candidates for tracking these patterns, being non-invasive, non-destructive, less costly, and faster. Barat et al. (2011) modelled salt transfer mathematically, and estimated NaCl and KCl diffusion coefficients on pork meat samples. Said et al. (2007) numerically simulated 3D salt diffusion and distribution in a pork belly side that had an irregular geometry and a very heterogeneous composition by developing a finite element-based model with a mesh created on a 3D geometry previously obtained from the analysis of X-ray CT images. Finite element methods offer a good way to solve, not only heat transfer equations (Cepeda et al., 2013), but also the mass transfer equations describing moisture and salt diffusion in meat-based food products subjected to salting and/or drying. Interestingly, Cevoli et al. (2014) recently used Comsol® Multiphysics software to develop 2D numerical models to study water transfers inside a salami-type dry-fermented sausage during the ripening process and post-packaging storage.

As previously stated, the final quality of dry-cured ham depends on how proteolysis has evolved during manufacturing in response to changes in various factors such as temperature, water content and salt content. Zhao et al. (2005) observed that salting depressed the potential activities of proteolytic enzymes such as cathepsin B and L down to only 9.31% and 13.66% of their original potential activity, thus confirming the inhibitory role of salt on proteolysis. Similar results were reported by Harkouss et al. (2014), who highlighted the promotive role of temperature, and the converse inhibitory role of salting and drying on the increase in proteolytic intensity measured in laboratory-prepared pork meat samples. In addition, these authors set up phenomenological models allowing proteolysis to be quantified in five different pork hindquarter muscles as a function of temperature, water content and salt content. However, quantitative modelling of salt diffusion, water migration, heat transfer and proteolysis patterns has never been attempted in dry-cured ham. We set out to build a multi-physical 3D finite element-based model developed via Comsol® Multiphysics software that would combine determination of proteolysis from the phenomenological models developed by Harkouss et al. (2014) with salt penetration, water migration and heat transfer

modelling in a real ham geometry. Here, as our objective was to develop a valuable tool to help professionals find new technological approaches to reducing salt content in dry-cured hams, we focus on the modelling and prediction of water and salt transfers, water activity and proteolysis during the early stages of the dry-curing ham process, i.e. the low-temperature salting and post-salting stages. In addition, the salting stage modelled here corresponded to a "limited salt input" salting procedure consisting in one-step 15-day salting of only the muscle part of a green ham, and not its rind.

2. Materials and methods

2.1. 3D ham geometry and meshing

Constructing an accurate representation of a 3D ham was a complex task. It was based on the analysis of a series of high-quality computed tomography images corresponding to 2D slices of a green ham weighing 10.3 kg. Following Said et al. (2007), we used automated tools for noise reduction, smoothing and contrast sharpening together with data manipulation tools such as re-sampling and rescaling. The image analysis was automated by applying specific tools such as thresholding to localize several parts of interest in the ham, namely rind, muscles, bone and the thin film of fat between the different muscles, in the CT images after specification of min/max signal intensity values. In all, 181 X-ray CT images of green ham were segmented using the specific software Mimics® (Materialise, Leuven, Belgium). The segmented objects were then simultaneously connected to form the 3D ham geometry. This geometry was then smoothed and meshed repeatedly to obtain a high-quality surface mesh (Fig. 1a). A volumetric tetrahedral mesh with extra-smooth boundaries was then obtained, corresponding to a ham 42 cm long, 32 cm wide, and 15 8 cm deep. Finally, the 3D ham model consisting of 202,000 tetrahedral meshes and containing five different groups of muscles was imported into Comsol® Multiphysics software (Fig. 1b). Fig. 1 shows the realism of the 3D geometry of dry-cured ham created using this procedure.

2.2. Proteolysis modelling

Harkouss et al. (2014) published a set of phenomenological models built to quantify proteolysis rate as a function of temperature, water content and salt content; the effect of pH on proteolysis evolution was neglected in their experimental study. Here, proteolysis was modelled by solving Eq. (1):

$$\frac{d\,PI}{d\,t} = R_i, \tag{1}$$

where PI is the proteolysis index (%), which characterizes proteolytic intensity. In Eq. (1), it was approximated that proteolysis rate could be calculated at each time step from the global phenomenological model proposed by Harkouss et al. (2014) in which four different pork muscles (semimembranosus, semitendinosus, biceps femoris and rectus femoris), which together make up the bulk volume of a pork ham, were considered together, due to their similar experimental proteolysis time course. This global phenomenological model is given by Eq. (2):

$$R_i = 8.286.10^{-4} - 1.024.10^{-2}.T + 1.147.10^{-4}.S + 1.466.10^{-4}.W - 2.62.10^{-4}.TS + 3.254.10^{-4}.TW - 1.746.10^{-6}.SW, \tag{2}$$

where T is temperature (°C), S is salt content (kg salt.kg dry