WATER MOBILITY AND DISTRIBUTION IN PORCINE MUSCLE *POST MORTEM* AND THE EFFECT OF CHILLING RATE

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Key words: water-holding capacity, water distribution, pork, chilling regime

Background

Water-holding capacity (WHC) is a major quality attribute of fresh meat (Andersen, 2000). However, the exact mechanisms determining the WHC of meat are far from understood. Especially, characteristics about proposed water populations in the meat and how they are interrelated with drip loss and how water populations are affected by intrinsic and extrinsic factors need to be studied further. NMR relation measurements provide information about the compartmentalisation and mobility of water in muscle and meat (Hazlewood et al.,1974). Moreover, NMR relation measurements are also shown to be able to determine potential drip loss in meat (Tornberg et al., 1993; Bertram et al., 2001). Consequently, this method seems appropriate to use for further elucidation of water mobility and distribution during the conversion of muscle to meat and how interior and exterior factors affect these.

Objective

The objective of the present study was to use Low-Field (LF) NMR relaxation measurements to characterize the proposed water populations in pork and investigate how the distribution and mobility of the water changes *post mortem* as influenced by the halothane gene (Heterozygote carriers (Hal-Nn) vs. wildtype) and chilling regime.

Methods

The macro- and microstructures of porcine meat of different technological quality (high to low WHC) were controlled using either chemical modulators (DMSO, Urea, NaCl) or physical treatments (mincing, homogenization, centrifugation). Subsequently, LF-NMR relaxation measurements (23.2 MHz Maran Benchtop Pulsed NMR Analyser, Resonance Instruments, Witney, UK) were carried out on well-characterised meat samples, and compared with microscopic investigations to further reveal the results in relation to physical features of the pork. Moreover, LF-NMR relaxation was continuously measured during the *post mortem* period of 12 porcine muscle samples from DPLY cross-breed slaughter pigs, which were carriers (Hal-Nn) and non-carriers (wildtype) of the halothane gene exposed to two commercially used cooling profiles.

Results and discussion

LF-NMR relaxation revealed the presence of three distinct water populations (T_{2b}, T_{21}, T_{22}) in meat (Figure 1a), which could be described due to the physical structure of the meat (Figure 1b). T_{2b} constitutes water tightly associated with macromolecules, T_{21} constitutes water located within highly organized protein structures, e.g. water in tertiary or/and quaternary protein structures and spatials with high myofibrillar protein densities including actin and myosin filament structures, and T_{22} constitutes the extra-myofibrillar water containing the sarcoplasmatic protein fraction.

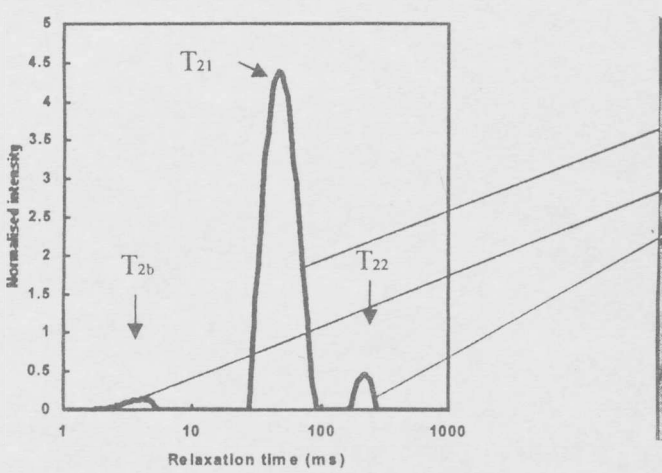

Figure 1a. Distribution of T_2 relaxation times in pork. T_2 data were performed with a τ-value (time between 90° pulse and 180° pulse) of 150 µs. Measurements were performed at 25°C, and data were acquired from 4096 echoes as 16 scans repetitions with a repetition time of 2 sec between two succeeding scans.

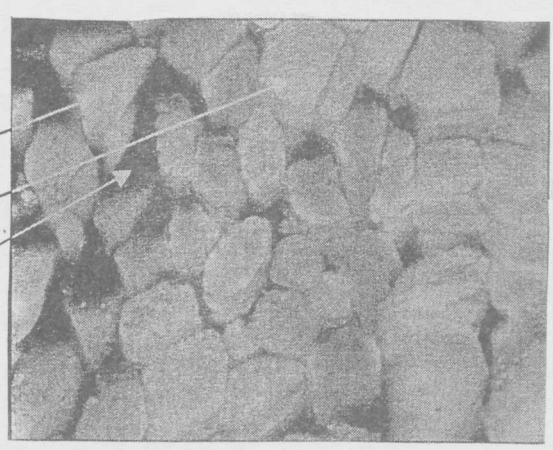

Figure 1b. Confocal microscopy of pork 24 h *post mortem* (10 x magnification) (TCS NT, Leica Microsystems, Wetzlar, Germany). Before examination the sample was covered with coverslips whereupon Nile red dissolved in acetone was settled, and the acetone was evaporated before mounting.

Comparison of WHC, determined by Honikel's method (Honikel, 1998), and the water populations determined by NMR revealed high correlation between the T_{22} population and WHC (Figure 3).

Moreover, changes in water mobility and distribution were followed *post mortem* using continuous LF-NMR measurements. Both chilling regime and genotype significantly affected changes in the characteristics (rate constants and populations) of T_{2b}, T_{21} and T_{22}, and hereby the WHC of the meat. Figure 4 displays the found changes in the populations of T_{22} (extramyofibrillar water) by time.

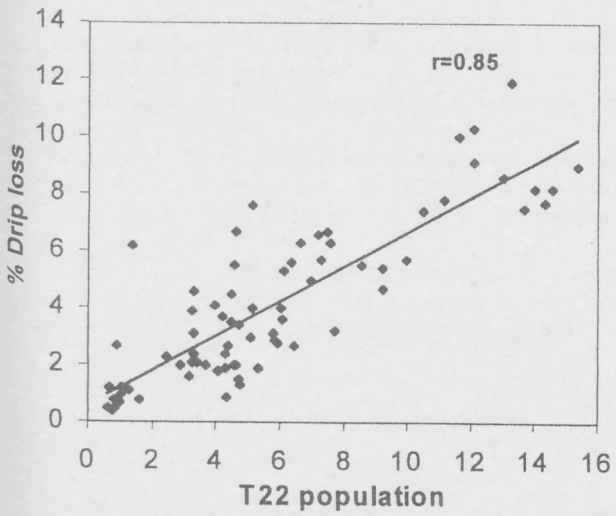

Figure 3. Relationship between T_{22} population and drip loss, determined by Honikel's method (Honikel, 1998).

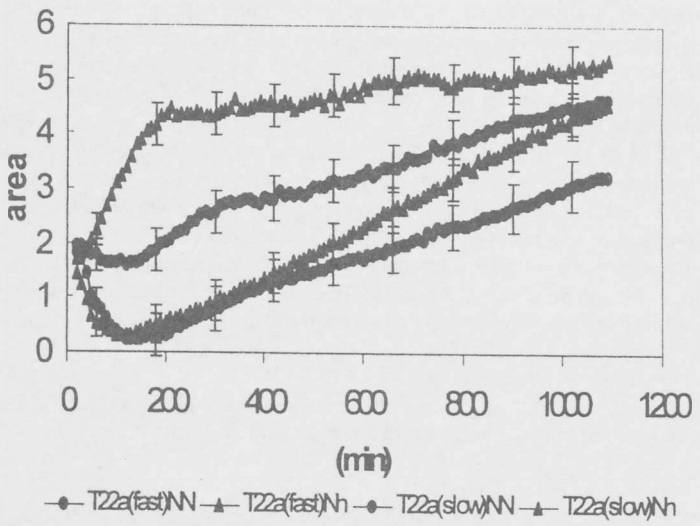

Figure 4. The *post mortem* course of the population of relaxation described by T_{22} for genotype HAL-Nn and HAL-NN and slow and fast cooling, respectively. LSMeans are given. Bars show standard errors.

Conclusions

The present study reveals that drip loss originates mainly from the extra-myofibrillar water population containing the sarcoplasmatic protein fraction. Moreover during the conversion of muscle to meat, the intrinsic water distribution is heavily affected by genotype and chilling regime through their effect on membrane stability.

References

Andersen, H. (2000): What is Pork Quality? In: Quality of meat and fat in pigs as affected by genetics and nutrition. EAAP publication No. 100, Zurich Switzerland, 15-26.

Bertram, H.C., Andersen H.J. & Karlsson A.H. (2001): Comparative study of low-field NMR relaxation measurements and two traditional methods in the determination of water holding capacity of pork. *Meat Science,* **57**, 125-132.

Hazlewood, C.F., Chang D.C, Nichols B.L. & Woessner D.E. (1974): Nuclear Magnetic Resonance transverse relaxation times of water protons in skeletal muscle. *Biophys. Journal*, **14**, 583-606.

Honikel, K.O. (1998): Reference Methods for the Assesment of Physical Characteristics of Meat. *Meat Science*, **49**, 447-457.

Tornberg, E., Andersson A, Göransson Å & von Seth G. (1993): Water and Fat Distribution in Pork in Relation to Sensory Properties. In: Pork Quality: Genetic and Metabolic Factors. Ed. E. Puolanne & D.I. Demeyer with M. Ruusunen & S. Ellis. CAB International.