MRI-aided texture analyses of compressed meat products

Franci Bajd a, b, Martin Škrlep c, Marjeta Čandek-Potokar c, Igor Serša a, b, *  

a Jožef Stefan Institute, Jamova 39, Ljubljana 1000, Slovenia  
b Faculty of Mathematics and Physics, University of Ljubljana, Jadranska 19, Ljubljana 1000, Slovenia  
c Agricultural Institute of Slovenia, Hacquetova 17, Ljubljana 1000, Slovenia

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ABSTRACT

Viscoelastic properties of food products can already be assessed by conventional (non-imaging) methods, such as compression-recovery creep (CRC), texture property analysis (TPA) and stress-relaxation (SR) methods. In the study, an alternative to these methods based on MRI of samples in a compression cell is proposed. Different commercial meat products were subjected to two different compression protocols. The first (protocol P1) was designed to mimic a CRC experiment and the second (protocol P2) was based on application of three different constant pressures (0, 160, 400 kPa). The samples were imaged either by consecutive 1D MR intensity profiles (protocol P1) or by 3D T2 mapping (protocol P2). Compression-induced samples changes were characterized by creep compliance obtained from the 1D profiles, while the T2 maps were analyzed by using first- and second-order statistical texture feature analyses. The approach enabled spatially-resolved assessment of viscoelastic properties and compression-induced structural changes of the examined samples.

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1. Introduction

Food industry produces a wide range of meat products representing a large share in global food market. The products differ with respect to the origin of raw material, biochemical composition and processing protocol. As a result of the interplay between these factors, the meat products differ also by the structure and texture properties that both play a crucial role in consumer acceptability (Morales et al., 2007). Therefore, standardized methods were developed in order to determine structural and textural traits of meat products. Evaluation of textural traits by sensory analysis could be slow and laborious, thus instrumental texture analyses are commonly performed in parallel for a complementary determination of meat product traits (Benedini et al., 2012; Meullenet et al., 1998). Most established techniques for characterization of meat products are texture profile analysis (TPA) (Zamri et al., 2006) and stress-relaxation (SR) experiments (Andres et al., 2008), in which the examined meat samples are subjected to a predefined strain and then the strain-maintaining force is measured as a function of time. In the last decade, a compression-recovery creep (CRC) method was introduced (Dolz et al., 2008), in particular for determination of viscoelastic behavior of low-oil-content meat emulsions. In the CRC method, the examined sample is subjected to an external stress, while the strain as a function of time is measured. Such viscoelastic responses can be theoretically analyzed by various viscoelastic models (Mainardi and Spada, 2011). This CRC technique was applied also to other, more compact meat products with various levels of meat fragmentation, such as finely, medium or coarsely ground sausages (Dzadz et al., 2015). For emulsion-like systems, a correlation between the TPA and CRC parameters was recently confirmed (Yilmaz et al., 2012).

The compression experiments (TPA, SR and CRC) represent a golden standard for characterization of texture features of food products (Chen and Opara, 2013). However, the experiments yield spatial-averaged parameters, while spatial distribution of structural changes (such as local deformations and possible cracks) induced in the sample during compression are inherently inaccessible by these experiments. Therefore, another, preferably nondestructive, methods are needed to assess these changes. Recently, a novel approach employing visible/near-infrared hyperspectral imaging was efficiently used for determination of spatial distribution of TPA parameters in salmon fillets (Wu et al., 2014). This approach is inherently limited to superficial layers of examined meat samples due to a relatively small penetration depth of visible/near-infrared light, while the sample interior remains inaccessible for the light and thus cannot be characterized.

Magnetic resonance imaging (MRI) was recognized as an
important biophysical method for nondestructive characterization of food products (Damez and Clerjón, 2008). For example, the method was proven useful for determination of water ingress into individual rice kernels during cooking (Mohoric et al., 2009), for determination of pores distributions in cheese (Musse et al., 2014), for a follow-up of dough fermentation (Bonny et al., 2004) and for a dynamical monitoring of dry-cured hams during their processing (Fantazzini et al., 2009). The characterization is based on spatial variations of water-proton density and apparent diffusion coefficient as well as on the intrinsic MR parameters, such as longitudinal ($T_1$) and transversal ($T_2$) NMR relaxation times, across the examined sample. Moreover, advanced MRI methods primarily developed for diagnosing various diseases were also efficiently translated to meat science. For example, diffusion-tensor imaging was employed for determination of fiber orientation in beef meat (Renou et al., 2003). Recently, a deformation vector field in beef muscle samples during cooking was determined (Bouhrara et al., 2012). The study proved MRI also a promising method for dynamical monitoring of meat structural changes during the mechanical/thermal processing.

Providing the voxel size is sufficiently small to avoid the partial volume effect, local intensity variations in MR images and MR-parameter maps enable clear visual distinction among differently processed meat samples as well as among different meat regions, e.g., lean meat vs. fat inclusions (Colliewet et al., 2005). More detailed characterization of meat products can be obtained by calculating first-order statistical texture features derived from image multidimensional histograms (Bajd et al., 2016). Even better characterization can be obtained by second-order statistical texture feature analysis employing the gray-level co-occurrence matrix (GLCM) method (Cernadas et al., 2005; Shiranita et al., 1998; Wu et al., 2014), which was first introduced by (Haralick et al., 1973). Recently, the GLCM method was efficiently employed for determination of the feeding background effect on texture properties of dry-cured and fresh Iberian ham (Perez-Palacios et al., 2010, 2011). In these studies, discrimination between hams of pigs fattened only with acorns and grass and those fattened with high oleic acid concentrates was confirmed based on second-order statistical texture features of platform-dependent $T_2$-weighted MR images. In combination with the artificial neural network modelling approach (Zhou and Li, 2007) and the data mining approach (Caballero et al., 2016), MRI was proven efficient for characterization of meat texture and sensory traits.

The aim of this study was to analyze various meat products (plain and cheese-filled poultry frankfurter sausages, smoked and dry-cured pork sausages, and dry-cured hams) during their compression by means of MRI. To this end, the meat samples were compressed to different levels of compression inside a specially designed MR-compatible compression cell. Sample changes were sequentially imaged by 1D profiles during compression and recovery as well as by 3D $T_2$ mapping in an uncompressed/compressed state. The obtained $T_2$ maps were analyzed by $T_2$ histograms and GLCM-derived texture features.

### 2. Material and methods

#### 2.1. Preparation of meat product samples

Five different meat products, classified in the following groups (G1–G5), were analyzed: plain poultry frankfurter sausage (G1, Pivka, Slovenia), cheese-filled frankfurter sausage (G2, Agricola Italiana Alimentare, Verona, Italy), smoked pork sausage (G3, Mesine dežele Kranjske, Ljubljana, Slovenia), dry-cured pork sausage (G4, PKK Karlovacã mesna industrija, Karlovac, Croatia) and dry-cured ham (G5) originating from our previous studies (Bajd et al., 2016; Skrlep et al., 2016). From each group, samples with a size of $12 \times 12 \times 27$ mm$^3$ were dissected from the bulk meat product in order to fit into an MRI-compatible compression cell with an inner diameter of 20 mm. The sample length of 27 mm was determined by the sensitive region of an MRI probe into which the cell was inserted. At least five samples were analyzed for each sample group.

#### 2.2. MRI-compatible compression cell

The compression cell had a cylindrical shape and was made of a hard plastic material (PE 1000). A 10 ml syringe with a 20 mm diameter piston was inserted into the cell and clamped to the cell housing. The syringe was connected to an external air pressure network with negligible pressure fluctuations via a pressure regulator. The compression force to a sample inside the cell was obtained by adjusting the pressure regulator to a desired pressure of up to 400 ± 10 kPa. The compression cell inserted inside the MRI probe is schematically shown in Fig. 1a.

#### 2.3. Compression protocol

The samples were examined by two different compression protocols (P1 and P2). The compression protocol P1 was designed to mimic a CRC experiment (Fig. 1b). In the protocol, pressure was gradually increasing in one minute intervals from zero to 160 kPa and back to zero in 40 kPa steps (four pressure steps up and four pressure steps down). The pressure intervals were interspersed with one minute intervals of zero-gauge pressure, i.e., each pressure interval was followed by one-minute decompression interval. The final decompression interval was 6.5 min long to enable following the final creep recovery of the sample. By the protocol viscoelastic response of at least three samples of each group was examined. In the compression protocol P2, parallel samples (at least two from each group) were MRI-examined in 3D after their compression to 160 kPa and 400 kPa. With both pressure protocols the pressure changes were instant. The pressure changes were enabled by using incompressible tubes of small volume and the pressure regulator valve that instantly equalized the pressure between the pressure cell and either the external air pressure network (sample compression) or zero-gauge pressure (sample recovery).

#### 2.4. Creep response modelling

Creep behavior of the samples examined by the pressure...
Fig. 1. (a) An MRI-compatible compression cell for texture feature assessment of meat samples in an uncompressed and compressed state. (b) Time course of the applied compression protocol P1. (c) Schematic presentation of four-element Burger’s model. (d) An experimental setup for the CRC experiment followed by digital photography.
protocol P1 was characterized by creep compliance, which is defined as a ratio between relative strain $\varepsilon(t)$ and applied stress $\sigma$, i.e., $J(t) = \frac{\varepsilon(t)}{\sigma}$. Sample compression was described by three different stages of viscoelastic response, i.e., instantaneous, retarded viscoelastic and pure viscous response that correspond to the initial, intermediate and final stage of compression, respectively. Mathematically, the response of a compression phase was modeled by the four-component Burger’s model (schematically presented in Fig. 1c) comprising of Maxwell and Kelvin-Voight viscoelastic parts (Yang et al., 2006)

$$J(t) = \frac{1}{E_0} + \frac{1}{E_1} \left(1 - e^{-E_1 \varepsilon(t)}\right) + \frac{t}{\eta_0},$$

where $E_0$ is the instantaneous elastic modulus of Maxwell unit, $E_1$ is the retarded elastic modulus of Kelvin-Voight unit, while $\eta_0$ and $\eta_1$ correspond to the residual viscosity (Maxwell dashpot unit) and internal viscosity (Kelvin-Voight dashpot unit), respectively. The time dependence of creep compliance in the recovery phase upon compression stress discontinuation was modeled by a semi-empirical equation (Dolz et al., 2008; Yilmaz et al., 2012)

$$J(t) = J_\infty + J_{KV} e^{-t/C},$$

where $J_\infty$ is the residual compliance corresponding to the Maxwell dashpot deformation, $J_{KV}$ is the recovery compliance of Kelvin-Voight part, while $C$ is a stretch exponent constant.

### 2.5. MR imaging

Meat samples were imaged using an MRI scanner consisting of a 2.35 T (100-MHz proton frequency) horizontal bore Oxford superconducting magnet (Oxford Instruments, Oxon, UK) that was equipped with a Bruker micro-imaging gradient system (Bruker, Ettlingen, Germany) and controlled by a TecMag NMR spectrometer (TecMag, Houston, TX, USA). During the compression protocol P1, 2000 one-dimensional intensity profiles across the sample along the compression direction were acquired using the spin-echo sequence (Callaghan, 1991; Haacke et al., 1999) with the following imaging parameters: TE/TR = 8/600 ms, dwell time 5 μs, acquisition size 512 and FOV 60 mm. The samples subjected to the compression protocol P2 were imaged by $T_2$ mapping employing multi-spin-echo imaging with the following parameters: $\text{TE/TR} = 8/1050$ ms, number of echoes 16, dwell time 5 μs, matrix size $N \times M \times K = 128 \times 64 \times 16$ and FOV $60 \times 20 \times 20$ mm$^3$.

### 2.6. MR image post-processing

Sample deformations were evaluated in the laboratory frame of reference. Fully automated MR image segmentation was performed as follows. Multi-dimensional raw MRI data were Fourier transformed to obtain MR images of the corresponding dimensionality. One-dimensional MR intensity profiles were used to calculate strain curves, i.e., relative compression-induced sample size changes. Then, creep compliance as a function of time was calculated by normalizing the strain curves to the corresponding applied stress values. Three-dimensional $T_2$ maps were calculated from 3D $T_2$-weighted MR image datasets by fitting mono-exponential function to multi-spin echo images in a pixelwise manner (Vidmar et al., 2015). The fitting analysis was performed only in hyper-intense sample regions with sufficiently high SNR to yield reliable fits, while the hypo-intense regions were omitted from the analysis (Bajd et al., 2016).

The calculated 3D $T_2$ maps were analyzed for first-order statistical texture features ($T_2$ histograms) as well as for second-order statistical texture features based on 2D GLCM, $p(i,j;\Delta x, \Delta y)\in G_{c,G}$ with $G = 128$ being a number of gray levels (the values with $0 < T_2 < 130$ ms were sorted in 128 equidistant bins)

$$p(i,j;\Delta x, \Delta y) = \frac{N}{\sum_{i=0}^{N-1} \sum_{j=0}^{M-1} (1 \text{ if } T_2(n,m) = i \text{ and } T_2(n+\Delta x, m+\Delta y) = j \text{ otherwise})}{.} \quad (3)$$

In the matrix, each element $p(i,j;\Delta x, \Delta y)$ equals the number of instances that two pixels separated by a distance $(\Delta x, \Delta y)$ have in a 2D $T_2$ map gray levels $i$ and $j$. To obtain a normalized neighborhood-averaged 2D GLCM $p(i,j)$, four different 2D GLCMs $p(i,j;\Delta x, \Delta y)$ with the following inter-pixel distances $(\Delta x, \Delta y) = (0,0), (1,0), (0,1), (1,1)$ were averaged and then normalized:

$$p(i,j) = \frac{\sum_{i=0}^{N-1} \sum_{j=0}^{M-1} (p(i,j;0,0) + p(i,j;1,0) + p(i,j;0,1) + p(i,j;1,1))}{\sum_{i=0}^{N-1} \sum_{j=0}^{M-1} (p(i,j;0,0) + p(i,j;1,0) + p(i,j;0,1) + p(i,j;1,1))} \quad (4)$$

Second-order statistical texture features were calculated from the normalized neighborhood-averaged 2D GLCM. In the analysis, the following eleven texture features were calculated: angular second moment (ASM) or uniformity or energy, entropy (ENT), dissimilarity (DIS) contrast (CON) or inertia, inverse difference moment (IDM) or homogeneity, variance (VAR), cluster shade (SHA), cluster prominence (PRO) and maximum probability (MAX). These features are defined as (Clausi, 2002; Soh and Tsatsoulis, 1999; Yang et al., 2012):

$$\text{ASM} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i,j)^2 \quad (5)$$

$$\text{ENT} = - \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i,j) \log(p(i,j)) \quad (6)$$

$$\text{DIS} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i - j)^2 \cdot p(i,j) \quad (7)$$

$$\text{CON} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i - j)^2 \cdot p(i,j)^2 \quad (8)$$

$$\text{IDN} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{1}{1 + |i - j|} \cdot p(i,j) \quad (9)$$

$$\text{COR} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{(i - \mu_x)(j - \mu_y)}{\sigma_x \sigma_y} p(i,j) \quad (10)$$

$$\text{IDM} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{1}{1 + (i - j)^2} \cdot p(i,j) \quad (11)$$

$$\text{VAR} = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \left(\frac{(i - \mu_x)^2}{\sigma_x^2} + \frac{(j - \mu_y)^2}{\sigma_y^2}\right) p(i,j) \quad (12)$$
SHA = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i + j - \mu_x - \mu_y)^3 p(i, j) \quad (13)

PRO = \sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i + j - \mu_x - \mu_y)^4 p(i, j) \quad (14)

MAX = \max_{i,j} \{p(i, j)\} \quad (15)

where the mean values for the columns and rows of the GLCM are

\mu_x = \frac{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} i \ p(i, j)}{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i, j)} \quad \text{and} \quad \mu_y = \frac{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} j \ p(i, j)}{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i, j)},

whereas the corresponding standard deviations are defined as

\sigma_x = \sqrt{\frac{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (i - \mu_x)^2 \ p(i, j)}{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i, j)}} \quad \text{and} \quad \sigma_y = \sqrt{\frac{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} (j - \mu_y)^2 \ p(i, j)}{\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} p(i, j)}}.

Fig. 2. Stacks of consecutive color-coded 1D MR intensity profiles of representative samples of all examined meat product groups G1-G5 that were subjected to the pressure protocol P1, along with the corresponding creep compliance curves during four different applied pressure values ranging from 40 kPa to 160 kPa. The white arrow indicates released soft cheese from the G2 sample. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)
respectively.

2.7. Creep response measurements by digital photography

Representative samples of all sample groups were analyzed by a creep experiment in which the samples were subjected first to pressure of 40 kPa for one minute and then allowed to spontaneously recover at stress discontinuation for another minute. Creep response of the samples was followed by sequential digital photography. Image acquisition parameters were: image matrix $640 \times 480$, image spatial resolution $70 \, \mu m$ isotropic and 25 frames per second. The acquired images were first thresholded to segment the sample from the remaining background, then central profiles along the direction of compression were used to extract

Fig. 3. Central-slice $T_2$ maps of the representative samples of all examined meat products G1-G5 subjected to the compression protocol P2: the maps prior to compression (left column) as well as the maps after compression with 160 kPa (middle column) and with 400 kPa (right column). The graph shows two representative $T_2$ curves that correspond to fat regions ($T_2 = 63 \pm 4 \, ms$, circles) and to dry lean meat regions ($T_2 = 21 \pm 5 \, ms$, squares) of the uncompressed G4-group sample.
sample size changes as a function of time, from which the corresponding creep compliance curves were calculated. The experimental setup is shown in Fig. 1d.

All data analyses, MR image and digital photography analyses as well as creep compliance modelling, was performed within the Matlab® programming environment (MathWorks, Inc., Natick MA, USA).

3. Results

In Fig. 2 results of the compression protocol P1 (Fig. 1b) applied to the representative samples of all sample groups (G1-G5) are shown by stacks of consecutive color-coded 1D MR intensity profiles (left column) and by the corresponding creep compliance curves (right column). The profile stacks demonstrate different viscoelastic behavior of the examined samples seen by five different time curses of sample size change. The curves with pressure of 40 kPa were also fitted by models given by Eqs. (1) and (2). Largest sample size changes were obtained with the smoked (G3) and dry-cured (G4) pork sausage samples. The changes were also accompanied with uneven variations in the corresponding MR intensity profiles due to a heterogeneous nature of the samples. Similarly, the viscoelastic response was prominent also with the plain (G1) and cheese-filled (G2) frankfurter sausage samples, where MR intensity increase was associated with densification of the homogenous emulsion-like sausage samples. With the cheese-filled (G2) sample, the pressure value of 80 kPa was sufficient for a release of soft cheese from the sample. This release was enhanced due to the absence of a sausage casing around the sample. The dry-cured ham sample (G5), however, had the largest response only to 0 kPa 160 kPa 400 kPa

Fig. 4. \( T_2 \) histograms and central-slice GLCMs of the same representative samples as shown in Fig. 3 that were obtained prior to (squares) and after compression with 160 kPa (circles) and 400 kPa (triangles).
the first compression step with a pressure of 40 kPa, while its response to other pressure steps was significantly lower. The corresponding creep compliance curves in Fig. 2 (right column) were calculated from the profile stacks and thus exhibit similar time dependence. The creep compliance curves of the frankfurter sausage samples (G1, G2) exhibited typical creep compliance, while the smoked and dry-cured pork sausage samples (G2, G3) had somewhat retarded creep compliance after stress discontinuation. Most unusual creep compliance was measured with the dry-cured ham samples (G5) where stress discontinuation only minimally resulted in sample relaxation.

In Fig. 3 results of the compression protocol P2 applied to another representative samples of all sample groups (G1-G5) are shown by central-slice $T_2$ maps. As can be seen, the samples in an uncompressed state (left column) differed by spatial distribution of $T_2$ values. The frankfurter sausage samples (G1, G2) exhibited relatively homogenous structure, while the pork sausage samples (G3, G4) contained clearly discernible lean meat regions (higher $T_2$ values) and fat regions (lower $T_2$ values). Similarly, individual marbling fat inclusions were discernible also with the dry-cured ham sample (G5). As a result of the structural differences seen in the $T_2$ maps, the samples also differently responded to the applied pressure. As can be seen in $T_2$ maps of the samples compressed by 160 kPa (middle column), the effect of compression was most pronounced with G1, G2 and G5 groups, where the samples after the applied pressure filled nearly the entire remaining space in the compression cell. The pork sausage samples (G3, G4) responded to the applied pressure by bending and by comparatively smaller volume change along the direction of the applied pressure. With the highest pressure of 400 kPa (right column), all samples filled the entire remaining space in the compression cell. With all the examined samples, the sample volume changes were associated also with texture changes as well as with a compression-induced release of liquid from the samples (individual pixels with high $T_2$ values on superficial sample layers).

Fig. 4 shows compression-induced sample changes, quantified by means of first-order (pixel histograms) and second-order (GLCM) statistical texture properties obtained by analysis of $T_2$ maps. Specifically, the left column in Fig. 4 shows normalized $T_2$ histograms (obtained from the entire 3D $T_2$ maps) of the same representative samples as displayed in Fig. 3, while the right column shows the GLCMs of the corresponding central-slice $T_2$ maps. Both, the histograms and GLCMs are displayed for an uncompressed and compressed state with 160 kPa and 400 kPa. The differences in texture properties among the uncompressed samples can be seen in distinctly different shapes of $T_2$ histograms as well as in different GLCM patterns. The uncompressed dry-cured ham sample (G5) contained a relatively low amount of marbling fat and thus exhibits narrow $T_2$ distribution as well as a well localized peak in GLCM. On the contrary, the structure of the dry-cured pork sausage sample (G4) was heterogeneous due to a large amount of added coarse-grained fat inclusions, thus resulting into a broader $T_2$ histogram as well as in a decentralized GLCM pattern. Sample compression resulted in altered $T_2$ histograms and GLCMs. $T_2$ histogram distribution peaks on average decreased and slightly left-shifted on account of the sample volume change and partial sample desiccation due to a possible compression-induced liquid release. The histogram shape change was most distinct with the G4 sample, where the initially relatively broad distribution peak split into a low-$T_2$ peak and a high-$T_2$ peak with an increasing pressure. The compression-induced GLCM pattern alterations were the largest with the samples exhibiting initially sharp GLCM patterns (G1, G2 and G5).

Fig. 5 shows a pairwise comparison, 0 kPa vs. 160 kPa (left column) and 0 kPa vs. 400 kPa (right column), for the eleven GLCM-derived texture features (Eqs. (5)–(15)) of all sample groups (G1–G5). For each sample group, the results were calculated from texture features of eight sequential central slices. Differences in the texture features between the uncompressed and compressed states are expressed by the corresponding p-values displayed on the top of each graph. Largest differences in texture properties were obtained with the emulsion-like samples (G1, G2) and with higher pressure (right column). The differences were less significant with pork sausage samples (G3, G4) exhibiting initially heterogeneous structure. The effect of compression on the dry-cured ham sample (G5) seen by changes in texture features was only minor.

Fig. 6 depicts results of the CRC experiment followed by digital photography. Graphs in the left column correspond to creep compliance curves of representative samples of all sample groups that were obtained by analysis of sequential digital images. Representative digital photographs of the samples in two states, initial uncompressed (0 kPa, 0 s) and compressed (40 kPa, 50 s), are shown in Fig. 6, middle and right column, respectively. Along with the measured creep compliance curves (solid symbols) best-fit model curves of Eqs. (1) and (2) (solid black lines) are shown as well. Best-fit parameters of the models are given in Tables 1 and 2.
4. Discussion

The aim of this study was to develop an MRI-compatible compression cell for evaluation of compression-induced texture feature changes of various food samples. The cell, which was operating in a constant pressure mode, enabled study of creep compliance as well as spatially-resolved assessment of sample structural changes due to the applied pressure. In the study, the method was demonstrated on five different commercial meat products differing in viscoelastic properties that were in different stages of compression measured by consecutive 1D MR intensity profiles and by 3D $T_2$ mapping.

Creep compliance of the samples was determined based on 1D sample deformations that were measured by consecutive 1D MR intensity profiles along the direction of the applied pressure. Sample deformations were calculated from the measured profiles and were therefore limited in spatial resolution by imaging resolution. Effects of limited spatial resolution can be well seen in creep compliance curves, e.g. G4 sample in Fig. 2, that are stepwise. As the profiles were obtained using readout gradients the profiles were prone to chemical shift artefacts. These were efficiently reduced by using sufficiently high signal acquisition frequency bandwidth. An alternative approach for the creep measurement could be a use of an optical system for detection of compression piston shifts. Such

Table 1

<table>
<thead>
<tr>
<th>Meat product group</th>
<th>$E_0$ [MPa]</th>
<th>$E_1$ [MPa]</th>
<th>$\eta_0$ [MPa s]</th>
<th>$\eta_1$ [MPa s]</th>
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<tbody>
<tr>
<td>G1</td>
<td>0.47 ± 0.05</td>
<td>0.18 ± 0.01</td>
<td>104 ± 16</td>
<td>0.22 ± 0.02</td>
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<tr>
<td>G2</td>
<td>0.17 ± 0.01</td>
<td>0.29 ± 0.03</td>
<td>78 ± 16</td>
<td>0.68 ± 0.15</td>
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<tr>
<td>G3</td>
<td>5.8 ± 2.0</td>
<td>0.27 ± 0.03</td>
<td>108 ± 10</td>
<td>0.24 ± 0.02</td>
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<tr>
<td>G4</td>
<td>2.1 ± 0.7</td>
<td>1.56 ± 0.37</td>
<td>190 ± 70</td>
<td>6.1 ± 3.6</td>
</tr>
<tr>
<td>G5</td>
<td>0.16 ± 0.01</td>
<td>0.34 ± 0.04</td>
<td>160 ± 10</td>
<td>1.33 ± 0.52</td>
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Table 2

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<tr>
<td>G1</td>
<td>1.20 ± 0.05</td>
<td>6.31 ± 0.40</td>
<td>0.72 ± 0.09</td>
<td>0.63 ± 0.07</td>
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<tr>
<td>G2</td>
<td>2.60 ± 0.12</td>
<td>5.98 ± 0.24</td>
<td>0.53 ± 0.03</td>
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<tr>
<td>G3</td>
<td>1.20 ± 0.04</td>
<td>3.13 ± 0.20</td>
<td>0.77 ± 0.08</td>
<td>0.48 ± 0.05</td>
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<td>G4</td>
<td>0.64 ± 0.05</td>
<td>0.72 ± 0.08</td>
<td>0.79 ± 0.12</td>
<td>0.11 ± 0.03</td>
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<tr>
<td>G5</td>
<td>6.3 ± 2.0</td>
<td>3.2 ± 2.3</td>
<td>0.25 ± 0.14</td>
<td>0.38 ± 0.20</td>
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</table>

Fig. 6. Results of the CRC experiment followed by digital photography: creep compliance curves of representative G1-G5 samples obtained with 40 kPa along with the corresponding digital photographs with two different pressure values (0 kPa and 40 kPa).
system could have a much better precession than the approach used in the study. In our study, 3D structure of the examined samples was determined by using $T_2$ mapping because the mapping is relatively fast (3D scan took only 20 min per sample) and was found reliable in determination of meat product structure (Bajd et al., 2016). In addition, the mapping enables assessment of intrinsic meat product MR properties (spatial distribution of transversal relaxation time) and is inherently independent on excitation RF field in-homogeneity. Alternatively, other maps, such as $T_1$ or ADC, could also be used as a replacement or supplement to the used $T_2$ maps. According to our previous studies done on various biomaterials (Bajd et al., 2016; Vidmar et al., 2015) ADC maps have broader histograms and are less specific for samples with low water contents. $T_1$ was demonstrated efficient for meat characterization (Fantazzini et al., 2009), however, it requires relatively long scan times when using a conventional inversion-recovery approach for the mapping.

In the study, first- and second-order statistical texture analyses of the corresponding $T_2$ maps were used to better characterize sample texture properties in an uncompressed and compressed state. Interestingly, both analyses were found efficient in discrimination between the two states, however, in a different manner. While the first-order analysis ($T_2$ histogram) provides only information on compression-induced $T_2$ distribution changes of the sample as a whole, the second-order analysis (GLCM) provides also information on compression-induced spatial redistribution of $T_2$ values on a predefined pixel neighborhood. All GLCMs exhibit considerable compression-induced pattern changes that are manifested in changes of different texture features. Among eleven studied texture features most discriminative were: contrast (CON), variance (VAR), cluster shade (SHA) and cluster prominence (PRO). Those four features showed most significant changes between uncompressed and compressed state (0 kPa vs. 400 kPa). With heterogeneous samples, larger differences in second-order texture features would be accounted by considering larger pixel neighborhoods. The discrimination between the states could be improved further by using the principal component analysis (Huang et al., 2014) provided that sufficiently large number of samples is included in the study. Some aspects of the study could be further improved. First, the confined cylindrical geometry of the MR probe and also of the compression cell along with comparatively large sample sizes determined the type of sample deformations. These were dominant in the axial direction and constrained in the lateral direction, implying that the corresponding MRI-based CRC model parameters would not be directly comparable to the results in Tables 1 and 2. On the other hand, absolute sample sizes were small, therefore, more samples should be analyzed in order to account for intragroup differences. Sample size restrictions can be overcome by employing MRI systems designed for larger samples such as whole body clinical MRI systems or open-design low-field systems that have also reduced susceptibility artefacts. Second, 3D $T_2$ maps had anisotropic resolution to reduce scan time and to improve SNR, however, this has as a consequence thicker slices which implied GLCM analysis only in 2D (in-plane). Third, the pressure regulator had only manual control. More precise pressure adjustment would be obtained using a spectrometer-controlled electronic pressure regulator. Such regulator could prevent also from overloading the cell, especially with soft samples, where in the present study nonlinear viscoelastic response was often obtained with high pressures.

5. Conclusions

In the study it was demonstrated that MRI enables assessment of compression-induced changes in food or soft biological materials. It was shown that the changes can well be characterized by creep compliance obtained from 1D MR intensity profiles as well as by $T_2$ mapping followed by texture feature analyses. The method is an interesting alternative to the current gold standard methods for texture feature assessment.

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