Quantitative Field-Cycling T_1 Dispersion Imaging

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Introduction:

Recent years have seen renewed interest in the development and use of relaxometric imaging to generate parametric images showing differences in T_1-dispersion between tissues. In particular, it is of interest to measure the variation of T_1 (or its reciprocal, R_1) in the range of magnetic fields between about 30 mT and 80 mT, where "quadrupole dips" occur [1,2]. These reductions of T_1 are observable at field values where the proton NMR frequency is equal to the ^{14}N nuclear quadrupole resonance (NQR) frequency, namely at 49 mT (2.1 MHz) and 65 mT (2.8 MHz). Quadrupole dips occur in samples containing ^{1}H—^{14}N bonds in immobilised proteins, and have been observed in small muscle samples [1,3] as well as in humans [4,5]. Previous work has shown that subtracting field-cycled inversion-recovery images obtained on and off quadrupole dips can highlight regions of muscle [5] and that T_1-dispersion images can be formed in a similar fashion, by collecting field-cycled images without, as well as with inversion [3]. In this work we have extended these ideas in order to generate "ΔR_1" images, the intensity of which should be proportional to the concentration of immobilised protein [2].

Methods:

Jiao and Bryant [2] showed that ΔR_1 is proportional to a sample's protein concentration, where

$$\Delta R_1 = R_1^{QD} - R_1^{0} \qquad \text{(Eq. 1)}$$

Here, R_1^{QD} is the measured R_1 value at the field where a dip should occur (e.g. 65 mT) and R_1^{0} is the predicted R_1 value at the same field in the absence of the effect (obtained by interpolation).

A field-cycled inversion-recovery imaging pulse sequence was used. An initial polarisation period at 450 mT was applied, at the end of which the magnetisation was inverted by a 10 ms adiabatic fast passage (AFP). (AFP was used for inversion, to provide immunity from B_1 and B_0 field inhomogeneity.) The field was then switched to its evolution value, around 65 mT, for approximately 150 ms. Then the field was returned to 450 mT and the signal was read out using a 90° pulse. In imaging experiments, conventional gradients were also applied during this detection period. The pulse sequence was implemented in an interleaved fashion, so that image data was also collected without the initial inversion, to allow the calculation of R_1 on a pixel-by-pixel basis. In order to generate a ΔR_1 image, k-space data was collected with and without inversion at three evolution magnetic field values: 56 mT, 65 mT and 75 mT. The R_1^{0} value at 65 mT was calculated by linear interpolation of the R_1 values measured at 56 mT and 75 mT. R_1^{QD} was calculated directly from the data obtained at an evolution field of 65 mT, and finally a ΔR_1 image was generated using Eq. 1.

The imager used for these experiments was a new field-cycled MRI system with signal detection at 450 mT. It employs a double, co-axial magnet system. The detection field is provided by a 450 mT superconducting magnet (820 mm bore). Inside it is located an actively-shielded, resistive magnet that is used to partially offset the 450 mT field, under control of the imager's console (Tecmag Inc., USA) via a high-precision, home-built DAC module. The field can be switched between levels (e.g. 65 mT to 450 mT) in 40 ms. The actively-shield field-offset coil (Tesla Engineering Ltd., UK) incorporates gradient and shim coils, and the free bore inside these is 120 mm. A birdcage resonator is used for NMR (Tx/Rx) at 19.14 MHz, and the maximum sample diameter is 60 mm.

Results:

The sample used in our initial tests of the ΔR_1 imaging method was a hen's egg. Non-imaging measurements of R_1 dispersion have shown that a raw egg exhibits the usual monotonic decrease with evolution field (data not shown), but that a "hard boiled" egg shows distinct quadrupole dips, arising from cross-linked protein in the albumin (egg white). Figure 1 shows an R_1 dispersion curve obtained from a sample of heat-treated hen's egg albumin; the peaks at 49 mT and 65 mT are clearly visible. The dashed line is indicative of the linear fit of R_1 between 56 mT and 75 mT, from which ΔR_1 was calculated in the imaging experiments. Figure 2 shows a calculated ΔR_1 image of an intact, heat-treated hen's egg. Mid-grey represents zero ΔR_1, with positive values being brighter and negative darker than this. The matrix size is 128x128, FoV 100x100mm, slice thickness 5 mm, NEX 4, T^{evol} 150 ms, TR 800 ms. Region-of-interest measurements on the image show mean values of ΔR_1 as 0.68 s^{-1} in the albumin and -0.02 s^{-1} in the egg yolk.

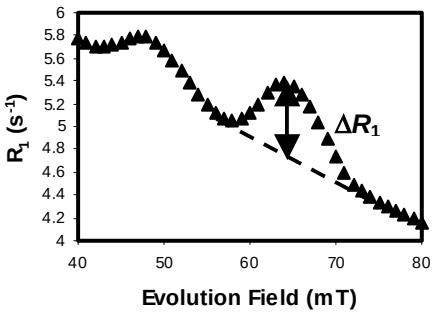

Figure 1: Measured R_1 dispersion of heat-treated hen's egg albumin

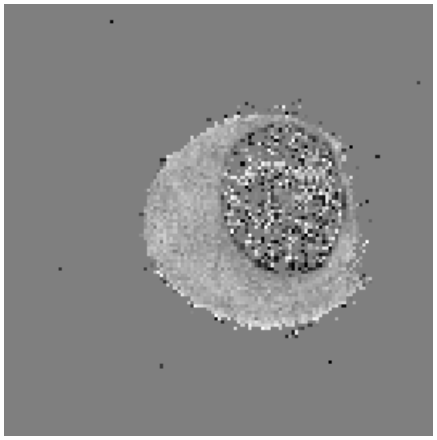

Figure 2: Calculated ΔR_1 image of intact, heat-treated hen's egg. Mid-grey corresponds to ΔR_1=0

Discussion and Conclusions:

The image shown in Fig. 2 demonstrates the feasibility of the detection of immobilised protein *via* a calculated ΔR_1 image. The image shows a consistent intensity (proportional to ΔR_1) in the albumin. Although the region of the yolk is noisy, the fact that the mean value of ΔR_1 is close to zero indicates that the system is behaving as expected.

The results presented here represent an initial pilot study of the ΔR_1 imaging method. In the future we will investigate the possibility of protein quantification by this method, using samples with known, independently verified, protein concentrations. It is hoped that in the future field-cycled relaxometric imaging, and ΔR_1 imaging in particular, may develop into a clinically useful tool, perhaps in the diagnosis and monitoring of muscle-wasting diseases.

References:

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