MR Imaging with T_1 Dispersion Contrast

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Introduction. We have developed a new contrast mechanism to provide protein contrast with MRI. This technique uses prepolarized MRI, which offers flexibility in the strength and duration of the magnetic field by using two pulsed electromagnets: a strong magnet to polarize the sample and a low-field homogeneous magnet for signal readout [1]. For tissues whose T_1 varies with magnetic field (T_1 dispersion), changing the field strength allows the tissue magnetization to decay with a new value of T_1. The difference between two images taken after allowing the magnetization to evolve at different field strengths yields an image with T_1 dispersion contrast: tissues with flat T_1 dispersion curves are dark and tissues with rapidly changing T_1 dispersion curves are bright [2]. In particular, tissues with high protein content, such as muscle tissue or white matter, exhibit rapid changes in their T_1 dispersion curves near 50 mT and 65 mT due to cross-relaxation with nitrogen nuclei in the protein backbone [3,4]. We have created images with protein-content contrast from differences in T_1 dispersion between fat or unbound water (no protein content), which have roughly constant T_1 over a small field range, and muscle tissue (high protein content), which has a rapidly varying T_1 near the quadrupole dips. We have demonstrated this technique on *ex vivo* samples [5] and *in vivo* on the wrist and foot of normal volunteers. This technique may prove useful for monitoring muscle viability in the extremities for patients with diabetic neuropathy, or for enhancing contrast of lesions in white matter caused by diseases such as multiple sclerosis.

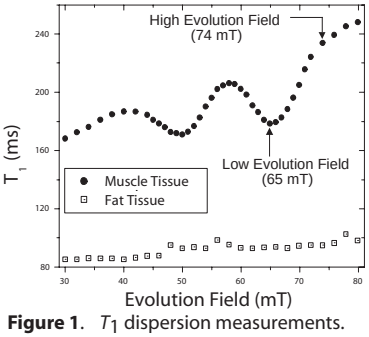

Figure 1. T_1 dispersion measurements.

Methods. Figure 1 shows T_1 dispersion measurements taken with our prepolarized MRI scanner on muscle and fat samples [6]. Between the two evolution fields we chose (indicated with arrows), the T_1 of the muscle tissue changes by about 50 ms (25%), while the T_1 of the fat sample stays virtually constant. We exploit the different slopes of the two T_1 dispersion curves using the pulse sequence shown in Fig. 2. A strong polarizing pulse (0.4 T) is followed by an evolutionary pulse (65 mT or 74 mT), and then the RF excitation and readout is performed at a lower field (52 mT). Final images with T_1 dispersion contrast are created both by direct subtraction of the high and low field data and by cluster analysis. Cluster analysis can determine which voxels had different T_1 values in the two images, and masking removes voxels whose T_1 was the same in each image.

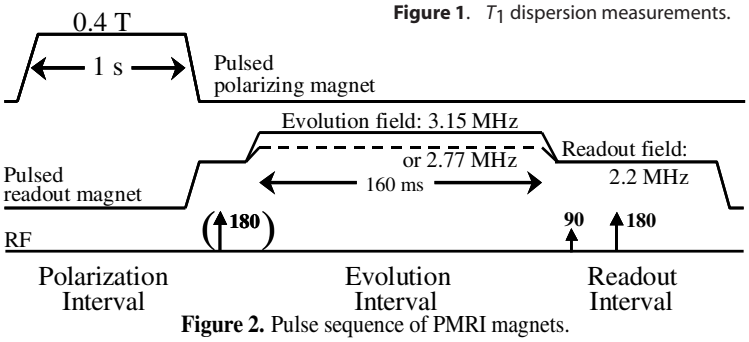

Figure 2. Pulse sequence of PMRI magnets.

Results. In our *ex vivo* test, we imaged three samples: muscle tissue and fatty tissue (both from chicken), and water doped with copper sulfate (T_1~100 ms). Figure 3(a,b) shows two images taken with different evolutionary field strengths: (a) 58 mT evolutionary field, and (b) 50 mT evolutionary field. Figure 3(c) shows the direct subtraction of the two images. In the resulting image, the signal from the fat and water samples (no protein content) has been almost entirely subtracted out, while the signal from the muscle sample (high protein content) is still significant.

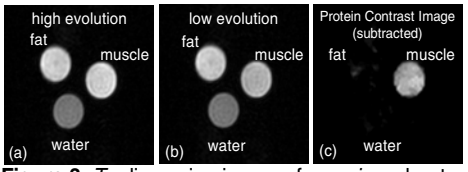

Figure 3. T_1 dispersion image of *ex vivo* phantom.

We then imaged the arm and foot of two normal volunteers. Figure 4 (top row) shows images taken at the two different evolutionary field strengths. Figure 4 (bottom row) shows T_1 dispersion images generated by subtraction and by masking using cluster analysis. The high evolution field image was masked to eliminate pixels that had the same intensity in both images. The masking threshold was determined by calculating the theoretical difference in intensity between muscle tissue in the high and low field evolution images (23%), and then setting the threshold halfway between the calculated difference and unity (no difference, meaning identical T_1 in the two images). Regions of fat (no protein content) which appear bright in the original images (a,b) are dark in the images with T_1 dispersion contrast.

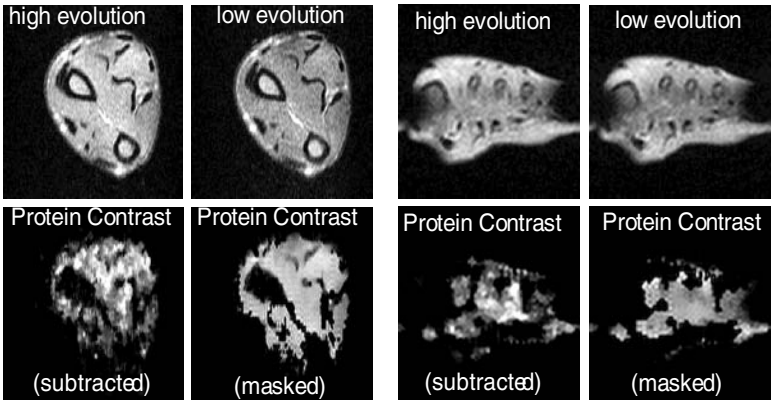

Figure 4. T_1 dispersion image of an *in vivo* wrist (left) and foot (right) of normal volunteers. 8 cm FOV, 1 cm slice, 5:45 min scan time.

Discussion. We have demonstrated a method for creating T_1 dispersion contrast in images using the difference between two images taken at different evolutionary field strengths. Species whose T_1 does not change between the two evolutionary field strengths are subtracted or masked out, while species whose T_1 varies between the two evolution fields remain. Our T_1 dispersion images show contrast between high-protein muscle tissue, which appears bright, and fat and unbound water, which both appear dark. This technique may provide a new contrast mechanism for imaging disorders that affect protein content, such as myopathies in muscle tissue or demyelinating diseases in white matter.

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